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Enzyme Engineering

Editorial

Finding Gene Mutations by the Enzyme: Chips for a Simple and Highly Sensitive Enzyme Mismatch Cleavage Method

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INTRODUCTION

Determination of unknown DNA variations is one of the substantive matters in many fields of molecular biology. Sanger sequencing has been used to the routine for this purpose. However, when you need to examine a large sized DNA or abundant samples, this method is bothersome, expensive and time consuming. Recently, Next Generation Sequencing (NGS) has been used in various purposes of mutation screening [1]. This massive sequencing technology is suitable for a scale of genome size screening, as well as to screen the list of genes that cause similar phenotypes, such as Maturity Onset Diabetes of The Young (MODY) [2]. If enough samples are gathered at once, NGS is a hopeful and fascinating strategy, because pooling of samples lowers the running cost per sample. But if you are intended to examine 1050 kb of DNA sequence by single experiment, you require an efficient and convenient screening method. Historically, Single-Strand Conformation Polymorphism (SSCP) and Hetero duplex Analysis (HA) were the most commonly used methods for this purpose [3]. But, the sensitivity of these methods was not satisfactory for the rigorous experiment. Although many of the modified PCR based mutation screening methods have been produced, none of these become popular due to the low sensitivity and/or inconvenience. Two modified methods of HA, Denaturing Gradient Gel Electrophoresis (DGGE) and Temperature Gradient Gel Electrophoresis (TGGE), were developed to enhance the migration delay of hetero duplex DNA in the gel by changing the gel component or temperature [4]. Subsequently, have insusceptible framework is to some degree sick pre pared to create a defensive enemy of tumor resistant reaction against most malignant growths. In any case, a huge advancement has been made in designing key parts of T cell invulnerability for creating a defensive enemy of tumor immunity. Although these methods potentially have an advantage over HA, they require special equipment for running or making the gel. Thus, these modified methods have not become as popular as the original HA. Denaturing High Performance Liquid Chromatography (DHPLC) is a type of mobility shift assay that does not involve electrophoresis, but instead detects mutations based on the decreased retention time of the hetero duplex in an HPLC column. Although this new technology achieves high sensitivity, time- consuming optimization of the mutation detection conditions for each DNA sequence is required to obtain the maximum sensitivity [4].

REFERENCES

1. Richardson C, Jull G, Hides J, Hodges P. Therapeutic exercise for spinal segmental stabilization in low back pain. London: Churchill Livingstone;1999.
2. Crisco JJ, Panjabi MM, Yamamoto I, Oxland TR. Stability ofthe human ligamentous lumbar spine. Part II: Experiment. Clin Biomech.7:27Y32, 1992.
3. Marshall PW, Murphy BA. Core stability exercises on and off a Physioball.ArchPhysMedRehabil.2005;86(2):242-9.
4. Akuthota V, Ferreiro A, Moore T, Fredericson M. Core stability exercise principles. Curr Sports Med Rep. 2008;7(1):39-44

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