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Article 11. Discussion on Gene Sequencing and Classification of DNA Genetic Markers

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Abstract

This article firstly critiques the DNA marker application on classification of genetic variation, and then the conceptions of gene recombination, gene communication and gene mutation are re-defined and re-classified.

Key words: DNA marker, Genetic Variation and Classification, Gene Recombination, Gene Communication, Gene Mutation.

1.Critical discussion of DNA marker application

Nowadays, for the analysis of genetic similarity in species or subspecies by DNA sequencing technology, the selected DNA sequence fragments from gene bank only reveals a small part of the genetic information compared with the total genetic information contained by the whole genomes. Therefore, the significant difference derived from very limited/bias genetic information is likely to be a misleading conclusion. There are several reasons:

First, using DNA sequence fragment primers to amplify the chemical reaction, the information obtained is only the repetitive primer sequences of gene fragments (such as SSR marker) and its relative molecular weighted among the total tested gene sequences in a experiment, but it does not reflect the spatial arrangement and combination information of various sequences on the genome. However, the arrangement and combination information of different gene sequences in the genomes is the main contribution factor of genetic variation, because most of the gene sequences revealed by DNA primers are highly conserved sequence fragments in the evolutionary process. Its own changes of DNA sequences are rare, which mainly depends on the change of arrangement and combination of various conserved sequences to achieve genetic variation in reproduction process for a population.

Secondly, in the past research, ovum cell and sperm cell are seldom separately distinguished to analyze each genetic contribution rate to their offspring. The

mass/weight of DNA molecules in egg cells is much larger than DNA in sperm cells, so the genetic contribution rate of maternal DNA to offspring DNA is significantly higher than that of sperm suppliers. Consequently, statistic classification of genetic variation must input this statistic factor to distinguish. In comparison, the genetic contribution rate of bio-electromagnetic waves (life signal waves) by sperm supplier to offspring is much higher than maternal parents (I have also discussed this in biophysics articles [2]).

Consequently, because the amount of genetic information tested by gene sequencing technology accounts for limited/bias proportion of the total genetic information of the genome, the significant difference in results reflected by multivariate statistics is likely to be a misleading conclusion, which may be corrected by molecular structural biology technology. My another article has further compared the DNA sequencing technology with the molecular structural biology in this theme [1].

Gene mutation is a common method for viruses to adapt to various environmental changes in population reproduction, and this change includes both biotic and abiotic environmental conditions. However, it is expected that only a small proportion of occurrences in gene mutation may be directly related to the pathogenicity of virus' invasive biology against host cells. Therefore, we should not overstate Big.

2.Gene recombination, gene communication and gene mutation

My another article has re-classified the conceptions among gene recombination, gene communication and gene mutation [1]: the DNA sequences in the gene pool are divided into two types for better understanding: one type contains the conserved and repeated DNA sequence regions, which are expressed as fundamental life functions, and the other is consisted of the DNA binding regions between these conserved DNA sequence regions, in which the DNA sequences are more active and irregular. In the conserved and repeated DNA sequence regions, the DNA sequences are highly stable in cell division process, and gene mutation seldom occurs. In comparison, gene mutation may occur more frequently in the DNA binding regions in cell division process. Gene recombination is considered as the spatial re-arrangement and re-combination between these conserved DNA sequence regions in cell division process. In the gene recombination process, cell mainly changes the DNA sequences in the binding regions, without altering the DNA sequences in the conserved and repeated DNA sequence regions during cell division process. In this way, cells pass on gene variation to offspring cells without significantly altering fundamental life functions expressed by the conserved DNA sequence regions (otherwise it may become the cancer cell). However, in the conserved and repeated DNA sequence regions, the DNA sequences can be commonly altered via gene communication between two parents in the sexual reproduction process.

Base on the new definition, it is to discuss different DNA molecular markers and gene

sequencing technology next:

For the genetic variation between individuals, it is advised to adopt Simple Sequence Repeats (SSR), whose primer initiates the synthesis of repeatitive and conserved sequence regions, because these conserved and repeated gene regions express as fundamental life functions. For other DNA molecular markers, the gene sequence regions initiated by the primers may be from the DNA binding regions, which are irregular (tend to be random sequences in cell division process within an individual) and do not determine the fundamental life functions, so the results of genetic variation classification may be less convincible.

Secondly, for these conserved and repeated gene regions, it is easy to identify the qualitative genes and quantitative genes separately. Obviously, the different repeated gene sequences between various conserved regions are the qualitative genes, expressed as different fundamental life functions, while the length/relative molecular weight of each repeated and conserved gene region is the quantitative genes. Correspondingly, these characteristics are consistent with the isozyme theory discussed by my another article [3]: the different functional groups between various isozyme families represent qualitative genes and the relative molecular weight of different enzyme species within an isozyme family is the quantitative gene. My article proposes that the relationship between conserved gene regions and corresponding isozyme expression is the main gene coding for fundamental life functions, rather than the irregular and random gene sequence regions.

For the results of gene sequencing technology, the gene sequences between each repeated gene sequence units do not have to be completely the same. For example, according to the gene sequencing results of TALIxoc gene region, in total 14.5 units of repeated gene sequence are found, but the gene sequences between these repeated gene sequence units are not exactly the same (more than 90% similarity) [4].

关键知识点译文：

1.DNA 标记技术应用的批判性讨论

如今应用 DNA 序列片段对各物种或是亚种进行遗传相似性的分析技术中，其中所选用的 DNA 序列片段与整个基因组遗传信息总量相比，仅仅为其中的非常有限或是偏差性的遗传信息，因此所得出的显著性区别很可能是一种误导性结论。有以下三点理由：

一、应用 DNA 序列片段引物进行扩增化学反应，所得到的信息仅仅是引物重复序列的片段（如 SSR 标记），但是没有反映出各种不同序列在基因组上的空间排列组合信息。而基因组上不同基因序列的排列组合信息为遗传变异特性的主要

贡献因子，因为 DNA 引物所揭示的基因序列中绝大部分序列为进化历程中高度保守的序列片段，极少发生 DNA 自身序列更改，主要依靠各种保守型的序列之间进行排列组合的变化产生遗传变异特性。

二、很少区别卵细胞与精子细胞分别对子代 DNA 遗传贡献率的区别。对于有性生殖的高等多细胞生物，卵细胞 DNA 质量远远大于精子细胞 DNA 质量，因此母系 DNA 对子代 DNA 的遗传贡献率要显著高于精子供应者。从而遗传变异特征的分类统计必须输入这个统计因子进行区分。相比而言，精子供应者对子代生命信号波（生物电磁波）的遗传相似性的贡献率会显著高于母系亲本代（本人在生物物理学论文中已经阐明[2]）。

三、由于所测试的遗传信息量占基因组遗传信息总量的比例很小或是偏差性的样本信息，以至于测试结果所反映出的显著性区别很可能是一种误导性结论，而这种误差可以通过结构生物学方法来更正。我的另一篇论文比较了基因测序技术与结构生物学方法之间的区别[1]。

四、基因突变是病毒在种群繁殖过程中为了适应多种环境变化的一种常用方法，这种环境条件变化既包括有生命的环境条件、也包括无生命环境条件。病毒基因突变发生量中仅仅有一小部分的概率会与与病毒入侵生理的致病性直接相关联。因此不应过分夸大。

2.基因重组、基因交流与基因突变

本人在另一篇文章中对基因重组、基因交流与基因突变的概念进行了重新定义和分类[1]。为便于阐释，可将基因库中的 DNA 序列划分为两类：一类为保守且重复的 DNA 序列区域，主要对应生命活动的基本功能；另一类为分布于上述保守 DNA 序列区域之间的 DNA 连接区段，其序列特征表现出更高的活跃性和不规则性。

在保守且重复的 DNA 序列区域中，DNA 序列在细胞分裂过程中通常具有较高的稳定性，因此基因突变较少发生。相较而言，DNA 连接区段在细胞分裂过程中更容易发生基因突变。基因重组可被理解为细胞分裂过程中各保守 DNA 序列区域之间在空间上的重新排列与再组合。在这一过程中，细胞主要改变的是连接区段中的 DNA 序列，而保守且重复 DNA 序列区域本身的序列通常不发生改变。通过这种方式，细胞一方面能够将遗传变异传递给子代细胞，同时由保守 DNA 序列区域所决定的基本生命功能不会产生显著影响（否则该细胞可能转变为癌细胞）。然而，在有性生殖过程中，借助双亲之间的基因交流，这些保守且重复的 DNA 序列区域中的 DNA 序列也能较为普遍地发生更改。

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