出國報告（出國類別：參加國際學術會議）

第 51 屆流行病學研究學會年度會議
(Society for Epidemiologic Research 51st Annual Meeting)

服務機關：國防醫學院
姓名職稱：周雨青副教授
派赴國家：美國
出國期間：107 年 6 月 16 日至
107 年 6 月 23 日
報告日期：107 年 7 月 11 日

摘要

（200-300 字）

流行病學研究學會(Society for Epidemiologic Research, SER)於 1968 年建立，目的在培育流行病學研究，是北美洲最大且歷史最悠久的流行病學學會。每年舉辦的年度會議遍及美國、加拿大各地，而今年在美國巴爾的摩舉辦的是第 51 屆流行病學研究學會年度會議。每年大會固定舉辦四天，研討會節目表包括工作坊(workshops)、口頭報告(含 plenary and symposia)及海報展示(poster presentations)等，今年來自世界各地參加人員共計 1230 人，發表論文共計 893 篇。本人除了發表海報展示外，也聆聽了專題演講及幾個特定主題的研討會，這些聆聽對於我未來從事教學、研究工作，以及參與政府衛生政策工作的成效評估，都有莫大的啟發與幫助。感謝科技部提供經費，國防部核定公假，使我能夠吸取新知、標竿學習、並與國際接軌，也讓世界能夠看見台灣。

目次

本文

一、目的

本次參加國際學術會議最主要的目的是發表海報展示論文，我的題目是「 OAF 基因 DNA 甲基化是一個台灣大腸直腸癌新穎的生物標記：取自 3 個公用自料庫進行資料探勘所發現且經過甲基特異聚合酶連鎖反應所確認(OAF is a novel DNA methylation biomarker for colorectal cancer in Taiwan: data mining from three public databases and validated by methylation-specific PCR)」，此一題目是本人在執行科技部研究計畫(計畫名稱：國人大腸直腸癌分子流行病學研究：遺傳及外遺傳變異獨立與交互作用之探討；計畫編號：MOST 106－2314－B－016－018)的其中一項研究成果。其次為吸取新知並與國際接軌。

二、過程

本人於台灣時間6月16日晚上,自桃園國際機場搭乘中華航空前往美國,於美國時間 6 月 16 日晚上抵達洛杉磯國際機場並轉機，轉機後於 6 月 17 日上午抵達華盛頓杜勒斯機場，當日晚上抵達舉辦本次會議的飯店。由於是第一次來到美國參加學術研討會，擔心遲到或找不到場地，6 月 18 日用完早餐後，先行自會場了解每個口頭報告的場地、海報展示的場地、廠商展示的場地及報到的櫃台等，恰巧遇到小兒及孕產期流行病學研究學會(Society for Pediatric and Perinatal Epidemiologic Research,SPER)舉辦的年度會議，因此也逛了此一大會的會場，了解新知。6 月 19-22 日為正式會議期間，根據主辦單位統計，來自世界各地參加人員共計有 1230 人齊聚一堂，共襄盛舉，所有口頭報告及海報展示題目共計 893 篇，並匯集成一本厚度為 280 頁的論文摘要彙編，涵蓋的類別詳如下表所示。由於本人所發表的海報展示被主辦單位安排在第 1 展示區，於 6 月 19 日晚上七點至八點三十分，因此 6 月 19 日下午報到後，就立刻去張貼海報，並練習了幾遍。6 月 20、21 日早上聆聽了大型會議室的專題演講後，接著我就鎖定幾個有興趣的研討會聆聽，吸取新知、標竿學習並增廣見聞，晚上則是穿梭在海報展示會場，模仿學習、相互交流與請教學習。6 月 22 日搭機返回台灣，6 月 23 日早上抵達桃園國際機場。

Table. 2018 Abstract Categories

Aging	Molecular
Alternative Medicine	Neurology
Behavior	Nutrition/Obesity
Big Data	Occupational
Cancer	Other
Cardiovascular	Perinatal & Pediatric
Diabetes	Pharmacoepidemiology
Environment/Climate Change	Reproductive
Genetics	Respiratory
Global Health	Screening
Health Disparities	Social
Health Services/Policy	Substance Use
HIV / STI	Translational & Implementation Science
Infectious Disease	Women’ s Health
Injuries/Violence	
Men’ s Health	
Mental Health	
Methods/Statistics	

三、心得及建議

1.本人發表的研究主題主要是大腸直腸癌分子流行病學，然而海報展示當晚，針對此一議題，多半只能將自己的研究議題與來自世界各地的學者分享，接下來對方便沒有進一步的提問，可能是因為流行病學相當廣泛，所以議題多半相當特異，因此大多數的學者也都是來看看來自世界各地的學者都在關注哪些議題?而不會有進一步的討論。因此，本人特地也逛了一下海報展示的會場，真的沒有同是「大腸直腸癌分子流行病學」的研究議題。倒是聆聽了一些國外學者的海報展示報告，學習了他們的表達，展現了自信的一面，還是有很多值得學習的地方。

2.除了海報展示會場可以展現自我成果於國際舞台外，主辦單位安排於大型會議室的專題演講是一些流行病學前輩畢生奉獻在這個領域的心得及各小型會議室的專題報告是針對各個研究議題方法學的進展與評估(如：VIRTUOUS CIRCLES: NEW IDEAS AT THE INTERSECTION OF OBSERVATIONAL AND RANDOMIZED STUDIES 及 MISCLASSIFICATION OF UNDERREPRESENTED GROUPS: CARING ABOUT SMALLER CATEGORIES)，運用新穎的工具來評估流行病學研究(如：

MACHINE LEARNING IN EPIDEMIOLOGIC SCIENCE 及 BIG DATA IN EPIDEMIOLOGY: CHALLENGES AND OPPORTUNITES)，以及健康政策改變的評估(如：CHANGES IN UNITED STATES HEALTH POLICY: IMPLICATIONS FOR SUBSTANCE USE AND INJURY 及 PATTERNS, PREDICTORS, AND POLICY IN HIV/STI EPIDEMIOLOGY)。這些寶貴的聆聽對於我未來面對學生從事教學工作各面向的態度，研究工作的精進，以及參與政府衛生政策工作後的成效評估都有莫大的啟發與幫助。

3.本次會議除了我自己參加之外，本校公衛系暨研究所林老師及公衛所四位碩士班研究生共六人參加，且均有發表海報展示論文。來到會場除了遇到目前在哈佛大學從事博士後研究(本校公衛系 24 期畢業)的校友，也遇到同樣來自台灣的高雄醫學大學師生及國立成功大學醫學院附設醫院職業及環境醫學部醫師，大家都來到相同的會場發表研究成果，並與國際接軌，也讓國際能夠看見台灣，相信回到台灣後，我們會有更進一步的合作與交流。

4.非常感謝科技部核定的經費補助，使我能夠順利參加本次的國際學術會議，有機會面對面的分享研究成果，與相關領域的學者交流，並與國際接軌，對於往後的教學與研究工作都有相當程度的啟發與精進。

四、發表論文摘要

OAF is a novel DNA methylation biomarker for colorectal cancer in Taiwan: data mining from three public databases and validated by methylation-specific PCR

Yu-Ching Chou[1*], Fu-Huang Lin[1], Cheng-Wen Hsiao[2], Chien-An Sun[3], Chi-Hua Huang[1]

[1]School of Public Health, [2]Department of Surgery, Tri-Service General Hospital, National Defense Medical Center, Taipei, [3]Department of Public Health, College of Medicine, Fu-Jen Catholic University, New Taipei City, Taiwan
*Corresponding author: trishow@mail.ndmctsgh.edu.tw

Background: Colorectal cancer (CRC) has been a serious public health issue nowadays. Epigenetic alterations underlying the pathogenesis of CRC have been reported. It is imperative to develop new biomarkers to predict the occurrence of CRC. The purpose of this present study is to find novel genes having the potential utility of promoter methylation status to detect CRC risk.

Methods: Integrating three open source databases (Prediction of Clinical Outcomes from Genomic Profiles [PRECOG], Methylation and gene expression in Human Cancer [MethHC]

and University of California Santa Cruz [UCSC] Genome Browser), we selected the most influential genes as candidates. Subsequently, we recruited 134 CRC patients to verify the DNA methylation status of these candidate genes. OLIGO 7 primer analysis software was used to design and analyze PCR primers for adequate conditions. DNA promoter methylation status was performed using Methylation-Specific PCR (MS-PCR).

Results: We used PRECOG to select 763 genes which expression level in tumor tissues was disparate from normal ones, and to evaluate the methylation status of promoter in these genes by MethHC. Moreover, we used UCSC Genome Browser to verify whether the frequency of the CG rich sequence was higher than other regions. Based on the above steps, we found 69 influential genes. Considering cost and time, we randomly selected 5 genes from these 69 influential genes to do MS-PCR validation. Fortunately, one of the 5 genes named out at first homolog (*OAF*) can be detected in the biospecimens of CRC patients. The hypermethylation frequency of *OAF* promoter in tumor tissues was 47.8% significantly higher than 26.1% in normal ones (chi-square test, $p<0.001$).

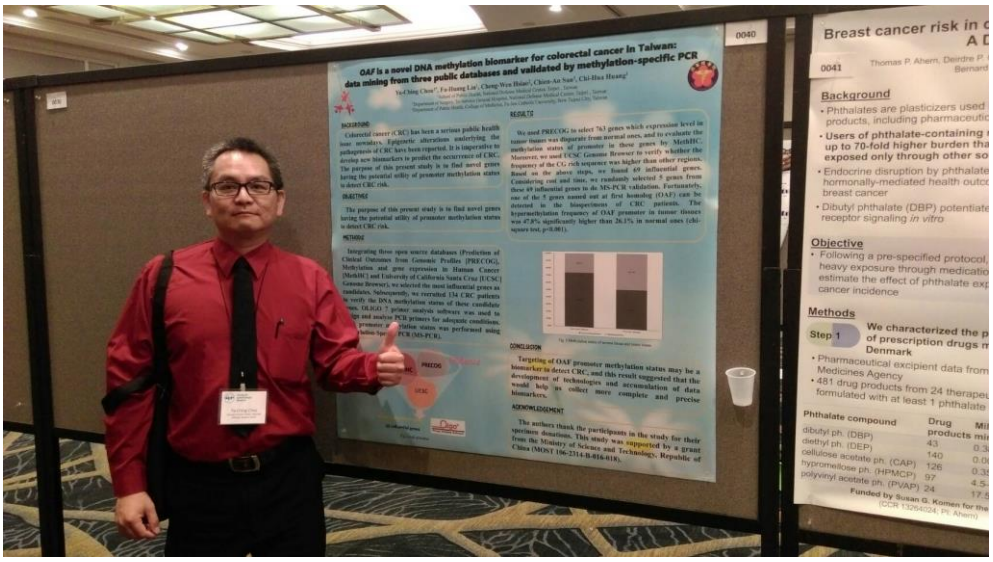
Conclusion: Targeting of *OAF* promoter methylation status may be a biomarker to detect CRC, and this result suggested that the development of technologies and accumulation of data would help us collect more complete and precise biomarkers.

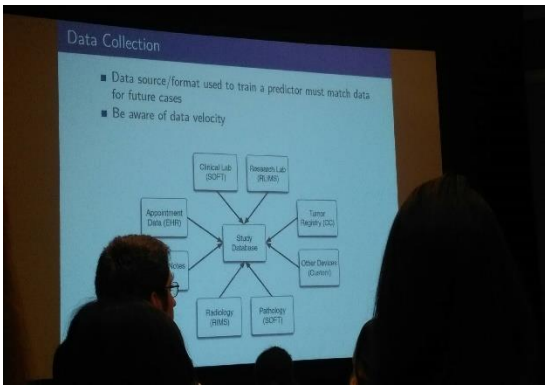
五、攜回資料名稱及內容

會議議程紙本 18 頁及自行網路下載 280 頁的論文摘要彙編(Abstract Book)。

六、其他(與會相關照片)


Factors to influence anxiety levels when facing medical problems in SDM participants
BACKGROUND
Society for Epidemiologic Research


OAF is a novel DNA methylation biomarker for colorectal cancer in Taiwan: data mining from three public databases and validated by methylation-specific PCR
Breast cancer risk in
Background
Objective
Methods


Data Collection
Data source/format used to train a predictor must match data for future cases
Be aware of data velocity
Clinical Lab (SOFT)
Research Lab (RLIMS)
Appointment Data (EHR)
Tumor Registry (CC)
Study Database
Other Devices (Cancer)
Radiology (RIMS)
Pathology (SOFT)

附錄

OAF is a novel DNA methylation biomarker for colorectal cancer in Taiwan: data mining from three public databases and validated by methylation-specific PCR

Yu-Ching Chou[1*], Fu-Huang Lin[1], Cheng-Wen Hsiao[2], Chien-An Sun[3], Chi-Hua Huang[1]
[1]School of Public Health, National Defense Medical Center, Taipei , Taiwan
[2]Department of Surgery, Tri-Service General Hospital, National Defense Medical Center, Taipei , Taiwan
[3]Department of Public Health, College of Medicine, Fu-Jen Catholic University, New Taipei City, Taiwan

BACKGROUND

Colorectal cancer (CRC) has been a serious public health issue nowadays. Epigenetic alterations underlying the pathogenesis of CRC have been reported. It is imperative to develop new biomarkers to predict the occurrence of CRC. The purpose of this present study is to find novel genes having the potential utility of promoter methylation status to detect CRC risk.

OBJECTIVES

The purpose of this present study is to find novel genes having the potential utility of promoter methylation status to detect CRC risk.

METHODS

Integrating three open source databases (Prediction of Clinical Outcomes from Genomic Profiles [PRECOG], Methylation and gene expression in Human Cancer [MethHC] and University of California Santa Cruz [UCSC] Genome Browser), we selected the most influential genes as candidates. Subsequently, we recruited 134 CRC patients to verify the DNA methylation status of these candidate genes. OLIGO 7 primer analysis software was used to design and analyze PCR primers for adequate conditions. DNA promoter methylation status was performed using Methylation-Specific PCR (MS-PCR).

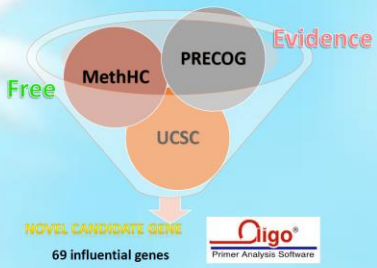


Fig. 1 study procedure

RESULTS

We used PRECOG to select 763 genes which expression level in tumor tissues was disparate from normal ones, and to evaluate the methylation status of promoter in these genes by MethHC. Moreover, we used UCSC Genome Browser to verify whether the frequency of the CG rich sequence was higher than other regions. Based on the above steps, we found 69 influential genes. Considering cost and time, we randomly selected 5 genes from these 69 influential genes to do MS-PCR validation. Fortunately, one of the 5 genes named out at first homolog (OAF) can be detected in the biospecimens of CRC patients. The hypermethylation frequency of OAF promoter in tumor tissues was 47.8% significantly higher than 26.1% in normal ones (chi-square test, $p<0.001$).

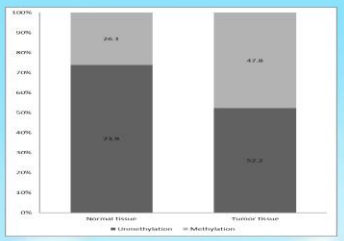


Fig. 2 Methylation status of normal tissue and tumor tissue

CONCLUSION

Targeting of OAF promoter methylation status may be a biomarker to detect CRC, and this result suggested that the development of technologies and accumulation of data would help us collect more complete and precise biomarkers.

ACKNOWLEDGEMENT

The authors thank the participants in the study for their specimen donations. This study was supported by a grant from the Ministry of Science and Technology, Republic of China (MOST 106-2314-B-016-018).