teratogenic factors playing a role. They can occur isolated or in association with multiple syndromes. Although common, there are few published studies focusing on the subject. The aim of this study is to describe the ocular anomalies found within a population of patients with OFC.

Methods A retrospective analysis of medical reports of patients that attended or are attending the clinic of Cleft Lip and Palate multidisciplinary group at Centro Hospitalar São João in Porto - Portugal over a period of 27 years between January 1992 and December 2018. OFC types were classified according to Spina classification: cleft lip (CL), cleft lip and palate (CLP), isolated cleft palate (CP) and atypical clefts (AC).

Results In total, 617 patients were included from which 106 (17.2%) had ocular anomalies, which were the most frequent type of anomaly within the study group; 58.8% were females. The most frequent ocular findings were myopia (30%), strabismus (21%) and astigmatism (14%). Other relevant findings were the presence of coloboma in 8.5%, short palpebral fissure in 8.5% and microphthalmia in 6.6%. Ocular anomalies were mostly related to CP (61.7%) followed by CLP (26.2%) and CL (10.3%). From the total sample of 106 patients, 70% had an identified syndrome, the most common being the Pierre Robin Sequence or Syndrome. Other systems were affected as well with 38% of patients showing other craniofacial anomalies and 39% cardiovascular anomalies.

Conclusions Ocular anomalies are frequent in the general population namely refractive errors such as myopia. Despite that, an important number of syndromes and congenital malformations are associated to ocular anomalies and OFC are among those. Although a significant number of patients with ocular anomalies were syndromic, not all OFC patients had other associated malformations. Therefore, awareness of the possible ocular malformations associated with OFC could provide a quick diagnosis and management of the affected patients.

P128 A RETROSPECTIVE AUDIT OF MICROARRAY TESTING PERFORMED IN THE DEVELOPMENTAL CLINIC AT A TERTIARY PAEDIATRIC CENTRE

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Background Array comparative genomic hybridisation (microarray) testing is a high resolution genetic test which detects microscopic and sub-microscopic chromosomal aberrations¹. In recent years, it has become the first line genetic investigation in children presenting to paediatric services with unexplained global developmental delay (DD), intellectual disability (ID) and autism spectrum disorders (ASD)^{1, 2}. Previous studies have shown that the diagnostic yield of microarray testing is between 15 and 20%².

Objectives The aim of this retrospective audit was to investigate the use of microarray testing of children presenting to a specialist developmental clinic, comparing the clinical indication against proposed national and international guidelines^{1, 2}, as well as, documenting abnormal results identified and their correlation with clinical phenotype with a view to refining the screening protocol.

Methods A total of 164 microarray tests performed on patients presenting to the clinic in 2017 were reviewed. The clinical indication prompting testing was documented. The

overall number of copy number variants in the population studied was determined and each CNV was characterised and its clinical significance assessed. All results had previously been disclosed to patients and families and all data anonymised.

Results The most common clinical indications for the 164 microarray tests included ASD, DD, and speech and language delay accounting for 99, 26, and 11 cases respectively. Other less common indications included gross motor delay, ID, and developmental coordination disorder (< 10). A total of 42 copy number variants were identified in 36 (29%) patients. Of the 42, 16 (9.8%) were associated with a previously documented genetic abnormality on the Online Mendelian Inheritance in Man database, 3 (1.8%) were variations of unknown significance and 23 (14%) were benign copy number variants (BCNV).

Of the 99 children with autism, 19 (19.2%) demonstrated a genetic aberration 8 (8.1%) of which were previously described on the OMIM database, 1 (1%) was a variation of unknown significance and 8 (8.1%) were BCNVs.

Conclusion Advances in genetic testing have transformed investigation in children with developmental abnormalities and there is an expectation that such investigations will be performed. Within the group of children with a diagnosis of autism, the explanation and understanding of the abnormality can be difficult. This presentation will explore further the clinical phenotype and genetic results of the children in this study with discussion regarding guidance for genetic testing in this patient group.

P129 RISK FACTORS FOR DEVELOPMENTAL DYSPLASIA OF THE HIP: 10-YEAR EXPERIENCE

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Aim Risk based screening for developmental dysplasia of the hip (DDH) with ultrasound is common. However, risk factors vary from one country to the other since data are insufficient to give clear recommendations. We aimed to evaluate the risk factors for developmental dysplasia of the hip (DDH).

Methods In this retrospective case-control study; the health records of all children, who were followed up between 2004 and 2014 at a well-child unit were investigated for the diagnosis of DDH. Of 9758 children, 57 children were found to have abnormal ultrasonographic findings and these constituted the case group. As the control group, healthy 228 children who matched the case children in birth months were selected. Two groups were compared for the risk factors.

Results A total of 19516 hips of 9758 children were examined for DDH. 97 hips of 57 children were found to have abnormal ultrasonographic findings (according to Graf classification). When the two groups were compared; breech presentation, multiple pregnancy and torticollis were identified as risk factors. The female sex was also found to have a significantly high prevalence among the children in the case group. Limited hip abduction, positive Ortolani and Barlow signs were important clinical findings in the case group.