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Environmental metagenomic assessment and its usefulness in the present pandemic

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Environmental metagenomic assessment and its usefulness in the present pandemic

Dear Editor, a new emerging disease is usually an important problem. Many new diseases have resulted in a worldwide problem, including the present Coronavirus disease 2019 (COVID-19) pandemic.

Some good examples of pandemics in world history are the Spanish flu and COVID-19. During early stage, it is usually hard to have an effective diagnosis and treatment of the new diseases.

Many new diseases can be transmitted through atypical modes, including contact to a contaminated surface. Environmental contamination is a new consideration during outbreak. The contamination in the surrounding environment might occur and cause disease spreading.

Metagenomics study is a new approach that can provide clues and evidence whether the new disease is transmittable due to contamination or not.

Scientifically, metagenomics study is a specific biomedical process. It starts from the collection of samples from the surrounding environment, and then, a standard molecular genomic study on the collected sample is done. The main aim of the test is the identification of the existence of the pathogenic agent in the studied samples. The metagenomics approach can answer the question on the existence of pathogenic contamination [1]. In case that there is a contamination, the characteristics can be further analyzed. Phylogenomics and evolutionary genomics can be used for grouping, classifying, and tracing for the origin of the new pathogen.

The metagenomics approach is based on the standard genomics concept. For *in vitro* studies, a standard microbial ecology study is used. The standard microbial ecology sample collection guidelines are applicable. The quality control and standardization are important requirements [2]. In brief, sufficient samples have to be collected according to the presampling statistical plan. After collection of the sample, the standard genomics processing will be done. All analyses have to follow the standards under appropriate quality control [3]. The concept of laboratory quality cycle from preanalysis to postanalysis is required.

Regarding the data manipulation, the computation informatics technology is useful for further analysis. The incidence and prevalence data from metagenomics study are useful for planning of disease control. The interactive distribution

map based on geographical information system technology can be further generated [4] (Clarke, 1996). This applied geographical pathology can help evaluate environmental effects from climatic, geographical, geological, and meteorological parameters. With the data of dynamicity of disease, the prediction and future trend analysis is possible. This is an actual clinical epidemiology work to correspond to a pandemic.

Similar to other omics approaches, there are many new available online metagenomics tools for clarification and prediction. However, the limitations of the metagenomics study on new pandemic still exist. First, as the metagenomics approach is mainly based on collected environmental sample, the quality management is necessary. Second, it is necessary to have a statistical correction for false-positive and false-negative results. This step is required before generalization of the metagenomics data [4]. Good sampling and sample size calculation are needed [5]. Finally, there are also limitations of the computational tool, especially for error when there is a very large data set [6,7].

In conclusion, environmental metagenomics analysis is a useful tool for pandemic containment. It should be considered as an important part for public health management of the present crisis.

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