

Euro Clinical Microbiology 2020 Reflections on Wuhan Viral Pneumonia (2019-nCov)

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The new decade started with a devastating outbreak of Wuhan viral pneumonia which is currently known is 2019-nCoV and questions about this new coronavirus remain. On December 31, 2019, a mystery cluster of pneumonia-like symptoms were reported in late 2019 from Wuhan Province in China. As the alarming confirmed cases as well as fatalities in China continues to rise, the global health community may face a pandemic potential of 2019-CoV. Although the epidemic is not declining as of February 2020, some insights can be reflected. The source of Wuhan viral pneumonia as reported by the Chinese health authorities, was presumably related to the Hunan Seafood Market in the city of Wuhan. Most recently, researchers at South China Agricultural University who tested more than 1000 samples from wild animals, reported a 99% match between the genome sequences of a virus found in pangolins and those in 2019-nCoV infected patients - such observation must be further validated. The Chinese scientists posted the full genome of the 2019-nCoV in GenBank. The genome sequences obtained from the nine infected patients (a cohort of 10 patients) were markedly similar and exhibited about 99% sequence homology within the patient cohort and was closely related (with 88% identity) to two bat-derived severe acute respiratory syndrome (SARS)-like coronaviruses. Analysis of the clinical specimens also showed the virus belongs to a subfamily of betacoronavirus. Further investigation revealed 2019-nCoV share same receptor with SARS-CoV, Angiotensin-converting enzyme-II. The virus appears to be more virulent in elderly and those with comorbid conditions. Although asymptomatic transmission has been reported in Germany, much questions remain about the biology of asymptomatic carriers since our current understanding of the mode(s) of transmission this this novel virus is limited. It is now evident 2019-nCoV is the third epidemic of the coronavirus family in the past decades which has crossed species infecting vulnerable and at-risk individuals. Much of the investigational work has been attributed to the infected patients, and to date, there are no published papers on human handlers of the animals serving as the source of the virus. What has been documented so far is like outbreaks caused by SARS-CoV and MERS-Cov, this novel outbreak causes severe respiratory syndrome indicating a virulent capacity of the virus causing viral pneumonia especially in elderly and those with comorbid conditions with an average fatality rate of almost 3% in Hubei province. Understanding the virulent factor in an error-prone RNA-dependent RNA polymerase virus such as 2019-nCoV is highly important in order to access the efficacy viral transmission as mutations and recombination of viral polymerase frequently occurs. It has been reported in critically ill patients who present with acute respiratory distress syndrome, there is reduction in peripheral blood lymphocytes. This finding in the context of adaptive immune response should be fully investigated since lymphocytes appear to be responsible in immunopathogenic events for Wuhan viral pneumonia. Particularly, the evidence of viral presence in peripheral lymph organ may provide insight for further understanding of immunopathogenesis of 2019-nCoV, let alone it provides better understanding of the pathogenic process in lung microenvironment.

To effectively unlock the ambiguous mode of transmission (so far animal-human, person-to-person, symptomatic carriers, and super spreaders have been reported) international research exchanges are urgently needed to coherently address so many questions about the biological, immunological and pathological characteristics of this novel virus. It appears the transmission of 2019-nCoV occurs fast by the means of miniscule contact droplets or possibly via airborne transmission. Measures to prevent or reduce transmission should be implemented in populations at risk applying the principles of public health prevention and control with emphasis on contact tracing and surveillance issues. In addition, deeper investigation of the specific immune response to acute infection will shed more lights on pulmonary and systemic inflammatory responses associated with 2019-nCoV. The immune response to coronaviruses in general is presumed to be triggered by the innate immune system when it recognizes the corona family viruses. Regarding the presumptive silent carriers of the virus in the endemic regions who present non-respiratory symptoms such as diarrhea, nausea and vomiting, should be promptly evaluated for possible coronavirus infection. Because of several uncertainties of 2019-nCov, the full scientific evidenced-based investigations necessitate stakeholders of various agencies collaborate and communicate efficiently through transparency, openness, and most importantly, unbiased data sharing – One Health concept. One Health integrates collaboration and communication of a broad range of biological, microbiological, biomedical and other related disciplines to focus on 2019-nCoV parameters such as animal reservoir(s), transmission route(s), epidemic curve, viral kinetics in the host system, clinical microbiological findings, unusual symptoms presentation in few clusters, and most importantly, autopsy findings that will help to foster more effective care and preventive strategies.

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