

is similar to SARS-CoV RBD and there are important interactions between several key amino acid residues of RBD receptor-binding motif and ACE2 [8].

However, our data show the differences of interaction with considerably less favorable binding energies between these viruses with ACE2 [19], as shown in this Table 7.1. Thus, the loops observed in the spike protein of COVID-19 in the amino acids mutation (substitutions or deletion) considered as key factor with ACE2 binding [20]. Mutations in the spike protein could change the physiochemical activity of a virus which increases viral pathogenesis [21]. The presence of square bracket in (Fig. 7.2a, b) around the interaction region might be promoting the interface with ACE2 receptor, which illustrate the binding to this receptor and interaction between amino acid residues (Table 7.2).

Interestingly, mutational site could play an important clue to determine the host receptor specificity [22] for the viral spike protein which is responsible for increasing infection and viral spreading. The comparative studies to determine the impact COVID-19 and SARS CoV mutational site are quite similar with respect to receptor binding domain, which helpful and required to predict possible zoonotic event in the future as well as develop therapeutics. However, the present data might play a significant role into develop antiviral drugs and vaccines to stop the COVID-19 disease with unpredictable death.

7.5 Conclusion

Drug/vaccine development against the COVID-19 is a challenging for scientific community worldwide due to their frequent recombination events. We need explore this study on system biology to accelerate the structural and functional details of the life cycle of the COVID-19 and their mode of action. Again, as a preventive measure and strict observation of viral changes in different hosts for the prediction of an event is important aspect. Based on the current research progress, ACE2 is considered as the host potential target site for the treatment of coronavirus infection to block COVID-19 from entering host cells.

References

1. Yu T, Xia J, Wei Y, Wu W, Xie X, Yin W, Li H, Liu M, Xiao Y, Gao H, Guo L, Xie J, Wang G, Jiang R, Gao Z, Jin Q, Wang J, Cao B (2020) Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. *Lancet* 395:497–506
2. World-Health-Organization (2003) Update 49—SARS case fatality ratio, incubation period. Available online: https://www.who.int/csr/sars/archive/2003_05_07a/en/. Accessed 31 Jan 2020
3. World-Health-Organization (2020a) Middle East respiratory syndrome coronavirus (MERS-CoV). Available online: <https://www.who.int/emergencies/mers-cov/en/>. Accessed 31 Jan 2020