**Title: Diagnostic yield of Whole Exome and Whole Genome Sequencing in pediatric neurological disorders*. A UAE Tertiary hospital experience***

**Background and Objectives**

Whole exome (WES) and Whole genome (WGS) sequencing is becoming part of routine clinical and diagnostic practice in children with neurological disorders. The yield of WES and WGS critically depends on the characteristics of the patient population. Little is known about the diagnostic yield of WES and WGS in non-Caucasian populations.

**Methods**

We prospectively investigated the utility of WES and WGS in Emirati children presenting with undiagnosed neurological disorders where conventional genetic (microarray / gene panels) and metabolic testing were inconclusive. Clinical presentations were classified into five categories: isolated developmental impairment, epileptic encephalopathy, movement disorder, CNS malformation, and miscellaneous.

**Results**

A total of 84 children were identified (male, n = 47; female, n = 38) over a two-year period (2020 / 2021). Median age at time of inclusion was 19 months (Range 2 weeks – 18 years). 43% presented with developmental impairment, 21% with epileptic encephalopathy. CNS malformation and movement disorders comprised of 18% and 10% of cohort respectively. WES diagnostic sensitivity was 38% and additional yield with WSG was 23%, VUS of pathogenic significance were seen in 27% in our cohort and rtesting of WES added 10% additionally. Median Time to diagnosis was 8 months, consanguinity rate was high up to 61%, and 40% of them had positive family history of similar presentation. In our cohort we identified 6 novel genes.

**Conclusion**

Our study supports the clinical use of WES and WGS for children with neurological disorders to enable more accurate counselling regarding prognosis, recurrence risk, avoids unnecessary medical investigations and may change care in future. Additionally variants of pathogenic relevance from middle east population will allow to integrate new genomic data.