The Proximal Origin of SARS-COV-2

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This letter to the editor may be cited as: Azmat A, Kamran N, Aziz N, Bashir S, Arif S, Ullah I. The proximal origin of SARS-COV-2. Pak J Chest Med 2020; 26 (3):113

To the Editor,

As the Novel coronavirus brought the world's great economies to a screeching halt. The quest of time to find the origin of this COVID-19 virus started. It was presumed that this animal virus was transferred from a bat to a human in the wildlife market of Wuhan city, China. The assumption brought fear and anxiety about the capability of animal virus crossing species boundaries to infect humans. Major concerns regarding the virus are the re-adaptation of it in another animal species, posing a greater risk for re-emergence. Others include its adaptability progress in humans. The real thirst among microbiologists/scientist is to decode its mutation strategy. However, the recognition of SARS-COV-2 close associates in other animal species improved our understanding of viral function.[1]

Significant features of SARS-COV-2 are advanced receptor binding domain (RBD) and polybasic sites revealed by the RaTG13 bat sequencing. It would likewise be useful to further acquire progressively hereditary and practical information about SARS-CoV-2.[2] The recognizable proof of a potential middle host of SARS-CoV-2, just as the sequencing of the infection from early cases, would comparatively be exceptionally enlightening. The current cases of coronavirus pneumonia should be catered with utmost care while gathering effective data for analysis.[3]

The genetic sequencing of SARS-COV-2 enabled access to its behavioral patterns in humans. This scientific proof is suggestive of its formation through the process of natural selection. A great number of studies have to be conducted to gather strong evidence to revoke other conspiracy theory of its being a biochemical agent. Since we witness its characteristic features, we don't accept any kind of lab-based situation is conceivable. Progressively more logical information could swing the parity of proof to support one speculation over another. Acquiring related viral sequencing from animal sources would be the most conclusive method for finding viral genesis.[4]

References

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