

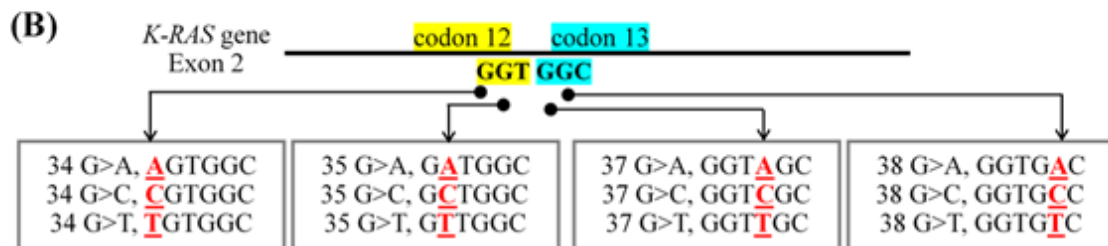
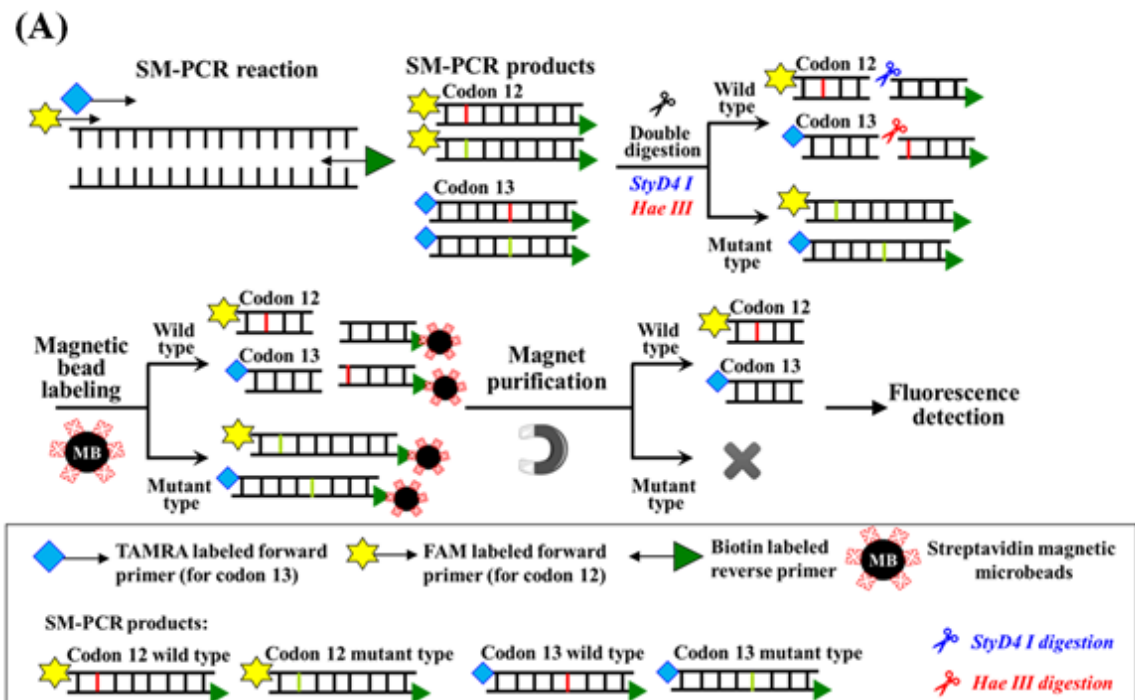


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- ▶ 以開發新穎分析技術為主，其研究內容包括線上濃縮毛細管電泳法開發、基因檢測方法開發、特殊引子及探針設計及應用、奈米粒子合成及應用等。

近幾年來，由於大眾開始對健康與預防醫學的重視，使得【基因檢測】成為相當被重視的國家發展主題與學術研究項目。基因檢測（Genetic Test）是偵測染色體結構中之 DNA 序列是否存在變異位點或探討基因的表現程度，提供受檢者與醫療研究人員評估一些基因遺傳相關疾病、體質或個人特質的依據，也是精準醫學檢測的一種方法。然而，現行基因檢測技術經常需要使用到一些昂貴耗材或大型儀器等，為了使得基因檢測技術更簡單、方便、準確且快速，實驗室開發了『單鹼基對錯配 PCR 技術搭配磁珠基因捕捉平台』，並應用於快速檢測 *K-RAS* 基因上之密碼子 12 和 13 遺傳變異，其檢測原理如圖形摘要所示。本方法於 PCR 之引子設計時，會於靠近基因變異處刻意設計 1 鹼基對與真實基因錯配，此錯配之引子將基因放大後，其基因序列即會含有錯配之鹼基對，之後應用 streptavidin 修飾之磁珠將此錯配鹼基對之放大基因片段捕捉與純化，最後即可利用錯配之鹼基對搭配所含之基因變異，設計限制酶酵素只將要分析的基因型放大片段分解。本研究成功得以單一技術同時分析 *K-RAS* 基因上之密碼子 12 和 13 上之 2 個基因變異點位，此方法方便、簡單且快速，且該方法具有通用性，只要設計適當的錯配引子及適合的限制酶酵素即可應用於不同基因之檢測，相當地適合應用於分析各種不同類型的基因變異。



StyD4I digestion HaeIII digestion

The mismatch of codon 12 primer Codon 12 Codon 13 The mismatch of codon 13 primer

ACTTGTGGTAGTTGGA **CC**↑**TGGTGG**↓**CC**TAGGCAAGAGTGCCTTG

ACGATACAGCTAATTCAGAATCATTTTGTGGACGAATATGATCCAACAATAG

AGGTAAATCTTGTTTAAATATGCATATTACTG

【具體成果】

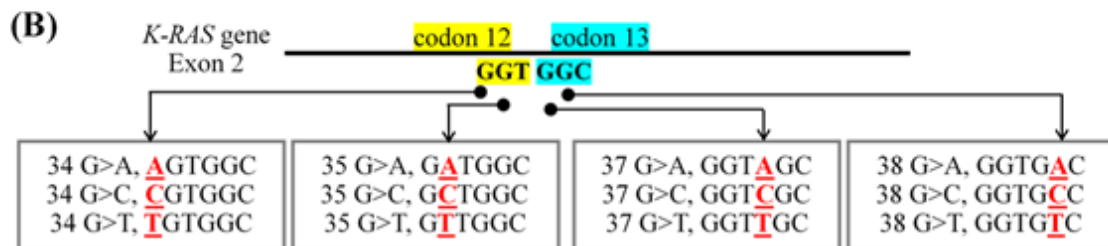
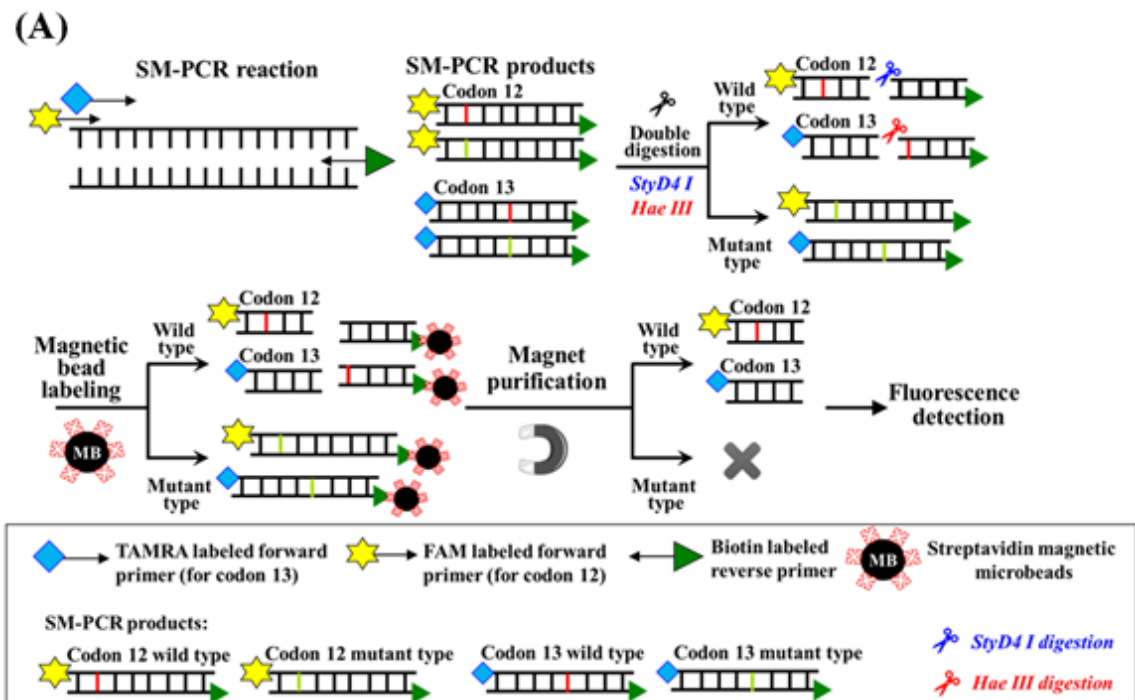
5 年內有多篇優質期刊發表，並擁有多國多項專利，且 2 項中華民國與美國專利正在申請中。



【研究團隊】王俊棋、柯黃盛、賴可朋、蘇郁晴

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In recent years, as the public has begun to pay more attention to health and preventive medicine, [genetic testing] has become a highly valued national development theme and academic research project. Genetic Test is to detect whether there are mutation sites in the DNA sequence in the chromosome structure or to explore the degree of gene expression. It provides subjects and medical researchers with a basis for evaluating some genetically related diseases, physical constitution or personal characteristics. It is also a method of precision medical testing. However, current genetic testing technology often requires the use of some expensive consumables or large instruments. In order to make genetic testing technology simpler, more convenient, accurate and faster, the laboratory developed "single base pair mismatch PCR technology with magnetic bead gene capture" Platform" and is applied to rapidly detect genetic variations in codons 12 and 13 of the K-RAS gene. The detection principle is shown in the graphical abstract. When designing primers for PCR, this method will deliberately design a base pair mismatch with the real gene near the gene mutation. After the mismatched primer amplifies the gene, the gene sequence will contain the mismatched base pair. Then streptavidin-modified magnetic beads are used to capture and purify the amplified gene fragment of the mismatched base pairs. Finally, the mismatched base pairs can be used to match the genetic variation contained in it, and restriction enzymes can be designed to amplify only the genotype to be analyzed. This study successfully used a single technology to simultaneously analyze two genetic mutation sites on codons 12 and 13 of the K-RAS gene. This method is convenient, simple and fast, and it is universal. As long as appropriate mismatch primers and suitable restriction enzymes are designed, it can be applied to the detection of different genes. It is quite suitable for analyzing various types of genetic variations.



StyD4I digestion HaeIII digestion

The mismatch of codon 12 primer

Codon 12 Codon 13

The mismatch of codon 13 primer

ACTTGTGGTAGTTGGA **C** **T** **GGTGG** **C** TAGGCAAGAGTGCCTTG

ACGATACAGCTAATTCAGAATCATTTTGTGGACGAATATGATCCAACAATAG

AGGTAAATCTTGTTTAAATATGCATATTACTG

Concrete Results: In the past 5 years, we has published many articles in high-quality journals, and has multiple patents in many countries, and 2 patents in the Republic of China and the United States are pending.

【Research Team】

Team Members: Chun-Chi Wang, Hwang-Shang Kou, Ke-Peng Lai, Yu-Chin Su



Research Team Introduction: This team focuses on developing novel analytical technologies. Its research content includes the development of online concentration capillary electrophoresis methods, the development of genetic detection methods, the design and application of special primers and probes, the synthesis and application of nanoparticles, etc.

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