

# Appendix I

## (Oral Free Paper Session)

### ORAL PRESENTATION 5:

#### **Clinical application of whole exome sequencing for paediatric undiagnosed diseases in Hong Kong – experience from first sixty cases**

Mak CCY, Chu YWY, Wong WL, Leung GKC, Chung BHY

Department of Paediatrics & Adolescent Medicine, LKS Faculty of Medicine, The University of Hong Kong, Hong Kong

#### **Background and aims**

By using next generation technology to sequence all the coding regions of the genome, whole-exome sequencing (WES) is now a more affordable and an increasingly important tool in diagnosing unsolved diseases. Worldwide, there has been growing collaborative efforts to solve rare and undiagnosed diseases using WES technology, with a diagnostic yield of up to 30%. We introduced the use of whole exome sequencing to paediatric patients with rare diseases in Hong Kong, and share our findings of the first 60 cases.

#### **Methods**

Sixty children with undiagnosed diseases referred to the genetics service in Queen Mary Hospital were recruited. These patients had all been assessed by a geneticist and genetic counsellor with conventional cytogenetic and molecular testing performed where appropriate. For those where a genetic diagnosis could not be obtained, the patients were offered singleton whole-exome sequencing. The results were validated and the relevant literature reviewed to determine the pathogenic nature of the mutation.

#### **Results**

A diagnostic rate of pathogenic causal variants was found in over 25% of patients, comparable to internationally reported figures. In addition to mutations in known rare diseases, we also discovered extended phenotypes of known syndromes and mutations contributing to newly described syndromes.

#### **Conclusion**

We share our experience in establishing WES as a useful tool for obtaining difficult diagnoses, as well as a valuable research tool to discover new genetic causes of rare diseases. The overall aim is not only to help more families to raise awareness and reach a diagnosis in the local population, but also to establish a pipeline to deal with the challenges of future application of next generation sequencing in the diagnosis of rare paediatric diseases.

#### **Acknowledgements**

*SK Yee Medical Research Foundation*

*The Society for the Relief of Disabled Children*