is the first report of a PPTID in a patient with DICER1 syndrome. This association highlights the clinical implications of molecular evaluation in pediatric brain tumors, for both immediate therapeutic decisions and long-term surveillance.

## RARE-54. MOLECULAR ANALYSIS OF ROSETTE-FORMING GLIONEURONAL TUMOR AT MIDBRAIN; REPORT OF TWO CASES <u>Hajime Handa;</u> Kitasato University, Sagamihara, Kanagawa, Japan

Rosette-forming glioneuronal tumor (RGNT) is a tumor that primarily arises at posterior fossa. We experienced two rare cases of RGNT located at midbrain and investigated their molecular features. Case 1 is a 23-year-old female, and Case 2 is an 18-year-old male. Both cases were surgically removed by the occipital transtentorial approach. Histological analysis demonstrated a biphasic pattern of neurocytic and glial components. The former consisted of neurocytic rosettes and perivascular pseudorosettes, and the latter was GFAP positive, corresponding to the diagnosis of RGNT. Both cases have an excellent clinical course without receiving chemotherapy or radiation therapy. Small residual tumors of both cases shrunk and maintained for 27 and 12 months, respectively. Case 1 underwent DNA methylation array and a subsequent DNA methylation-based classifier, indicating that the case matched RGNT with a 0.99 calibrated score. Also, we identified FGFR1 K656 mutation. Pyrosequence analysis of other genes such as IDH1 R132, IDH2 R172 BRAF T599, BRAF V600, H3F3A K27, H3F3A G34, HIST1H3B K27, TERT C228, FGFR1 N546 had no mutations. RT-PCR of KIAA1549-BRAF fusion was not detected. DNA methylation status of Case 2 is under investigation. Pyorosequence analysis identified TERT C228 mutation but did not identify other mutations such as FGFR1 N546 and K656. Midbrain RGNT corresponds to the histological and molecular features of RGNT. RGNT needs to be differentially diagnosed in the case of a midbrain tumor.

## RARE-55. CHALLENGES AND SPECIFIC STRATEGIES FOR CONSTITUTIONAL MISMATCH REPAIR DEFICIENCY SYNDROME IN LOW RESOURCE SETTINGS. ON BEHALF OF THE INTERNATIONAL RRD CONSORTIUM IN LOW RESOURCE SETTINGS PANEL

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Germline biallelic mutations in one of the mismatch repair genes (MSH2/ MSH6/MLH1/PMS2 results in constitutional mismatch repair deficiency (CMMRD), a condition associated with multiple tumors arising from multiple organs during childhood, and these individuals rarely reach adulthood. The paucity of information with respect to these conditions leads to mismanagement and may be a factor in the high mortality of patients with CMMRD. Two international consortia, the European CARE4CMMRD, and the international replication repair deficiency (RRD) consortium, are addressing the many challenges associated with this condition. To address specific issues surrounding the management of CMMRD in low and middle income countries (LMIC), a multidisciplinary taskforce of 11 specialists from nine countries was formed. Preliminary conclusions are: 1) Immunohistochemistry for CMMRD should be considered for all patients with suggestive clinical features. In countries where CMMRD is common, malignant gliomas, colon cancers and T cell lymphomas should be stained routinely as the prevalence of CMMRD in these tumors can exceed 40%. 2) Temozolomide should not be used in the management of malignant glioma. By contrast, preclinical studies have suggested increased sensitivity to nitrosoureas. For the management of CMMRD related lymphoma and leukemia, mercaptopurines should not be avoided or discontinued as a part of the standard of care before more data are collected. 3) Management with checkpoint inhibitors should be limited to centers with intensive care units and expertise in complex supportive care to manage side effects of immune therapy. 4) Surveillance protocols have demonstrated long term survival benefits and should be implemented in LMIC.

## RARE-56. PERITONEAL SEEDING OF A DIFFUSE LEPTOMENINGEAL GLIONEURONAL TUMOR IN A CHILD

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Diffuse leptomeningeal glioneuronal tumors (DLGNT) are rare neoplasms of the central nervous system and have been included in the 2016 update of the WHO classification. This is the first description of a DLGNT disseminating to the peritoneal cavity via a ventriculoperitoneal shunt (VPS) in a child. We describe an 11-year old girl who received a VPS for a Dandy-Walker malformation at the age of seven, and was diagnosed with a spinal pilocytic astrocytoma with leptomeningeal metastases six months later. She received chemotherapy (SIOP-LGG protocol) with partial response, and had progressive disease eight months after therapy cessation. Following a novel biopsy, the diagnosis was revised to a DLGNT, with a KIAA1549-BRAF fusion and loss of 1p. She received vinblastine, but was clinically progressive and craniospinal radiotherapy was initiated. 13 months later, she suddenly presented with ascites. The inferior vena cava was compressed due to the ascites, and an abdominal drain was placed, with massive fluid release. Abdominal MRI indicated an omental cake and peritoneal contrast enhancement. Bone metastases were suspected in the iliac and femoral bones. Anatomopathological examination of the ascites showed an atypical cell population, with irregular, hyperchromatic and enlarged nuclei resembling the primary tumor. The cells were positive for synaptophysin, MAP2 and weakly positive for S100. Pan-NTRK staining was negative. The diagnosis of a metastatic localization of the DLGNT was made, due to seeding of tumoral cells via the VPS. Treatment with a MEK-inhibitor was initiated, but was stopped due to progressive disease and she died 3 weeks later.

## RARE-57. PEDIATRIC CHORDOMA: WHOLE EXOME SEQUENCING OF 11 PEDIATRIC CHORDOMA SAMPLES

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Chordoma is a rare tumor and while SMARCB1 alterations have been observed in poorly differentiated chordomas, conventional chordomas are not well understood. We interrogated nuclear and mitochondrial genomes of 11 chordoma samples from 7 children. Frozen tumor tissue DNA was extracted and whole exome libraries generated using Agilent SureSelect Human All Exon V6 kit plus mtDNA genome capture kit. Libraries were sequenced using Illumina Nextseq 500. MuTect2, VarDict and LUBA variant callers were used with allele frequency cutoff 2%. Potential germline variants were filtered bioinformatically. In total, 656±74 high-confidence somatic variants, including 368±43 nonsynonymous variants per sample were detected. Of 2,607 combined unique nonsynonymous variants, 95% were missense. Remaining high impact variants were frameshift (37%), stop gain (39%), splice acceptor/ dongr (22%) start and stop loss (2%). Of the unit donor (22%), start and stop loss (2%). Of the unique nonsynonymous variants, 137 fall within Cosmic Cancer Census Genes, including high impact variants in SETD2, MLLT4. No previously reported TBXT, CDKN2A, PI3K, LYST mutations identified. Tumor Mutation Burden/ Megabase was 10±1. The mitochondrial analysis revealed heteroplasmic m.11727C>T MT-ND4 missense variants in three tumors resected at different time points from the same patient, and another heteroplasmic m.1023C>T rRNA mutation from the primary and recurrent tumors of another patient. Intriguingly, two Children's Brain Tumor Tissue Consortium patients with chordoma had identical heteroplasmic m.10971G>A MT-ND4 nonsense mutations. Pediatric chordomas appear to lack somatic nuclear mutations. Observing recurrent mitochondrial mutations across multiple tumors from the same and/or different patients is striking, suggesting they may be implicated in tumorigenesis and be potential diagnostic markers.