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Hypertension and sex related differences in mortality of COVID-19 infection: A systematic review and Meta-analysis

Background: Hypertension is the leading cause of cardiovascular diseases and premature deaths. Hypertension plays a striking role in mortality and morbidity in case of Coronavirus Disease 2019 (COVID-19) infection; however, numerous studies have reported contradictory findings.

Objective: To assess the relationship of hypertensive disease and mortality of COVID-19 infection and to assess the sex and age differentials on the association.

Methods: We have conducted a systematic review of published literatures that identified the relationship between hypertension and mortality of COVID-19 infections. Nineteen articles were selected following structured inclusion and exclusion criteria for systematic review and analyses. A total of 21,684 hospital admitted COVID-19 patients were included in this review and meta-analysis from 19 studies. The studies covered the six months of the pandemic from December 2019 to May 2020.

Results: In the pooled analysis, the median age of patients was 58 years, and the proportion of male patients was 58.8%. In contrast, we estimated 33.26% of hypertensive and 19.16% of diabetes mellitus patients in the studies. Hypertension was found to be associated with COVID-19 mortality (“Risk ratio (RR) = 1.45, [95% confidence interval (CI): 1.35 - 1.55]; I2 = 77.1%, p - value < 0.001”). The association in the meta-regression was affected by sex (p - value = 0.050). The association was found to be stronger in the studies with males ? 55% and age ? 55 years (“RR = 1.65, [95% CI: 1.52 - 1.78]; I2 = 77.1%, p - value < 0.001”) compared to male < 55% or age < 55 years (“RR = 1.11, [95% CI: 0.94 - 1.28]; I2 = 72.2%, p - value < 0.001”).

Conclusion: Hypertension was significantly strong associated with COVID-19 mortality which may account for the contradiction in the many studies. The association between hypertension and mortality was affected by sex and there were significantly higher fatalities among older male patients.

Research Article **Published Date:- 2020-10-28**

Evaluation of the antibacterial and anticancer activities of marine Bacillus subtilis ESRAA3010 against different multidrug resistant Enterococci (MDRE) and cancer cell lines

Fifty nine isolates belonging to six species of Enterococci namely, Enterococcus faecalis, Enterococcus faecium, Enterococcus raffinosus, Enterococcus durans, Enterococcus mundtiiand Enterococcus avium (n = 35, 15, 4, 3, 1 and 1 isolates, respectively) were obtained from different clinical specimens including urine, pus, blood, wound, sputum and synovial fluid. The highest numbers of Enterococci were recorded from the pus (20 isolates, 33.90%) followed by urine (12 isolates, 20.34%) while the lowest frequency was observed with synovial fluid samples (2 isolates, 3.39%). These isolates showed different multidrug resistant patterns with the lowest resistant for linezolid (n = 5, 8.48%), followed by teicoplanin (n = 14, 23.73%) and vancomycin (n = 20, 33.90%) while they exhibited the highest resistant against penicillin (n = 53, 89.83%), oxacillin (n = 50, 84.75%), erythromycin (n = 49, 83.05%) and streptomycin (n = 47, 79.66 %). On the other hand, a free living marine bacterium under isolation code ESRAA3010 was isolated from seawater samples obtained from the fishing area Masturah, Red Sea, Jeddah, Saudi Arabia. The phenotypic, chemotaxonomic, 16S rRNA gene analyses and phylogenetic data proved that isolate ESRAA3010 is very close to Bacillus subtilis and then it was designated as Bacillus subtilis ESRAA3010. It gave the highest antagonistic activity against all clinical Enterococcus faecalis, Enterococcus faecium, Enterococcus raffinosus, Enterococcus durans, Enterococcus mundtiiand Enterococcus avium isolates under study with minimum inhibitory concentration (MIC) ranged from 4 to 56 µg/mL, 4 to 12 µg/mL, 4 to 8 µg/mL, 4 to 8 µg/mL, 8 µg/mL and 4 µg/mL, respectively as well as minimum bactericidal concentration (MBC) (8 to 64 µg/mL, 4 to 16 µg/mL, 4 to 12 µg/mL, 4 to 16 µg/mL, 12 µg/mL and 8 µg/mL, respectively). Moreover it showed anti-proliferative activity against colon (HCT-116), liver (HepG-2), breast (MCF-7) and lung (A-549) carcinomas with IC50 equal to 39, 50, 75 and 19 µg/mL, respectively which indicates its prospective usage in the upcoming decades.

Research Article **Published Date:- 2020-10-21**

Can the Wondfo® SARS-CoV-2 IgM/IgG antibodies be used as a rapid diagnostic test?

Background: An outbreak of novel coronavirus (SARS-CoV-2) disease (COVID-19) has rapidly spread worldwide. The aim of this study was to evaluate and validate the performance of the Wondfo® lateral-flow immunochromatographic assay that detect SARS-CoV-2- IgG, IgM antibodies (Wondfo® IC), using the results obtained by the fluorescence immunoassay test as reference diagnostic.

Material and methods: 97 serum specimens collected and analyzed by four independent laboratories of Sergipe/Brazil was used for validated the Wondfo® SARS-CoV-2 IgM/IgG antibodies test. The COVID-19 positive serum specimens were determined by fluorescence immunoassay technique, used as reference standard.

Results: An overall of 97 serum specimens show 39 (39/97) SARS-CoV-2 IgG positive specimens, 33 (33/97) SARS-CoV-2 IgM positive specimen and 25 non-reagent specimens (25/97). However, the Wondfo® IC assay detected only 9 (9/97) IgM/IgG positive specimen and 25 (25/97) no-reagent specimen. A weak correlation was found between the outcomes of the Wondfo® IC assay and fluorescence test. The accuracy between the two tests was 32.08%. The sensitivity, specificity, positive predictive value, and negative predictive value of Wondfo® IC assay were of 11.12%, 100%, 100% and 25.27%, respectively. Moreover, no false positive sample was determinate, whereas 88.89% of false negative results were found.

Conclusion: The Wondfo® IC test failed in providing a quick, valid, and reliable results and appears not to be a good alternative for clinical use in detecting pandemic coronavirus. However, if the limitations of the rapid test are known, some correction factors can be used in order to adjust the epidemiological data.

Research Article **Published Date:- 2020-07-03**

Statistical and equation model analysis on COVID-19

Background: An infectious disease caused by a novel coronavirus called COVID-19 has raged across the world since December 2019. The novel coronavirus first appeared in Wuhan, China, and quickly spread to Asia and now many countries around the world are affected by the epidemic. The deaths of many patients, including medical staff, caused social panic, media attention, and high attention from governments and world organizations. Today, with the joint efforts of the government, the doctors and all walks of life, the epidemic in Hubei Province has been brought under control, preventing its spread from affecting the lives of the people. Because of its rapid spread and serious consequences, this sudden novel coronary pneumonia epidemic has become an important social hot spot event. Through the analysis of the novel coronary pneumonia epidemic situation, we can also have a better understanding of sudden infectious diseases in the future, so that we can take more effective response measures, establish a truly predictable and provide reliable and sufficient information for prevention and control model.

Methods: We establish different models according to the different developments of the epidemic situation, different time points, and different response measures taken by the government. To be specific, during the period of 2020.1.23-2020.2.7, the traditional SIR model is adopted; during the period of 2020.2.8-2020.3.30, according to the scientific research results, it was considered that the novel coronary pneumonia has a latent period, so in the later phase of epidemic development, the government has effectively isolated patients, thus we adopt the SEIQR model accordingly. During the period of 2020.3.31-2020.5.16, because more asymptomatic infected people were found, we use the SEIQLR model to fit. Finally, through a SEIR simulator, considering the susceptible number, the latent number, the infected number, the cured number, death number and other factors, we simulate the change of various numbers of people from the beginning to the next 180 days of novel coronary pneumonia.

Findings: The results based on the analysis of differential equations and kinetic models show that through the prediction of the model established in the first phase, the epidemic situation of novel coronary pneumonia in Hubei Province was controlled at the end of March, which is in line with the actual situation. The rest of Hubei province, except for Wuhan, lifted control of the departure channel from 0:00 am on March 25, and Wuhan was also unblocked on April 8. Through the establishment of the second-phase model, it is found that the epidemic situation will reach its peak in mid-February. For example, the quarantine admission of the hospital declined after mid-February, which is inseparable from the measures to build square cabin hospitals in early February so that more and more patients can be admitted. The model established in the third phase shows that the epidemic had been completely controlled by the end of May, which is also in line with the reality. Because in mid-May, the Wuhan government conducted a nucleic acid test on all the citizens to screen for asymptomatic infected persons to fundamentally control the spread of novel coronary pneumonia.

Interpretation: Hubei Province, as the center of the initial outbreak of novel coronary pneumonia, people were forced to be isolated at home during the Spring Festival, the most important Chinese holiday, and the whole society was in a state of suspension of work and study. The Chinese government had taken many measures in response to the epidemic, such as shutting down the city, vigorously building square cabin hospitals, and prohibiting people from gathering. At the beginning of May this year, the epidemic in Hubei Province was finally effectively controlled. For ordinary citizens, we should not cause unnecessary panic about the unknown novel coronavirus. Instead, we should fully understand and be familiar with this virus. In addition to the relevant medical knowledge, we should also understand the spread of infectious diseases through appropriate mathematical models. By mathematical models, we can understand the degree of harm of infectious diseases, when to control it, how to stop it, and use scientific views to reveal the original face of the novel coronavirus to the public without causing social panic.

Mini Review **Published Date:- 2020-02-13**

Progress of chemical components and biological activities of Fructus Amomi

Fructus Amomi is “one of the top four south authentic Traditional Chinese Plant Medicines”, widely distributed in tropical and subtropical districts of China, such as Fujian, Guangdong, Guangxi, Hainan, etc., which has ever been used in clinical for treatment of the digestive diseases. In addition, it has also been used as spices. In recent years, some research about its components together with pharmacological activities have been reported. In this Mini review, we mainly describe the recent progress of the components and pharmacological activities of Fructus Amomi, to provide the reference for the relevant researchers.

Review Article **Published Date:- 2019-11-09**

Packaging challenge for COVID-19 drug

At present Corona virus is the most burning topic across the world. At present there is no drug available to cure 100%. So many companies are trying to make it possible as soon as they can. The basic characteristics of the product is “Non-Toxic made of sugars Carbohydrates”. A Galectin is a protein that recognizes carbohydrates and modulates intracellular and extracellular interactions primarily related to the immune system. In some cases Galectins act as a glue bringing molecules together. The major focus of the research is on extracellular interactions.