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Article 5. Gene Mutation, Pathogenesis and Gene Modification/ 基因突变、致病性机理与基因修改

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1. Gene Mutation and Its Pathogenesis (1)/基因突变及其致病性机理

Step 1. The host cells with apparent antibiotics of the same genetic strains are identified during the invasive simulation of a specific bacteria strain (Sample 1);

Step 2. The same bacteria strain is cultivated during radiation, leading to gene mutation (Sample-M) detected by FISH technology using transmission electron microscopy;

Step 3. Invasive simulation by Sample-M targeting the host cells with apparent antibiotics, identified in step 1, is conducted.

Step 4. The disease infection by Sample-M is observed.

Step 5. The bacteria cell division rate (quantity of cells / cultivation time) is observed and compared between cells with gene mutation and cells without gene mutation.

Hypothesis:

The bacteria with gene mutation leads to altered bio-signal which can be difficultly perceived by host cells with specific immunology against their parental bacteria (sample 1), and the infection rate by sample-M is higher than sample 1. The altered bio-signals caused by gene mutation of pathogen is further discussed below.

Discussion:

Gene mutation[1], leads to cells with faster cell division rate (DNA or RNA replication rate in virus) than their parental cells (or virus). This explains the sharply epidemic infection caused by bacteria or virus with gene mutation (such as AIV).

2. Gene Mutation and Its Pathogenesis (2)/基因突变及其致病性机理

As discussed previously, gene mutation pathogens leads to 'altered' or distortive bio-signal, which is hardly identified by host cells. Consequently, this section presents a novel method to train the host cells' 'memory' in terms of identifying the invasive virus family with gene mutation.

Step 1. The virus classification on the basis of FISH technology is conducted among different virus families, which is the morphological markers of DNA or RNA molecules, as designed in another article [3].

Step 2. The similar virus families (mild sample) to the pathogenetic virus family with gene mutation (pathogenetic sample) is identified in step 1 on the basis of morphological markers of DNA or RNA molecules; And the similar virus is less pathogenetic virus (such as becoming dormant in host cells after puncture), which is consequently called as 'mild' samples, but is classified into the similar virus family with close genetic distance to the pathogenetic virus family of gene mutated, according to the morphological markers of DNA or RNA molecules;

Step 3. The host cells are abstracted from the individual body, and subsequently divided into different samples that are cultivated separately. Then the 'mild' sample of virus family invades different samples of host cells separately in Lab, and the host cell samples with apparent antibiotics are identified as bio-sample A. This step is to train the specific immunology in host cells against the virus family with gene mutation.

Step 4. Then the virus family with gene mutation (pathogenetic sample) in Lab invades the host cells cultivated in step 3. The infection rate between host cells of bio-sample A cultivated in step 3 and host cells without previous 'mild' sample invasion training is compared;

Step 5. This method strengthens the immunology of host cells against this gene mutation virus family through similarity invasion simulation, so the infection rate in host cells of bio-sample A cultivated in step 3 may be reduced, compared with host cells without previous 'mild' sample invasion training.

Discussion:

The pathogenicity of virus invasion in this journal is explained by two process: one is to puncture the host cell membrane, and the other is the virus metabolism in host cells after puncture. In the first process of host cell puncture, both biochemical and biophysical mechanism are involved. For the biochemical factors, invasive pathogens produces the toxic enzyme to degrade the host cell walls before puncture, which has been reviewed in case studied by another article [4]. However, after this biochemical process, virus must invade host cells through puncturing cell walls, which is a kind of biotic and intelligent sports in biophysics rather than abiotic movement. This biophysical mechanism of pathogenesis has been seldom studied before, consequently

becoming the research gap to fill in in the future.

Consequently, host cells identify the bio-signal of invasive virus in the first stage of puncture process, in which the morphological bio-signal of invasive virus genome is the main bio-signal in biophysics (this bio-signal by gene mutation virus is similar to other virus families, rather than its parental virus family); the second stage is the pathogenic metabolism of invasive virus after puncture, and the main bio-signal depends on the gene expression of virus genome (this bio-signal by gene mutation virus is similar to their parental virus). This two process further explains the altered or distortive bio-signal caused by gene mutation virus. **Consequently, this training procedure helps host cells identify the morphological signals of gene mutated virus in biophysics, so that immunology is cultivated correspondingly.**

Please note:
If the host cells of sample A with apparent antibiotics can be hardly found in step 3, the biophysical training methods that help to establish immunology is designed in another articles [5]. It is expected that the specific zymograms of host cells with specific immunology against invasive gene mutation virus is closer to the specific immunology against their parental virus.

3. Gene modification of microbial vaccine/微生物疫苗的基因修改技术

Although the gene mutated bacteria or virus has been already commonly used in the production of microbial vaccine in the past [2], the biophysical simulation by adjusting different frequency or intensity of electromagnetic waves, as discussed in my article of this journal [5], points out a new way of cultivation of microbial vaccine below:

Step 1. Vaccine microbes are cultivated during simulation of electromagnetic wave conditions;

Step 2. Different frequency of electromagnetic wave (or different wavelength) are simulated, and labeled as F1, F2, ..., Fn;

Step 3. Under each simulated frequency of electromagnetic wave, different intensities of electromagnetic wave are simulated, and labeled as I1, I2, ..., and In; Then in total N×N bio-samples are cultivated under biophysical simulation;

Step 4. After sufficient reproduction process, gene mutated vaccine microbes is obtained and identified by FISH technology;

Step 5. Finally, this gene-mutated microbial vaccine is inoculated into host cells, and then pathogen invasion simulation is conducted for testing the effectiveness of vaccine.

For the pathogenic bacteria or virus, suitable/accurate gene mutation may reduce the pathogenicity of these pathogens against host cells, but keeps both metabolic and ecological traits which are similar to their parental and pathogenic bacteria or virus. The new strains engineered by this gene modification provides better way of microbial vaccine production than trans-gene microbes. The improved simulation method of time-varying electromagnetic waves has been designed in another biophysics article [6], which can be used to replace the static frequency and intensity specified in step 2 and step 3 above. The reasons of this gene mutated technology for gene modification is summarized as below:

The advantages of inoculation of microbial vaccine is not just to cultivate the host cell's memory in terms of immunology against their parental and pathogenic microbes, but also for the microbial vaccine to be dominant in host environment by competing with their parental and pathogenic microbes' invasion, because the microbial vaccine compete for the same 'ecological niche' with their parental and pathogenic microbes in host cell environment and shows symbiosis with host cells before their parental and pathogenic microbes invade. For example, if the vaccine microbe already 'occupies' a host cell with symbiosis, the metabolic substances of symbiotic vaccine microbe, as a kind of bio-signals, eliminates the re-invasion by their parental and pathogenic microbes. This is a common nature of host-invasion interactions. Secondly, the

microbial vaccine engineered and created by gene mutation leads to higher cell mutation rate than its parental pathogens so that eliminates the reproduction of parental pathogens which is identified as more pathogenicity against host cell. Consequently, the metabolites of symbiotic vaccine microbe itself are just a kind of effective antibiotics against similar genetic strains, and this competition-exclusion natural Law between different strains of microbes also partly explains that the symbiosis of rhizobium in Leguminosae species leads to antibiotics for biomedicine discussed in other article of this journal [7].

In this case, the host cells inoculated by symbiotic microbial vaccine can be utilized for exchange transfusion as remediation method, and the symbiosis would not need persist long-termly after cure, because the symbiosis of microbial vaccine may negatively influence the health due to competition for nutrition as well after cure.

Conclusion

Gene mutation is the natural adaptive process of cell evolution in response to environment changes. Moderate gene mutation can be utilized as gene engineering instead of clone Tech due to more nature!

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References:

[1].基因突变。搜狗百科，共享百科全书/Sogou Baike, Creative Commons.
[2].细菌疫苗。搜狗百科，共享百科全书/Sogou Baike, Creative Commons.
[3].Liu Huan. (2021). Classification of Virus by DNA Genetic Marker and Its Theory. Journal of Environment and Health Science (ISSN 2314-1628), 2021(02).https://doi.org/10.58473/JBS0001
[4].Liu Huan (2023). Original review of specificity in the interaction between pathogen invasion and host organism. Journal of Biological Sciences (ISSN 2958-4035), 2023 (04). https://doi.org/10.58473/JBS0022
[5].Liu Huan. (2021). Bio-signal Simulation of Electromagnetic Wave and Its Specificity on the Isozyme Expression. Journal of Environment and Health Science (ISSN 2314-1628), 2021(02).https://doi.org/10.58473/JBS0012
[6].Liu Huan. (2021). The Parameterization of Time-varying Electromagnetic Field for Biophysics Simulation. Journal of Environment and Health Science (ISSN 2314-1628), 2021(02). https://doi.org/10.58473/JBS0013
[7].Liu Huan. (2021). The Synthesis of Biological Antibiotics and Its Application on Bio-medicine. Journal of Environment and Health Science (ISSN 2314-1628), 2021(02).https://doi.org/10.58473/JBS0014