performed in two steps; first on CAs previously associated with seaso-

nal factors and second on all remaining CAs. CAs and monthly births were calculated back to month of last menstrual period after which trigonometric regression analysis was performed to explore seasonal trends in CA prevalence.

Our dataset confirmed seasonality for Ebstein’s anomaly (p<0.05), tricuspid atresia and stenosis (p<0.05), congenital hydronephrosis (p<0.001) and hip dislocation (p<0.001) and a new signal was generated for seasonality of situs inversus (p<0.001). We detected non-significant seasonal peaks for neural tube defects (p=0.0683) and spina bifida (p=0.0507) coinciding with influenza season. We were not able to detect seasonality for any other CAs. We were unable to confirm the associations between neural tube defects, some other anomalies and influenza.

The associations detected and the negative results provided can help future studies unravelling the etiology of CAs.

MOLECULAR ETIOLOGY OF CHILDHOOD HEARING IMPAIRMENT ASSOCIATED WITH NON-SYNDROMIC ENLARGED VESTIBULAR AQUEDUCT IN SOUTHEASTERN CHINA

Molecular etiology studies of non-syndromic EVA will provide important data to facilitate DNA diagnosis and genetic counseling of this disease.

Methods Mutation screening of SLC26A4 was performed in 126 probands with non-syndromic EVA in Southeastern China. Those detected with mono-allelic or no SLC26A4 mutation were subjected to mutation screening of FOX11 and KCNJ10.

Results Bi-allelic, mono-allelic, and no SLC26A4 mutation were detected in 70.6%, 8.0% and 21.4% of the probands with non-syndromic EVA. Sixteen of the 40 SLC26A4 mutations detected were novel. While the c.919–2A>G mutation accounted for 41.3% of the novel mutations, the most significantly upregulated miRNAs were miR-548i (12.5 fold), miR-708 (10 fold), miR-181b (6.25 fold) and most downregulated miRNAs were miR-145 (~2.52 fold) and miR-640 (~2.3 fold) compared to control group in microarray profiling.

Conclusion The c.919–2A>G mutation of SLC26A4 is highly prevalent and should be the primary target of genetic testing for patients with non-syndromic EVA in Southeastern China. The spectrum of the other SLC26A4 mutations, however, is highly heterogeneous and differs from those reported in Taiwan or other regions of mainland China. Mutations in FOX11 or KCNJ10 were not the major cause of non-syndromic EVA in Southeastern China.

WHOLE GENOME MICRORNA EXPRESSION PROFILING IN CHILDHOOD ACUTE LYMPHOBlastic LEUKEMIA: A PROSPECTIVE EVALUATION

Whole genome microRNA expression profiling consisting of 1136 miRNAs was performed in peripheral blood and bone marrow samples of patients. Diagnosis, differential diagnosis, outcome and prognosis associated with aberrant microRNA expressions were prospectively evaluated.

The aim of the study is to evaluate the associations between microRNAs (miRNAs) and childhood acute lymphoblastic leukemia (ALL). Forty-three children with ALL and 14 age-matched controls were included in the study. Microarray expression profiling