中文題目：台灣高流行率 PKD2 R803*突變

英文題目：High Prevalence of PKD2 R803* Mutation in Taiwan

作　　者：林穎志[1]黃道揚[2]

服務單位：高雄醫學大學附設中和紀念醫院內科部[1]腎臟內科[2]

Introduction：Autosomal dominant polycystic kidney disease (ADPKD) is the most common hereditary kidney disease. It has a prevalence of 1 in 400 to 1 in 1000 live births. We successfully developed a high-through put to analyze PKD1 and PKD2 mutations in our cohort.

Methods：A total of 170 families were analyzed in our cohort. A simplified long-range PCR was performed in the PKD1and PKD2. The products from each long-range PCR were combined and diluted as the template for the second multiplex PCR. Fluidigm 48.48. Access Array system was used to perform the second multiplex PCR followed by barcode PCR. A 2x300 MiSeq run contained 48 to 96 samples and the FASTQ data were analyzed by CLCbio Genomic Workbench. Microsatellite analysis of PKD2 region was performed in a total of six D4S regions. A 2-step PCR method was used with a universal fluorescence tag and data were analyzed by Peak Scanner 2 (Applied Biosystems).

Results：The PKD2 mutation represented 25% of our cohort, where the recurrent PKD2 R803* mutation accounted for 15% of KMU ADPKD cohort. Microsatellite analysis of the PKD2 region indicated at least two different but closely related PKD2 founders existed in the PKD2 individuals in Taiwan. Compound heterozygous PKD1 mutations were found in ADPKD individuals where hypomorphic mutation existed. De novo mutation was also identified in atypical ADPKD family without kidney disease history. The combination of a truncation mutation plus a hypomorphic mutation leaded to an early renal failure requiring renal replacement therapy.

Conclusion：The benefits of our method is a high-throughput and cost-effective method for mutation analysis in the ADPKD individuals. Our method can provided genetic study for all ADPKD individuals for prognosis estimation, genetic consultation, and personalized precision medicine.