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Article 6-3. The Identification of Pathogen Phenotype for Biophysical Simulation /生物物理模拟试验中病原体表现型的确定方法

Author: Liu Huan (1983-), Master of Science (First Class Honours, 2009), The University of Auckland.

DOI:10.58473/JBS0010 Retrieval from official database: www.crossref.org

Latest revised on 29/05/2023.

Methods

Step 1. The host cells of the same genetic strain (such as the blood cells of rat) are abstracted, which are divided into several cell samples, and labeled as S1, S2, S3, Sn;

Step 2. The simulation of a specific virus (or bacteria) invasion targeting the host cells is conducted by inoculating this pathogen in Lab, immediately after host cells are abstracted from host body;

Step 3. The samples of host cells with apparent antibiotics are identified in this pathogen invasion simulation; and the samples of host cells without apparent antibiotics are also continuously observed until they are 'eaten up' by the specific invasive pathogen;

Step 4. The separation of virus from each sample of host cell without apparent antibiotics are conducted independently by centrifuge in Lab, and the metabolomics test is conducted in each invasive virus sample as well as background virus sample without participating in pathogen invasion simulation. The method of metabolomics test is designed in another article [1].

Step 5. By comparing the background samples with the invasive pathogen samples, it is to identify the specific isozyme family and specific enzyme species within an isozyme family at molecular weight level, which plays the key role in the pathogen invasion process.

Step 6. The specific enzyme species within an isozyme family can be identified and separated by Non-denaturing polyacrylamide gel electrophoresis in isozyme experiment, and the correspondingly specific enzyme materials can be collected from the electrophoresis pipes for further enzyme activity analysis. The specific enzyme concentration can be still measured by spectrophotometry in water solution after Non-denaturing polyacrylamide gel electrophoresis to indicate the enzyme activity expression by each invasive pathogen sample.

Discussion:

The different phenotypes of an invasive virus (or bacteria) strain would be identified specifically in this method, which would be more exactly targeting the specificity of host-invasive interaction.

Please note: the simulation of a specific virus (or bacteria) invasion targeting the host cells should be conducted immediately after host cells are abstracted from host body, otherwise the uniform cell cultivation in Lab lead to the homogeneity of host cells, so that different phenotypes of an invasive pathogen can be hardly detected. However, if virus samples, which are separated from host cell without apparent antibiotics after step 3, re-invade the host cells with apparent antibiotics identified in step 3, virus infection would occur, due to the evolution of new virus phenotypes.

The theory of this method attempts to demonstrate that the host cells are usually heterogeneity in host body, and pathogens usually can only start to infect a small proportion of host cells at first, evolving into new virus phenotypes. Then the new virus phenotypes re-invade other host cells, resulting in infection of the majority of host cells in body.

Please note: This is the revised materials in book “Proceedings for Degree of Postgraduate Diploma in Environmental Science (3rd Edition).” Published in 2016. The ‘chapter’ content mentioned in this article is in previous book. Firstly Revised on 05/01/2021; Secondly Revised on 08/02/2021; Thirdly Revised on 26/09/2021; Fourthly Revised on 25/12/2021. This journal article is previously published as: Liu Huan. (2021). Article 10-3. The Identification of Pathogen Phenotype for Biophysical Simulation. Journal of Environment and Health Science (ISSN 2314-1628), 2021(02)., which is converted into Journal of Biological Sciences (ISSN 2958-4035). Both Journals belong to the same publisher, Liu Huan. The previous journal article is closed to the public, but the previous reference is still valid. Latest revised on 19/04/2023; 29/05/2023.

References:

[1].Liu Huan. Metabolomics (1) --- The Systematic Chemistry Fingerprints Between Genotype and Phenotype and its Application on the Conservation Genetics. Journal of Environment and Health Science. Feb. 2021.https://doi.org/10.58473/JBS0005