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Editorial

Proteomics and Its Application in Pandemic Diseases

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Pandemics create havoc in human life and are not simply old-world problems. A series of recent viral outbreaks including HIV, influenza, Ebola, Zika, and SARS-CoV-2 have elevated to pandemics. The recent and ongoing coronavirus disease (COVID-19) caused by SARS-CoV-2 has caused more than 1 081 868 deaths and infected more than 37 888 384 humans worldwide, as reported by the World Health Organization (WHO). Prevention, early diagnosis, and early treatment are the keys to pandemic management. Proteomics can play an important role in understanding host−pathogen interactions, diagnosing infections, developing vaccines, and creating therapeutics for pandemic-causing pathogens such as SARS-CoV-2. Notably, COVID-19 emerged in Wuhan, China and was first reported as pneumonia with an unknown cause to a WHO China country office on December 31, 2019. Furthermore, it was elevated to a pandemic by WHO on March 11, 2020. COVID-19 is a serious threat for patients with comorbidities such as compromised immune systems, respiratory diseases, cardiovascular diseases, hypertension, diabetes, and other diseases. This disease has destabilized the healthcare systems and economies worldwide. COVID-19 can infect any age, gender, or ethnicity and can infect healthy people. Body fluids including nasal aerosol and saliva are major modes of transmission for spreading COVID-19. Unfortunately, there are no clinically approved vaccines or curative drugs for it. Efforts are being made to develop vaccines and therapeutics against the deadly SARS-CoV-2 to save lives. There are several emergency drugs for COVID-19, including remdesivir, dexamethasone, and favipiravir. Early treatment with favipiravir and remdesivir may be beneficial during the ongoing COVID-19 pandemic. Both favipiravir and remdesivir are prodrugs that inhibit the RNA-dependent RNA polymerase (RdRp) enzyme and prevent virus replication.

RdRp is one of the favorite targets for antiviral drug discovery. In this "Proteomics in Pandemic Disease" Special Issue, Zhao and Bourne have suggested four classes of binding modes for RdRp binding pockets that can help the *in silico* screening of RdRp inhibitors. Nucleotide analogues such as triphosphates of sofosbuvir, alovudine, AZT, abacavir, lamivudine, and emtricitabine can inhibit the RdRp of SARS-CoV-2, as studied by Chien et al.

Furthermore, Zeng et al. proposed 41 drugs for repurposing, including dexamethasone for COVID-19, using the deep-learning framework and AI methodology. Moreover, by a computational approach including homology modeling, molecular docking, molecular dynamics simulations, and binding affinity calculations, Martin and Cheng found potential targets for toremifene in SARS-CoV-2, such as heptad repeat 1 (HR1) and methyltransferase nonstructural protein (NSP) 14. Using *in silico* studies, Barros et al. found that the antimalarial drug metaquine and anti-HIV antiretroviral saquinavir interact with four SARS-CoV-2 receptors, including Nsp9 replicase, main protease (Mpro), NSP15 endoribonuclease, and spike protein (S protein), interacting with human ACE2; therefore, they may be repurposed for COVID-19 treatment. The bioinformatics analysis of BCG antigens by Glisic et al. suggested that four bacterial proteins, Rv0934, Rv3763, Rv3875, and Rv2997, have similar properties as the S1 protein of SARS-CoV-2; therefore, they might be effective against SARS-CoV-2. A molecular docking and dynamics simulation analysis suggested that noscapine binds with the main protease of SARS-CoV-2 and produces conformational changes (Kumar et al.). Furthermore, Maffucci and Contini used an *in silico* approach to find drug candidates against the main proteinase and spike protein of SARS-CoV-2. This led to the finding that indinavir, polymyxin B, daptomycin, terlipressin, and thymopentin can be repurposed against the SARS-CoV-2 infection. Interestingly, the studies by Stamatakis et al. suggested that the antigenic peptides generated from the S1 spike glycoprotein of SARS-CoV-2 using aminopeptidases ERAP1, ERAP2, and IRAP might be helpful in selecting better epitopes for immunogenic studies and the design of a vaccine for COVID-19.

Metabolites in SARS-CoV-2 patients were analyzed by NMR and mass spectrometry with the observations of an increase in the α-1-acid glycoprotein, an increased kynurenine/tryptophan ratio, low total and HDL apolipoprotein A1, low HDL triglycerides, high LDL and VLDL triglycerides, elevated glutamine/glutamate, and Fischer's ratios that are consistent with diabetes, coronary artery disease, and liver dysfunction risk (Kimhofer et al.). By using NMR spectroscopy, Loo et al. reported that inactivation by heat causes the degradation of lipoproteins and changes in various metabolic information in SARS-CoV-2-infected plasma samples. Saunders et al. described the coronavirus-specific web portal (https://metatryp-coronavirus.whoi.edu/) in METATRY V2.0 that can be used for coronavirus proteomics research. This web portal is helpful for finding peptide biomarkers and specific taxonomic groups.

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The prevalence of pandemic diseases has necessitated method development for their detection. A mass-spectrometry-based method was developed by Ihling et al. for gargle solution collected from SARS-CoV-2-infected persons. Gouveia et al. developed a nanoLC-MS/MS method to quantify several virus-specific peptides from COVID-19 patients for proteo-typing of SARS-CoV-2 using nasopharyngeal swabs in a 20 min MS acquisition window. Furthermore, the nanoLC-MS/MS acquisition method for COVID-19 clinical samples reported that the peptides ADETQALPQR and GFYAQGSR from nucleocapsid proteins were detected within a 3 min window. Nikolaev et al. developed a method for the detection of the SARS-CoV-2 virus using nasopharynx epithelial swabs by the identification of the viral nucleocapsid N protein from the virus. They inactivated the virus by heating, the addition of isopropanol, followed by trypsin digestion and then analyzed it by mass spectrometry. In addition, D'Alessandro et al. reported serum proteomics from COVID-19 patients and observed the up-regulation of IL-6, complement cascade, and inhibitory components of the fibrinolytic cascade in COVID-19 patients compared with the control. Zhou et al. reported the quantitative proteomics of porcine-deltacoronavirus (PDCoV)-infected IPEC-J2 cells (porcine small intestinal epithelial cells) using iTRAQ, which might be helpful to understand its pathogenesis.

Rosa-Fernandes et al. reported a method to study the ocular surface proteome, especially for infants exposed to the Zika virus during the gestation period without early clinical symptoms, and named it the cellular imprinting proteomic assay (CImPA). In the conjunctival epithelium of infants exposed to the Zika virus, neutrophil, eosinophil infiltration, and degranulation were detected by this proteomic assay. Furthermore, virus-like particles (VLPs) have been applied in vaccine therapies. Lavado-García et al. used quantitative proteomics to identify the changes in the secretome of VLPs and the coproduction of extracellular vesicles (EVs) under different conditions, including nontransfected and transfected with and without plasmid coding for HIV-1 Gag polyprotein.

Interestingly, a computational method was used to find an allosteric site on the SARS-CoV-2 spike protein by Di Paola et al., as its detection would weaken the spike−ACE2 interaction and thereby reduce the viral infection. Another study by Verkhivker suggests that the spike protein of SARS-CoV-2 may function as an allosteric regulatory engine fluctuating between dynamic functional states. Hadi-Alijanvand and Rouhani reported the higher binding affinity of the closed state of ACE2 for the S1 protein of SARS-CoV-2 compared with the open state of ACE2 by using a computational approach. Furthermore, Nadeau et al. used a computational approach to study the SARS-CoV-2-interacting human proteins using the GoNet algorithm.

Using a ferret model for the H1N1 2009 pandemic influenza A virus, Chen et al. reported the host glycomic response and its age-dependent severity. They suggested that a high level of mannose may be related to the severity of the influenza A virus due to the overactive innate immune system. In the case of the Ebola virus, Banerjee and Mitra proposed the tetrameric assembly model to the VP35 protein and suggested that the C-terminal of VP35 interacts with human protein kinase R to stop its autophosphorylation.

This Special Issue provides a platform to understand pandemic diseases. Here several topics have been encouraged that connect proteomics and pandemic diseases, including proteomic technologies, biomarker discovery, pathogenesis, mechanistic details of proteins, protein−protein interactions, signaling pathways, post-translational modifications, computational proteomics, prevention and vaccination, drug repurposing, and therapeutic agents and their mode of action. It will be thrilling to find the bridge between proteomics and pandemic diseases, especially for COVID-19.

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