Annals of Biomedical Science and Engineering

Volume - 4, Issue - 1

Review Article **Published Date:-2020-04-09 00:00:00**

The Trans-zoonotic Virome interface: Measures to balance, control and treat epidemics

The global virome: The viruses have a global distribution, phylogenetic diversity and host specificity. They are obligate intracellular parasites with single- or double-stranded DNA or RNA genomes, and afflict bacteria, plants, animals and human population. The viral infection begins when surface proteins bind to receptor proteins on the host cell surface, followed by internalisation, replication and lysis. Further, trans-species interactions of viruses with bacteria, small eukaryotes and host are associated with various zoonotic viral diseases and disease progression.

Virome interface and transmission: The cross-species transmission from their natural reservoir, usually mammalian or avian, hosts to infect human-being is a rare probability, but occurs leading to the zoonotic human viral infection. The factors like increased human settlements and encroachments, expanded travel and trade networks, altered wildlife and livestock practices, modernised and mass-farming practices, compromised ecosystems and habitat destruction, and global climate change have impact on the interactions between virome and its hosts and other species and act as drivers of trans-species viral spill-over and human transmission.

Zoonotic viral diseases and epidemics: The zoonotic viruses have caused various deadly pandemics in human history. They can be further characterized as either newly emerging or re-emerging infectious diseases, caused by pathogens that historically have infected the same host species, but continue to appear in new locations or in drug-resistant forms, or reappear after apparent control or elimination. The prevalence of zoonoses underlines importance of the animal–human–ecosystem interface in disease transmission. The present COVID-19 infection has certain distinct features which suppress the host immune response and promote the disease potential.

Treatment for epidemics like covid-19: It appears that certain nutraceuticals may provide relief in clinical symptoms to patients infected with encapsulated RNA viruses such as influenza and coronavirus. These nutraceuticals appear to reduce the inflammation in the lungs and help to boost type 1 interferon response to these viral infections. The human intestinal microbiota acting in tandem with the host's defence and immune system, is vital for homeostasis and preservation of health. The integrity and balanced activity of the gut microbes is responsible for the protection from disease states including viral infections. Certain probiotics may help in improving the sensitivity and effectivity of immune system against viral infections. Currently, antiviral therapy is available only for a limited number of zoonotic viral infections. Because viruses are intracellular parasites, antiviral drugs are not able to deactivate or destroy the virus but can reduce the viral load by inhibiting replication and facilitating the host's innate immune mechanisms to neutralize the virus.

Conclusion: Lessons from recent viral epidemics - Considering that certain nutraceuticals have demonstrated antiviral effects in both clinical and animal studies, further studies are required to establish their therapeutic efficacy. The components of nutraceuticals such as luteolin, apigenin, quercetin and chlorogenic acid may be useful for developing a combo-therapy. The use of probiotics to enhance immunity and immune response against viral infections is a novel possibility. The available antiviral therapy is inefficient in deactivating or destroying the infecting viruses, may help in reducing the viral load by inhibiting replication. The novel efficient antiviral agents are being explored.

Research Article **Published Date:-2020-03-11 00:00:00**

Mesoscopic irreversible thermodynamics of morphological evolution kinetics of helical conformation in bioproteins 'DNA' under the isothermal isobaric conditions

---

The morphological evolution kinetics and instabilities of alpha helical peptide 3.613, which involves large amount of stored torsional elastic deformation energy (3-40 eV/molecule), is formulated by the variational method based on the connection between the rates of internal entropy production and the changes in the global Gibbs free energy, assuming that one has isobaric irreversible processes under the isothermal conditions. The present mesoscopic nonequilibrium thermodynamic approach relies on the fact that the global Gibbs free energy of helical conformation involves not only the bulk Gibbs free energy of the amino-acid back bone structure but also the interfacial Gibbs free energy of the enclosing cylindrical shell or the cage associated with the side-wall molecular branches, and their interactions with the immediate surroundings. The proposed variational analysis applied directly on the proposed macro-model has furnished a nonlinear integral equation in terms of the normalized and scaled internal and external variables. This allows us to track down the motion of the total pitch height of the alpha polypeptide along the well-defined trajectories in the displacement-time space, dictated not only by the initial configuration of the helix but also through the gradients of the global Gibbs free energy of the strained helical conformation as the main driving force. In the negative manifold, there is a well-defined region below the dynamic instability regime, in which the helical conformation can evolve towards the nonequilibrium stationary states by expanding, or contracting, depending upon whether the interfacial free energy and/or the applied stress system are below or above the well-defined thresholds level dictated by the initial pitch height. The highest life time may be realized along that trajectory, which follows up the threshold level of the interfacial specific Gibbs free energy, which is gs = -315 erg/cm^2. In the upper region of the negative manifold, the helical conformations are driven by the very large applied uniaxial tension or the negative pressure induced by the thermal expansion, in the range of p > 1GPa and/or the strong negative interfacial free energies [3-4 pH] or their combinations, they show strong kinematic instabilities, which can cause not only the accelerated unfolding phenomenon but also cause large extensions that end up with the catastrophic decimations by ruptures and fragmentations. In the positive manifold, the aging behavior of the polypeptide follows up a S-shape path having rather speedy aging behavior compared to the negative manifold, which is separated from by a well-defined boundary, which represents the isochoric path having longest relaxation times, which can be achieved with great stability. Finally, one could attempt to estimate the upper limit of the relaxation time of aging for the modern hominin, from samples of exceptional preservations, relying on the present nonequilibrium theory as well as on the very limited knowledge on the post-mortem DNA and the present pitch heights of the modern hominin, which is found to be about 25,840 yrs, with a life expectation of 451,800 yrs. These figures are very close to those calculated for Neanderthals (SH), which are found to be 31,820 yrs and 499,100 yrs, respectively.

Research Article **Published Date:-2020-02-14 00:00:00**

Peptide-based antifouling aptasensor for cardiac troponin I detection by surface plasmon resonance applied in medium sized Myocardial Infarction

Highly selective and sensitive detection of cardiac troponin I (cTnI) is a powerful complement to clinical diagnosis of acute myocardial infarction (AMI). In this study, a strategy for cTnI detection was developed by constructing a universal biosensing interface composed of zwitterionic peptides and aptamers. The peptides were self-assembled onto gold chips, and some of them were biotinylated. The cTnI-specific binding aptamers were immobilized through the streptavidin-biotin system. Surface plasmon resonance (SPR) measurements revealed the preparation process. The developed aptasensor presents a linear detection with cTnI ranging from 20 ng/ml to 600 ng/ml and a detection limit of 20 ng/ml. The high immobilization of the aptamer enhances the sensitivity of the aptasensor and the calculated KD was 6.75 nM. Due to the outstanding antifouling property of the zwitterionic peptide, the developed aptasensor possesses a high resistance towards protein fouling. Moreover, the aptasensor has excellent selectivity and specificity towards cTnI in complex media. Hence, the proposed peptide-based aptasensor shows great potential for practical application in medium sized Myocardial Infarction (MI).
