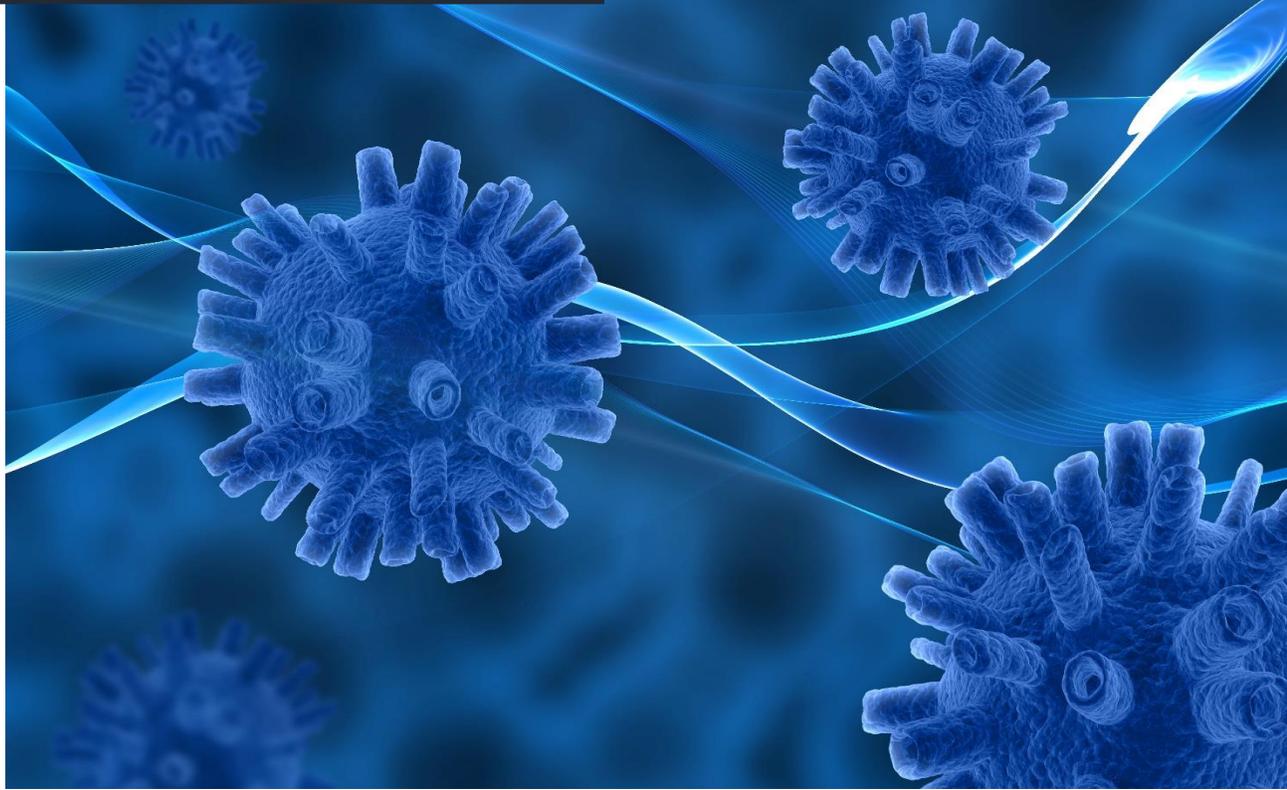# Hot Articles

"March | 2020"

Science and Technology

Title: [Encapsulation of grape seed extract phenolics using whey protein concentrate, maltodextrin and gum arabica blends](#)

Author: Kanta Yadav | Rajesh Kumar Bajaj | Surajit Mandal | Bimlesh Mann

Abstract

Grape seed extract (GSE) contain phenolic compounds that decrease the proclivity to various chronic diseases such as several types of cancer and cardiovascular diseases. The objective of the present study was to investigate the encapsulation of GSE polyphenols and their characterization. For this study, whey protein concentrate (WPC), maltodextrin (MD) and gum arabic (GA) were evaluated as encapsulating materials. For the preparation of stable microcapsules different WPC:MD/GA (5:0, 4:1, 3:2 and 0:5) ratios were assessed using ultrasonication for different time periods (20–40 min) followed by freeze drying. Encapsulation efficiency, antioxidant activity, particle size, surface morphology and release mechanism were determined. The GSE microcapsules coated with WPC:MD/GA ratio of 4:1 and 3:2 with core to coat ratio of 1:5 and prepared by sonication for 30 min were found to have highest encapsulation efficiency (87.90–91.13%) and the smallest particle size with maximum retention of antioxidant activity. Under optimized conditions, the low level release (43–49%) of phenolic compounds resulted under simulated gastric condition and significantly ($p < 0.05$) increased (88–92%) under simulated intestinal condition. Thus the results indicated blending of MD or GA with WPC improved the microencapsulation of GSE.

Database

SpringerLink

Title: [First two months of the 2019 Coronavirus Disease (COVID-19) epidemic in China: real-time surveillance and evaluation with a second derivative model](https://doi.org/10.1186/s41256-020-00137-4)

Author: Xinguang Chen | Bin Yu

Journal: Global Health Research and Policy

Doi: https://doi.org/10.1186/s41256-020-00137-4

Abstract

Background

Similar to outbreaks of many other infectious diseases, success in controlling the novel 2019 coronavirus infection requires a timely and accurate monitoring of the epidemic, particularly during its early period with rather limited data while the need for information increases explosively.

Methods

In this study, we used a second derivative model to characterize the coronavirus epidemic in China with cumulatively diagnosed cases during the first 2 months. The analysis was further enhanced by an exponential model with a close-population assumption. This model was built with the data and used to assess the detection rate during the study period, considering the differences between the true infections, detectable and detected cases.

Results

Results from the second derivative modeling suggest the coronavirus epidemic as nonlinear and chaotic in nature. Although it emerged gradually, the epidemic was highly responsive to massive interventions initiated on January 21, 2020, as indicated by results from both second derivative and exponential modeling analyses. The epidemic started to decelerate immediately after the massive actions. The results derived from our analysis signaled the decline of the epidemic 14 days before it eventually occurred on February 4, 2020. Study findings further signaled an accelerated decline in the epidemic starting in 14 days on February 18, 2020.

Conclusions

The coronavirus epidemic appeared to be nonlinear and chaotic, and was responsive to effective interventions. The methods used in this study can be applied in surveillance to inform and encourage the general public, public health professionals, clinicians and decision-makers to take coordinative and collaborative efforts to control the epidemic.

Database

SpringerLink

Title: A Blockchain-Based Trusted Data Management Scheme in Edge Computing

Author: Ma Zhaofeng | Wang Xiaochang | Deepak Kumar Jain | Haneef Khan | Gao Hongmin | Wang Zhen

Abstract

With rapid development of computing technologies, large amount of data are gathered from edge terminals or Internet of Things (IoT) devices, however data trust and security in edge computing environment are very important issues to be considered, especially when the gathered data are fraud or dishonest, or the data are misused or spread without any authorization, which may lead to serious problems. In this article, a blockchain-based trusted data management scheme (called BlockTDM) in edge computing is proposed to solve the above problems, in which we proposed a flexible and configurable blockchain architecture that includes mutual authentication protocol, flexible consensus, smart contract, block and transaction data management, blockchain nodes management, and deployment. The BlockTDM scheme can support matrix-based multichannel data segment and isolation for sensitive or privacy data protection, and moreover, we have designed user-defined sensitive data encryption before the transaction payload stores in blockchain system, and have implemented conditional access and decryption query of the protected blockchain data and transactions through smart contract. Finally, we have evaluated the proposed BlockTDM scheme security, availability, and efficiency with large amount of experiments. Analysis and evaluations manifest that the proposed BlockTDM scheme provides a general, flexible, and configurable blockchain-based paradigm for trusted data management with tamper-resistance, which is suitable for edge computing with high-level security and creditability.

Database

Title: [Multiplierless Filtered-OFDM Transmitter for Narrowband IoT Devices](https://doi.org/10.1109/JIOT.2019.2945186)

Author: AlaaEddin Loulou | Juha Yli-Kaakinen | Toni Levanen | Vesa Lehtinen | Frank Schaich | Thorsten Wild | Markku Renfors | Mikko Valkama

Abstract

In cyclic-prefix orthogonal frequency-division multiplexing (CP-OFDM)-based radio access, the coexistence of different technologies without precise time-frequency synchronization is limited due to high out-of-band (OOB) emissions. Therefore, the spectrum enhancement techniques play a key role in relaxing the synchronization and power control requirements. This allows a higher degree of opportunistic spectrum use with minimized interference. In addition, all the transmitting devices have to fulfill specific transmitted signal quality requirements, including the maximum OOB radiated signal power. With the orthogonal frequency-division multiplexing (OFDM)-based radio access, some additional signal processing for improved spectrum containment is commonly needed to achieve these requirements. The filtering and time-domain windowing are two fundamentally different approaches for spectrum enhancement. The filtered OFDM (F-OFDM) provides better spectrum localization than the time-windowing schemes [such as windowed overlap-add (WOLA)], with the cost of higher complexity. This article introduces low-complexity solutions for spectrally enhanced narrowband OFDM transmitters based on the use of lookup tables (LUTs). The proposed LUT approach, requiring only memory units and a low number of additions, allows to avoid all computationally expensive operations in online transmitter processing, as it builds the transmitted signal by summing the stored partial waveforms optimized offline. In certain cases, completely multiplication- and summation-free designs are possible. The transmitters of narrowband Internet of Things (NB-IoT) devices are natural applications for the proposed LUT approach, as they require additional digital baseband signal processing to reach the emission requirements. It is shown that the proposed LUT schemes can provide significant savings in real-time computations of NB-IoT devices, while fulfilling the 3GPP requirements.

Database

IEEE/IET Electronic Library (IEL)

Abstract

The industry standard advanced SPICE model (ASM)-GaN compact model has been enhanced to model the GaN high electron mobility transistors (HEMTs) at extreme temperature conditions. In particular, the temperature dependence of the trapping behavior has been considered and a simplifying approximation in the temperature modeling of the saturation voltage in the ASM-GaN model has been relaxed. The enhanced model has been validated by comparing the simulation results of the model with the dc $I - V$ measurement results of a GaN HEMT measured with chuck temperatures ranging from 22 °C to 500 °C. A detailed description of the modeling approach is presented. The new formulation of the ASM-GaN compact model can be used to simulate the circuits designed for extreme temperature environments.

Database

Abstract

The Co(−I) dihydrogen complexes, $[(\eta^2\text{-}H_2)CoML]^−$, where ML is the group 13 metalloligand, N(o-(NCH2PiPr2)C6H4)3M, and M is Al, Ga, or In, were previously reported (J. Am. Chem. Soc. 2017, 139, 6570−6573). In this work, the related Co(−I) end-on dinitrogen adducts, $[(N_2)CoML]^−$, were isolated and investigated as precatalysts for CO2 hydrogenation. The Co–Ga catalyst was highly active, achieving 19,200 formate turnovers with an initial turnover frequency of 27,000 $h^{−1}$ under 34 atm of 1:1 CO2/H2 and using Verkade's proazaphosphatrane as a base at ambient temperature. The Co–Al catalyst was moderately active, while the Co–In complex was inactive. Hence, tuning the group 13 ion greatly influences the catalytic activity at the Co site. To elucidate the role of the group 13 support, experimental and theoretical mechanistic studies of the Co–Ga and Co–Al catalysts were conducted. The Co(−I) H2 species are potent hydride donors with estimated thermodynamic hydricities ($\Delta G°_{H−}$) of 32.0(1) and 37.4(1) kcal/mol in CH3CN for M = Al and Ga, respectively. By acting as masked Co(I) dihydrides, the Co(−I) H2 species operate via an unusual Co(−I)/Co(I) redox cycle. After hydride transfer to CO2, the resulting intermediate is the Co(I) hydride complex, HCoML, which was independently synthesized and structurally characterized for M = Al and Ga. The Gibbs free energy for H2 binding, $\Delta G°_{bind}$ (1 atm), to generate $(\eta^2\text{-}H_2)HCoML$ was slightly more favorable for HCoGaL (−4.2(1) kcal/mol) than for HCoAlL (−2.7(1) kcal/mol). In the subsequent step, the deprotonation reaction to regenerate the initial catalyst was much more favorable for $(\eta^2\text{-}H_2)HCoGaL$ (pKa of 31.4, CH3CN) than for $(\eta^2\text{-}H_2)HCoAlL$ (pKa of 34.3). The straightforward substitution of Al with Ga perturbs the energy profile of the catalytic reaction ($|\Delta\Delta G°_{H−}|$ = 5.4 kcal/mol, $|\Delta\Delta G°_{bind}|$ = 1.5 kcal/mol, and $|\Delta\Delta G°_{Ka}|$ = 4.0 kcal/mol) and thus provides a thermodynamic rationale for the higher catalytic efficiency of Co–Ga over Co–Al.

Database

American Chemical Society Journal (ACS)

Abstract

A skin-gas cam that allows continuous imaging of transcutaneous blood volatile organic compounds (VOCs) emanated from human skin was developed. The skin-gas cam is able to reveal the relationship between the local skin conditions and transcutaneous blood VOCs in the field of volatile metabolomics (volatolomics). A ring-type ultraviolet (UV) light-emitting diode was mounted around a camera lens as an excitation light source, which enabled the simultaneous excitation and imaging of fluorescence. A nicotinamide adenine dinucleotide (NAD)-dependent alcohol dehydrogenase (ADH) was used to detect ethanol as a model sample. When gaseous ethanol was applied to an ADH-immobilized mesh that was wetted with an oxidized NAD solution placed in front of the camera, a reduced form of NAD (NADH) was produced through an ADH-mediated reaction. NADH emits fluorescence by UV excitation, and thus, the concentration distribution of ethanol was visualized by measuring the distribution of the fluorescence light intensity from NADH on the ADH-immobilized mesh surface. In this study, a new gas application method that mimicked the release mechanism of transcutaneous gas for quantification of the transcutaneous gas concentration was evaluated. Also, spatiotemporal changes of transcutaneous ethanol for various body parts were measured. As a result, we revealed a relationship between local skin conditions and VOCs that could not be observed previously. In particular, we demonstrated the facile measurement of transdermal gases from around the ear where capillaries are densely distributed below a thin stratum corneum.

Database

American Chemical Society Journal (ACS)

Abstract

This study aimed to develop and validate a mathematical model for predicting ozone propagation and distribution in a bench-scale storage silo of soybean and link the model results to its application as an antifungal. The reduction of potentially toxigenic fungi found in soybeans was also evaluated after the ozone treatment. Experimental validation consisted of the ozone application and concentration (ozone) monitoring at the experimental silo outlet. The soybean grains were analyzed prior to and after ozone treatment from different portions of the silo to evaluate the antifungal activity. After 30 minutes of ozone exposure, there was an 88% reduction in the amount of fungi present at the lower section, reaching total elimination with longer exposure times. Fusarium was the main genus found, and it was significantly reduced even with the shortest exposure (30 min). The results of the ozone propagation in soybeans will be useful to better understand its behavior within silos, in order for the elimination of biological contaminations to occur. The model showed ozone spread through the silo, and this treatment showed to be an effective alternative to control against potentially toxigenic fungi found in soybeans.

Database

Taylor & Francis Journals

Title:

Author: Yashpal Singh Malik | Shubhankar Sircar | Sudipta Bhat | Khan Sharun | Kuldeep Dhama | Maryam Dadar | Ruchi Tiwari | Wanpen Chaicumpa

Abstract

Coronaviruses are the well-known cause of severe respiratory, enteric and systemic infections in a wide range of hosts including man, mammals, fish, and avian. The scientific interest on coronaviruses increased after the emergence of Severe Acute Respiratory Syndrome coronavirus (SARS-CoV) outbreaks in 2002-2003 followed by Middle East Respiratory Syndrome CoV (MERS-CoV). This decade's first CoV, named 2019-nCoV, emerged from Wuhan, China, and declared as 'Public Health Emergency of International Concern' on January 30th, 2020 by the World Health Organization (WHO). As on February 4, 2020, 425 deaths reported in China only and one death outside China (Philippines). In a short span of time, the virus spread has been noted in 24 countries. The zoonotic transmission (animal-to-human) is suspected as the route of disease origin. The genetic analyses predict bats as the most probable source of 2019-nCoV though further investigations needed to confirm the origin of the novel virus. The ongoing nCoV outbreak highlights the hidden wild animal reservoir of the deadly viruses and possible threat of spillover zoonoses as well. The successful virus isolation attempts have made doors open for developing better diagnostics and effective vaccines helping in combating the spread of the virus to newer areas.

Database

Taylor & Francis Journals

Title:

Author: Domenico Benvenuto | Marta Giovanetti | Marco Salemi | Mattia Prosperi | Cecilia De Flora | Luiz Carlos Junior Alcantara | Silvia Angeletti | Massimo Ciccozzi

Abstract

The global spread of the 2019-nCoV is continuing and is fast moving, as indicated by the WHO raising the risk assessment to high. In this article, we provide a preliminary phylodynamic and phylogeographic analysis of this new virus. A Maximum Clade Credibility tree has been built using the 29 available whole genome sequences of 2019-nCoV and two whole genome sequences that are highly similar sequences from Bat SARS-like Coronavirus available in GeneBank. We are able to clarify the mechanism of transmission among the countries which have provided the 2019-nCoV sequence isolates from their patients. The Bayesian phylogeographic reconstruction shows that the 2019–2020 nCoV most probably originated from the Bat SARS-like Coronavirus circulating in the Rhinolophus bat family. In agreement with epidemiological observations, the most likely geographic origin of the new outbreak was the city of Wuhan, China, where 2019-nCoV time of the most recent common ancestor emerged, according to molecular clock analysis, around November 25th, 2019. These results, together with previously recorded epidemics, suggest a recurring pattern of periodical epizootic outbreaks due to Betacoronavirus. Moreover, our study describes the same population genetic dynamic underlying the SARS 2003 epidemic, and suggests the urgent need for the development of effective molecular surveillance strategies of Betacoronavirus among animals and Rhinolophus of the bat family.

Database

Taylor & Francis Journals