《生物科学杂志(ISSN 2958-4035)》
Journal of Biological Sciences (ISSN 2958-4035)

ChengZhu Science™

Serial in November, 2022

ChengZhu Science Research Center Limited

(Hong Kong Registration NO. 80561228)

Journal article DOI is registered via JiangXi Province ChengZhu Environmental Engineering Company Ltd, with Crossref membership (DOI prefix 10.58473)

出版人： 刘焕 香江出版社有限公司

Publisher: Liu Huan, Xiangjiang Publishing Company Ltd.



Copyrights Statements

Copying and Transferring is Forbidden!

版权申明

禁止复制、转载！

All the intellectual property (mainly including the original academic knowledges and brand logo) are prohibited to copy or transfer into other publications or websites. To cite this article, only short quote is acceptable, but copying or transferring any substantial part of this article is NOT allowed (Defined in <Copyright Ordinance> in Hong Kong). The original academic knowledge is the substantial part of an article as academic journal. For learning purpose, it is allowed to read our website in online video class only. This journal is published by Hong Kong Publisher, and the copyrights is regulated and protected by <Copyright Ordinance> in Hong Kong, China. This PDF document is accessible to public only through Hong Kong domain websites (natural-foundation-science.org), and its printed version is the formally published journal. Without permission, it is NOT allowed to print, issue and sale.

所有形式知识产权（主要包括原创型学术知识和品牌标识）禁止复制、转载到其他出版物和网站。如果需要引用这篇论文，仅仅允许简短引述，但是禁止复制、转载这篇论文中任何实质性部分（香港《版权条例》中定义）。作为学术杂志，这篇论文中的原创型学术知识即为作品的实质性部分。仅仅允许以学习为目的在线视频课堂阅读本公司网站。本杂志由香港出版社出版，其版权受中国香港《版权条例》监管和保护。此PDF文档仅仅通过香港主机网站向公众公开 (natural-foundation-science.org)，并且其印刷版本杂志为正式出版物。未经许可，不得印刷、发行、销售。

Article 6-1: Metebolomics and Immunology Cultivation /新陈代谢组学与免疫力培养

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

DOI: https://doi.org/10.58473/JBS0008

Formally published on 30/11/2022; Latest revised on 11/05/2026.

Abstract

This article designs a novel method to analyze the isozyme electrophoretograms across different isozyme families, targeting the cultivation of environmental adaptiveness or immunology, and the theoretical discussion of biochemistry dynamics in enzyme expression is provided.

Key words: Metabolomics, Immunology, Environmental Adaptiveness, Biochemistry Dynamics, Enzyme Expression.

Methods:

The same strain of microbes is divided into two samples for the bio-signal simulation:
1.There are two kinds of cultivation conditions simulated in Lab for microbe reproduction process: one is the 'comfortable' condition (Sample 1); the other is under UV-B radiation for cultivation (Sample 2). The microbe samples are collected after sufficient reproduction process (at least ten generations).

2.After sufficient reproduction process, the UV-B radiation simulation stops. Then both sample 1 and sample 2 are separately transferred into moisture simulation process: different moisture conditions of microbial cultivation are simulated in Lab, and labeled as T1, T2, ..., Tn.

3.Metabolomics tests are conducted after moisture simulation of T1, T2, ..., Tn respectively, resulting in different zymograms as: M1, M2, ..., Mn. The procedure of this test is presented in previous article of this journal as below [2]:

4."Each isozyme family is labeled as 1, 2, 3..., and E; It is hypothesized that the bands at the same line across different isozyme families are the enzyme species at the same locus (expressed by the same quantitative gene status), named as enzyme 'species i' (i = 1, 2, ..., I), and each isozyme family has the same amount (I) of enzyme species (Please note: this is different from the identification of real enzyme species. If there is

no band at this line for an isozyme family, its value is given to be zero but the (I) value is still counted as the serial number). Then there is a 3-dimension (I× E × N) matrix presented in this research. I is the total amount of enzyme species within an isozyme family; E is the total amount of isozyme families; N is the total amount of bio-samples that generate different zymograms among different simulated moisture conditions:

X= ⎪Xien⎪(i = 1, 2, ...I; e = 1, 2, ... E; n= 1, 2, ... N)

Xien is the occurrence of enzyme 'species i' in the isozyme 'family e' during simulated moisture condition Tn. The value of Xien is one or zero. If the electrophoresis band occurs at this locus, the value is one; otherwise it is zero. The matrix X is below:

$$\begin{vmatrix} X111 & X112 & ..... & X11n & X121 & X122 & ..... & X12n & ..... & X1e1 & X1e2 & ..... & X1en \\ X211 & X212 & ..... & X21n & X221 & X222 & ..... & X22n & ..... & X2e1 & X2e2 & ..... & X2en \\ ..... & ..... & ..... & ..... & ..... & ..... & ..... & ..... & ..... & ..... & ..... & ..... & ..... \\ Xi11 & Xi12 & ..... & Xi1n & Xi21 & Xi22 & ..... & Xi2n & ..... & Xie1 & Xie2 & ..... & Xien \end{vmatrix}$$

Matrix Se = Xe × (Xe)T , where Xe = ⎪Xin⎪(i = 1, 2, ...I; n= 1, 2, ... N); (Xe)T is the transpose of the matrix Xe. The matrix Xe is below:

$$\begin{vmatrix} X11 & X12 & ..... & X1n \\ X21 & X22 & ..... & X2n \\ ..... & ..... & ..... & ..... \\ Xi1 & Xi2 & ..... & Xin \end{vmatrix}$$

To conduct Principal Components Analysis (PCA) on matrix X, the overall matrix X can be divided by two sub-factors: PCA is firstly conducted on the basis of matrix Se, revealing the biochemical dynamics of an isozyme 'family e' among different simulated moisture conditions. In matrix Se, it is hypothesized that the variable in PCA represents the biochemistry dynamics of each enzyme 'species i'.

Matrix S = $\sum_{E}^{1} Se$ (e = 1, 2, ..., E)

PCA is further conducted on the basis of Matrix S (I×I dimension), revealing the biochemical dynamics among different isozyme families over the whole simulated moisture conditions. In Matrix S, it is hypothesized that the variable in PCA represents the biochemistry dynamics of each enzyme 'species i' across all the isozyme families."

5.However, for the comparison between sample 1 and sample 2, this article needs to present more procedures for subsequent analysis: in matrix Se, the biochemistry dynamics of the first three enzyme species, which contribute to the most variations by PCA in an isozyme family, are selected for comparison between sample 1 and sample 2; in matrix S, the biochemistry dynamics of the first three enzyme species, which contribute to the most variations by PCA across all the isozyme families, are selected for comparison between sample 1 and sample 2; the sum percentages of the first three enzyme species in an isozyme family (= the sum Variance Contribution Ratio (VCR) of the first three enzyme species in matrix Se), represent the total variation of an isozyme family over the whole simulated moisture conditions; the sum percentages of the first three enzyme species across all the isozyme families (= the sum Variance Contribution Ratio (VCR) of the first three enzyme species in matrix S), represent the variation of the total zymograms over the whole simulated moisture conditions. Finally, the sum VCP are compared between sample 1 and sample 2.

Discussion

1.The higher variation in biochemical dynamics of enzyme expression, the better environmental adaptiveness or immunology. It is deduced that the biochemistry dynamics of the first three isozyme families (the sum VCR), which explains the highest variation by PCA, determines the conclusion of this comparison;

2.It is expected that sample 2 leads to higher variation in biochemical dynamics of enzyme expression, in terms of the higher sum VCR, which is also revealed by the higher adaptiveness during drought stress or higher immunology.

3.The findings of this article further support the theory proposed by other articles of this journal: the memory of cells can be 'trained' by the biophysical simulation in site, indicated by the zymograms in metabolomics test. **Consequently, the memory of cells, in terms of identifying the bio-signals of a specific environmental factor (can be biotic or abiotic) triggering the gene expression for environmental adaptiveness or immunology, can be trained and strengthened by the biophysical simulation of other environmental factors, because multiple gene traits of environmental adaptiveness or immunology should be located in the same linkage group of genome.** The next article (biophysical simulation for blood cell division) further supports above theories (please note: the theory, 'memory' of gene expression, is also applicable on cell division in an individual) by assessment of resistance or immunology in host cells.

References:

[1]陶玲，任裙 （2004）。进化生态学的数量研究方法。第一章，第六节，第 49 页。中国林业出版社。ISBN：7-5038-3735-7。

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