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Pediatric brain tumor entities harbor a variety of gene fusions. Whilst other molecular parameters like somatic mutations and copy number alterations have become pivotal for brain tumor diagnostics, gene fusions are only less well covered by routinely applied methylation arrays or targeted next-generation sequencing of DNA. In a routine diagnostic setting we established and optimized a workflow for investigation of gene fusions in formalin-fixed paraffin-embedded (FFPE) tumor tissues by using RNA sequencing. Assessing different tools for calling fusions from raw data, we found relevant fusions in 66 out of 101 (65%) analyzed cases in a prospective cohort collected over 26 months. In 43 (43%) cases the fusions were of decisive diagnostic relevance and in 40 (40%) cases the fusion genes rendered a druggable target. Besides the relevance of pathognomonic fusions for diagnostics, especially the detection of druggable gene fusions yields direct benefit to the patients. This approach allows for an unbiased search for fusion events in the tested samples. Besides rare variants of established fusions which were not detected by prior targeted analyses, we identified previously unreported fusion events. Exemplified on KIAA1549:BRAF fusion, we in addition provide an overview of the detection accuracy of different methods, including breakpoint detection in DNA methylation array data and fusion gene detection in DNA panel sequencing data. Our data show that RNA sequencing has great diagnostic as well as therapeutic value by clinically detecting relevant alterations.

PATH-27. MUTATION DETECTION USING PLASMA CELL-FREE DNA IN CHILDREN WITH CENTRAL NERVOUS SYSTEM TUMORS

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BACKGROUND: The role of plasma cell-free DNA (cfDNA) as a cancer biomarker for tracking treatment response and detecting early relapse has been well described for solid tumors outside the central nervous system (CNS). However, the presence of a blood-brain barrier complicates the application of plasma cfDNA analysis for patients with CNS malignancies. METHODS: cfDNA was extracted from plasma of pediatric patients with CNS tumors utilizing a QIAmp® MinElute® kit and quantitated with Qubit 2.0 Fluorometer. Extensive genomic testing, including targeted DNA and RNA solid tumor panels, exome and transcriptome sequencing, as well as copy number array, was performed on matched tumor samples as part of the Texas KidsCanSeq study. An Archer® Reveal ctDNA28 NGS kit was then used for assaying the sensitivity of detecting tumor-specific mutations in the plasma of these patients. RESULTS: A median of 10.7ng cfDNA/mL plasma (Interquartile range: 6.4 – 15.3) was extracted from 78 patients at time of study enrollment. Longitudinal samples from 24 patients exhibited a median yield of 7.7ng cfDNA/mL plasma (IQR: 5.9 – 9.1). An initial cohort of 6 patients was identified with 7 somatic variants covered by the Archer® Reveal kit. Four of seven mutations identified in matched tumor specimens were detected in patient plasma at variant allele frequencies ranging from 0.2–1%. CONCLUSIONS: While challenging, detection of cfDNA in the plasma of pediatric patients with CNS tumors is possible and is being explored in a larger patient cohort along with pilot studies investigating cerebrospinal fluid as an additional source for tumor-specific cfDNA.

PATH-28. MOLECULAR DIAGNOSIS FOR CENTRAL DIAGNOSIS OF BRAIN TUMORS FROM 2016 TO 2019— A REPORT FROM THE JAPAN CHILDREN'S CANCER GROUP (JCCG)

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INTRODUCTION: Since 2016, the Japan Children's Cancer Group (JCCG) has established a nationwide network that prospectively provides pathological review and molecular analysis. METHODS: Patients who were diagnosed with brain tumors between ages 0 and 29 were eligible. The central office at National Center for Child Health and Development served as a hub for the hospitals involved and institutions conducting pathological and molecular analysis, and managed the patients' clinical information and tumor samples. Histopathology of all cases were centrally reviewed. Routine non-NGS based analyses were conducted based on histological diagnosis and included pyrosequencing for glioma-associated hot spot mutations and PFA/PFB classification for ependymoma, RT-PCR for RELA fusion and BRAF fusion, and nanostring for subgrouping medulloblastoma. In selected cases, methylation analysis, RNA sequencing and exon sequencing of 93 genes were performed in selected cases. RESULTS: In total, 985 cases were registered to this study in four years. Frozen samples were collected from approximately 80% of cases. The number increased from 152 in 2016 to 326 in 2019. They includes glioma (n=268), medulloblastoma (n=161), ependymoma (n=103), germ cell tumor (n=93), ATRT (n=29) and others. In 55 % of the glioma cases, at least one abnormality was detected by the routine analysis. The detailed analysis for atypical cases identified targetable alternations. DISCUSSION: This nationwide central diagnostic system has now been well established. Current issues and future prospective of the system will be discussed.

PATH-29. HIGH FREQUENCY OF CLINICALLY-RELEVANT TUMOR VARIANTS DETECTED BY MOLECULAR TESTING OF HIGH-RISK PEDIATRIC CNS TUMORS – PRELIMINARY FINDINGS FROM THE TEXAS KIDSCANSEQ STUDY

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BACKGROUND: DNA and RNA-based tumor sequencing tests have the potential to guide the clinical management of children with CNS tumors. However, data describing the utility of these tests are limited. METHODS: Children with high-risk or recurrent CNS tumors are included in the diverse cohort of patients enrolling in the KidsCanSeq study from six Texas sites. DNA and RNA from FFPE tumor is subjected to targeted sequencing using a 124-gene mutation panel and an 81-gene fusion panel. Tumor capture transcriptome sequencing, exome sequencing, and copy number array (as well as germline panel and exome testing) are also performed. Tumor variants are classified using AMP/ASCO/CAP consensus guidelines. RESULTS: A total of 74 children with high-risk/recurrent CNS tumors enrolled as of 1/28/20. Targeted tumor DNA and RNA panel testing was completed for 57 patients with varied diagnoses. At least one tumor variant with strong or potential clinical significance was identified in 43 of 57 (75%) tumors, with therapeutic significance in 20 of 57 (35%) tumors. The 38 therapeutically-relevant variants most frequently affected MAPK signaling (BRAF x9, EGFR x3, FGFR2, FGFR3, KRAS, NF1, NTRK2) and the AKT/mTOR pathway (PIK3CA x3, PTEN x2, mTOR, TSC1, PIK3R1). Most had not been detected by prior targeted diagnostic testing (27/38, 71%). CONCLUSION: Integrated DNA and RNA-based panel testing identified variants with potential to impact clinical decision-making in a majority of children with high-risk/recurrent CNS tumors. The comparative yield of panel testing vs. exome/transcriptome/array will be evaluated in the KidsCanSeq study cohort.

PATH-30. EXOSOMES AS A SOURCE OF PLASMA CTDNA TO IDENTIFY POINT MUTATIONS IN PEDIATRIC GLIOMA PATIENTS

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Surgery consists in the mainstay of treatment in most gliomas, but in many cases, a resection is not feasible. Liquid biopsy is an ideal tool providing a minimally invasive method through plasma or CSF sampling to assess cell-free tumor DNA (ctDNA). Here we explore the feasibility of detecting DNA in plasma exosomes (exoDNA) extracted from glioma patients and further investigate its use in identifying molecular alterations. Exosomes were isolated from 2ml of plasma from 24 patients (13 LGG, 8 HGG, 3 DIPG) and fully characterized by nanoparticle tracking analysis and transmission electron microscopy. DNA was extracted from 13 samples (exoDNA) so far. Five patients had confirmed point mutations in the primary tumor (3BRAFV600E; 1FGFR1N546K; 1H3.3), additionally, 3 samples were collected from clinically diagnosed DIPG patients to inquire H3K27M mutations. DNA was extracted successfully from all exosome samples; a pre-amplification step was needed and direct sequencing was carried out for BRAFV600E. FGFR1N546K and H3K27M mutations were sought in patients with positive tumors. Wildtype BRAF fragment was identified in 12/13samples (1 patient failed sequencing). However, none of the five tumor positive patients nor the DIPG patients had mutations detected at the exo-DNA level. There is growing evidence that CSF may be the ideal source of ctDNA in brain tumor patients, therefore although we could not detect mutations in plasma DNA we are currently analyzing CSF exoDNA and cell-free DNA to evaluate if this proves a successful strategy and weather exoDNA is more representative of the tumor content.

PATH-31. THE IMPACT OF MOLECULAR PROFILING OF PEDIATRIC CNS TUMORS ON TUMOR DIAGNOSIS AND MANAGEMENT - A SINGLE CENTER EXPERIENCE

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BACKGROUND: Next generation sequencing (NGS) plays a role in neuro-oncology research and in clinical diagnosis and management. Here, we describe how NGS for pediatric CNS tumors impacted clinical diagnosis and therapy at a single institution. METHODS: NGS was performed using the UCSF 500 Gene Panel (targeted sequencing platform covering about 500 cancer associated genes). Patients were selected for NGS based on tumor pathology /need to identify therapeutic targets. We collected data on patient demographics, tumor histology/pathway alterations/therapeutic targets/ therapy and used descriptive statistics for data analysis. RESULTS: Between January 2016 and July 2019, about one-third of patients with CNS tumors seen at our institution (N=29) were interrogated. NGS revealed pathway alterations in 20/29 patients. Treatment recommendations/modifications based on pathway alterations/therapeutic targets impacted the therapy of 18 patients. Patient groups: Medulloblastoma (N=6), alterations in WNT, SHH, and TP53 pathways (Vismodegib recommended for SHH pathway alteration but not used). **High-grade glioma** (N=4), alterations (with treatment changes) included, NF1(Trametinib, Everolimus); MSH2/ MLH1(Nivolumab); CDKN2A/CDKN2B/CDKN2C(Abemaciclib); EGFR (Osimertinib, Afatinib); H3K27M (Panobinostat/ONC201); BRAFV600 (Dabrafenib, Trametinib); **ATRT** (N=1) SMARCB1; Low Grade Glioma (N=10), BRAFV600(Vemurafenib) /BRAFKIAA1549 fusion (Trametinib)/ PIK3CA; **DIPG** (N=5), H3K27M/BCOR/ P53/ACVR/PIK3CA (LY3023414, Everolimus)/PDGFR(Dasatinib); Ependymoma (N=3), PFA/PFB/RELA Fusion. Seven patients were treated with targeted therapy + conventional therapy. In 8 patients targeted therapy remains an option but not yet needed. CONCLUSIONS: NGS of pediatric brain tumors is widely available and contributes to the diagnosis/therapy of pediatric CNS tumors. Optimal chemotherapy/targeted therapy combinations are areas of study.

NEUROPSYCHOLOGY/QUALITY OF LIFE

QOL-01. LONGITUDINAL COMPARISON OF NEUROCOGNITIVE TRAJECTORIES IN PEDIATRIC MEDULLOBLASTOMA PATIENTS TREATED WITH PROTON VERSUS PHOTON RADIOTHERAPY

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PURPOSE: By reducing dose to normal brain tissue, proton radiotherapy (PRT) may lessen neurocognitive risk traditionally associated with photon radiotherapy (XRT). We examined change in neurocognitive scores over time in pediatric medulloblastoma patients treated with PRT versus XRT. METHODS: Neurocognitive scores from 79 patients (37 PRT, 42 XRT) were examined. Patients were treated between 2007–2018 on the same treatment protocols that differed only by craniospinal modality (PRT versus XRT). Change in scores over time since diagnosis were compared between groups. RESULTS: Groups were similar on most demographic/ clinical variables: sex (67.1% male), age at diagnosis (mean 8.6 years), CSI dose (median 23.4 Gy), length of follow-up (mean 4.3 years), and parental education (mean 14.3 years). Boost dose ($p<0.001$) and margin ($p=0.001$) differed between groups. Adjusting for covariates, the PRT group exhibited superior outcomes in global IQ, perceptual reasoning, and working memory versus the XRT group (all $p<0.05$). The XRT group exhibited significant decline in global IQ, working memory, and processing speed (all $p<0.05$). The PRT group exhibited stable scores in all domains except processing speed ($p=0.003$). Posterior fossa syndrome imparted risk independent of modality. CONCLUSION: This is the first study comparing neurocognitive trajectories between pediatric patients treated for medulloblastoma with PRT versus XRT on comparable, contemporary protocols. PRT was associated with more favorable neurocognitive outcomes in most domains compared to XRT, although processing speed emerged as vulnerable in both groups. This is the strongest evidence to date of an intellectual sparing advantage with PRT in the treatment of pediatric medulloblastoma.

QOL-02. PERCEPTIONS OF LATE EFFECTS CARE NEEDS AMONG SURVIVORS OF PEDIATRIC BRAIN TUMOURS

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OBJECTIVES: Pediatric brain tumour survivors are at risk of long-term consequences of therapy. Comprehensive late effects care may mitigate these risks, but the best care model is unclear. We sought to describe the care experience and quality of life (QOL) of pediatric brain tumour survivors at the McMaster Children's Hospital joint adult/pediatric Neuro-Oncology clinic. METHODS: Cross-sectional survey data were collected. Care needs were assessed with the Cancer Care Experience Questionnaire (CCEQ), Cancer Worry Scale (CWS), and Self-Management Skills Scale (SMSS). Quality of life was measured utilizing the PedsQL Brain Tumor Module. Data were analyzed descriptively. RESULTS: Thirty-two childhood brain tumor survivors and/or their parents participated. Their malignancies included embryonal tumors (medulloblastoma/ATRT) (62%), ependymoma (22%), and germ cell tumours (16%). Among 77%, therapy included chemotherapy, surgery and radiation. Most respondents reported high quality cancer care, although some could not recall discussions of late effects risks and health promotion. Mean cancer worry scores were low (71.8 (± 28.4)). Survivors reported limited self-management skills (58.5 (±18.2)), with support required in clinic visits, arranging medical appointments, filling prescriptions and tasks of daily living. Overall median QOL scores were in the 'good' range (parental report 72.3 (±17.7), survivor 68.2 (±16.6)). CONCLUSION: In comparison to other childhood cancer survivor cohorts, this group of long-term brain tumour survivors appear to have similar QOL, fewer cancer worries, and increased need for aid with self-management. Given this, along with the positive care experience reported, this clinic model of care appears to meet the needs of this population.

QOL-04. INFLUENCE OF FAMILY, SCHOOL, AND HOSPITAL SYSTEMS IN SUPPORTING SURVIVORS OF PEDIATRIC BRAIN TUMORS WITH NEUROCOGNITIVE LATE EFFECTS

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OBJECTIVE: Pediatric brain tumor survivors (PBTS) are at risk for developing neurocognitive late effects that may interfere with academic and adaptive functioning. To mitigate the potential impact, some PBTS may implement strategies independently, while others may rely on system-level support from family, school, or hospital systems. Given the limited knowledge on survivor and family perspectives of these supports, we conducted a mixed-methods study involving PBTS and their caregivers to examine the