

Appendix I

(Oral Free Paper Session)

ORAL PRESENTATION 6:

Copy number variation in Hong Kong patients with autism spectrum disorder

Mak SL,¹ Leung GKC,² Mak CCY,² Chu YWY,² Mok GTK,² Tang TWF,³ Chan KYK,³ Kan ASY,³ Tang MHY,³ Lau ET,³ So KW,² Tao VQ,² Fung CW,^{2,4} Wong VCN,^{2,4} Lee SL,^{2,4} Chung BHY²⁻⁴

¹Department of Obstetrics and Gynaecology, Queen Elizabeth Hospital; ²Department of Paediatrics and Adolescent Medicine, Li Ka Shing Faculty of Medicine, The University of Hong Kong; ³Prenatal Diagnostic and Counseling Department, Tsan Yuk Hospital; ⁴Duchess of Kent Children's Hospital at Sandy Bay, Hong Kong

Background and aims

When offering chromosomal microarray for patients with autism spectrum disorder (ASD), as according to international standards, copy number variations of uncertain significance (CNV VUS) are frequently identified, which leads to challenges in genetic counselling. We aim to study the CNV findings in children with ASD in Hong Kong, and to gather information for reclassification of recurrent CNV VUS.

Methods

ASD patients from the Department of Paediatrics and Adolescent Medicine QMH/HKU were recruited if their Array Comparative Genomic Hybridization (aCGH) were done anytime from Jan 2011 to August 2014 in Prenatal Diagnostic Laboratory, Tsan Yuk Hospital. Diagnosis of ASD was made by developmental paediatricians and clinical psychologists using the criteria from Diagnostic and Statistical Manual of Mental Disorders, Fourth or Fifth Edition. NimbleGen CGX-135k oligonucleotide array and Agilent CGX 60k oligonucleotide array were used. Information was summarized from the literature and existing databases to re-classify CNV VUS occurring in our ASD cohort.

Results

Among 288 patients with ASD in our cohort, we identified 5 patients with pathogenic CNV (1.74%) and 5 patients with likely pathogenic CNV (1.74%). Among all the CNV VUS, one variant overlapping DPP10 (hg[19]chr2:116,534,689-116,672,358) was recurrently found in Chinese individuals. The frequency of this variant in our ASD cohort was 0.35% (1 in 288), and 0.96% (9 in 935) in our controls. ($P=0.467$, two-tailed Fisher's exact test). Similar CNVs were suggested to be ASD-related in previous studies recruiting mainly Caucasians. However, there were Chinese individuals with typical development possessing similar CNVs identified in independent sources (9 from our internal database, 1 from Singapore Genome Variation Project, 24 from The Singapore Prospective Study Program).

Conclusions

Our study explored the CNV findings in Hong Kong paediatric ASD patients. The CNV overlapping DPP10 may be a Chinese-related copy-number variation in Hong Kong Chinese, and we reclassified it to be likely benign in our locality. Our result emphasized the need to account for ethnicity to give the most precise interpretation of aCGH data.

Acknowledgements

The study was supported by SK Yee Medical Research Fund, SK Yee Medical Foundation and the Society for the Relief of Disabled Children, Hong Kong.