P29 SINGAPORE CHILDHOOD CANCER SURVIVOR STUDY – A MULTI-INSTITUTIONAL COLLABORATIVE STUDY ON LONG-TERM SURVIVORS OF CHILDHOOD CANCER

L. Aung ^{a,*}, S.M. Sabai ^b, Y.H. Chan ^c. ^a Division of Pediatric Hematology-Oncology, KK Women's and Children's Hospital, Singapore. ^b Division of Pediatric Hematology-Oncology, National University Hospital System, Singapore. ^c Biostatistics Unit, Yong Loo Lin School of Medicine, National University of Singapore, Singapore

Background: Worldwide, survival rates among childhood cancer patients are increasing; thus, assessing the risk of late effects and complications is important.

Methods: The Singapore Childhood Cancer Registry (1981–2005) included 704 patients from KK Women's and Children's Hospital and 626 from the National University Hospital (NUH). The Singapore Childhood Cancer Survivor Study (SIN-CCSS) consisted of all individuals who survived at least 2 or more years after treatment for cancer diagnosed during childhood or adolescence.

Findings: A total of 1043 (72.4%) of 1440 patients are alive, of which 839 (80.4%) are long-term survivors. 58.6% (n = 492) survivors had haematological malignancies, whereas 41.4% (n = 347) were diagnosed with various solid tumours. To date, 79 survivors have enrolled in the study at NUH. Mean age was 14.9 years (range 4.9–31.8); 55.7% were male, 11.4% were an only child, 58.2% were Singaporean, and 74.4% were Chinese. 27.8% continued to see the doctor once or twice per year and 12.7% of these visits were related to previous illness. Preliminary analysis shows that 21.8% of participants reported anxiety. Endocrine adverse effects were most common (40.4%), followed by respiratory complaints (37.9%).

Interpretation: At least 58% of those diagnosed with childhood cancer are long-term survivors. This is the first study of its kind in Singapore, looking at long-term survivors of childhood cancer with a multicultural and multiethnic approach. In the future, we plan to focus on prevention of late effects, aetiological (genetic and environmental) and outcomes research, and survivor education.

Funding: Singapore Cancer Syndicate.

The authors declared no conflicts of interest.

doi:10.1016/j.ejcsup.2011.02.030

P30 MICRORNA AS DIAGNOSTIC AND PROGNOSTIC MARKERS IN HUMAN HEPATOCELLULAR CARCINOMAS

Y.-H. Huang ^{a,*}, C.-T. Yeh ^{a,b}. ^a Liver Research Center, Department of Hepato-Gastroenterology, Chang Gung Memorial Hospital, Taipei, Taiwan. ^b Molecular Medicine Research Center, Chang Gung University, Taoyuan, Taiwan

Background: Human hepatocellular carcinomas (HCCs) are the fifth most common malignant tumours worldwide, and the third leading cause of cancer-related death. In view of the high postoperative recurrence rate, identification of potential biomarkers should be considered; these can be a diagnostic marker, prognostic marker, or target for cancer therapy. MicroRNAs (miRNAs) have been proposed to contribute to oncogenesis because they can function either as tumour suppressors or oncogenes.

Methods To search the useful index marker to predict postoperative recurrence rate of patients with HCC, adjacent noncancerous liver tissues from HCC patients with good prognosis (n = 6) and poor prognosis (n = 6) were collected. 270 miRNA expression profiles were analysed using a highly sensitive stem-loop reverse transcriptase (RT)-PCR method.

Findings: 20 miRNA candidates were found that were association with good and poor prognosis. Further screening of 216 adjacent non-cancerous liver tissues identified six miRNAs significantly correlated with disease-free survival (p < 0.021). Cox proportional-hazards analysis revealed that high expression of miR-A6 and miR-A18 were the most significant markers associated with poor disease-free survival (p = 0.013, hazard ratio [HR] 1.633 [95% CI 1.108–2.408]; p = 0.001, HR 1.929 [1.298–2.867], respectively). High expression of miR-A3 and miR-A19 were the most significant markers related to better disease-free survival (p = 0.012, HR 0.431, 95% CI [0.224–0.830]; p = 0.001, HR 0.529, [0.357–0.783], respectively). Additionally, in J7 cells transduced with anti-miR-A6 lentivirus, cell-growth suppression was observed and cell-cycle related molecules, including CDK2, CDK4, cyclin E, and cyclin D1, were underexpressed.

Interpretation: miRNAs associated with good and bad prognosis can serve as biomarkers for HCC.

Funding: Chang Gung Medical Research Council.

The authors declared no conflicts of interest.

doi:10.1016/j.ejcsup.2011.02.031

P31 EXPRESSION OF NEUROENDOCRINE MARKERS IN NON-SMALL-CELL LUNG CARCINOMAS AND ASSOCIATION WITH POST-OPERATIVE SURVIVAL

N. Naseem ^{a,*}, A.H. Nagi ^a, N. Reyaz ^b, M. Ashraf ^b, W. Sami ^a. ^a University of Health Sciences, Khayaban-e-Jamia Punjab, Lahore, Pakistan. ^b Gulab Devi Chest Hospital, Lahore, Pakistan

Introduction: Neuroendocrine differentiation has been suggested as a marker of poor prognosis in 10–30% of non-small-cell lung carcinomas (NSCLCs). We studied immunohistochemical expression of the neuroendocrine markers chromogranin A (CgA), synaptophysin (SYN), histidine decarboxylase (HDC), and neuron-specific enolase (NSE) in various subtypes of NSCLCs, and noted whether there was any association with post-operative survival.

Methods: 225 patients (mean age 45 years) diagnosed with NSCLCs were surgically treated at Gulab Devi Chest Hospital, Lahore, Pakistan from January, 2004, to January, 2006. Relevant clinical and laboratory data including age, sex, tumour location, and type of surgical procedure were recorded in separate proformas. After haematoxylin and eosin staining, paraffin-embedded tissue blocks of tumour specimens were stained immunohistochemically with monoclonal anti-CgA, anti-SYN, anti-HDC, and anti-NSE antibodies. A total of 153 patients were followed up for 4.5 years, and the shortest follow-up time was 13 months. COX proportional-hazard multivariate analysis was applied to observe