The consequences of SMARCB1 loss in Atypical Teratoid Rhabdoid Tumor (ATRT) have been extensively studied and cheapest tools. The concordance between the two expression-based profiling was 19/21. EPIC-arrays and RNAseq or Nanostring were concordant in 26/30 and 30/35 samples, respectively. The concordance was perfect for methylation-defined MYC subtype. Finally, 17/20 tumor samples classified by EPIC-array as IHC, 5/10 tumors classified as SMARCB1+ were SHH by methylation but consistently MYC by IHC. Nanostring and RNAseq. There was 90–100% of concordance for TYR subgroup (all techniques). We have designed a gene panel-based expression signature that shows promising concordance with RNAseq and methylation profiling. Nanostring assay and IHC will predict ATRT subgroup classification for MYC and TYR subclass, but less so for methylation-defined SHH ones.

ATRT-26. META-ANALYSIS OF TREATMENT MODALITIES IN METASTATIC ATYPICAL TERATOID/RHABDOID TUMORS IN CHILDREN

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BACKGROUND: Metastatic atypical teratoid/rhabdoid tumors (AT/RT) are aggressive central nervous system tumors that present during infancy and are associated with dismal outcomes. Patients receive multimodal treatment including surgical resection, systemic chemotherapy and one or more of radiation therapy (XRT), craniospinal irradiation (CSI), and autologous hematopoietic cell rescue (AuHCR). We performed whole-genome CRISPR/Cas9 screening we describe functionally essential SMARCB1 dependent pathway/membrane biomarkers, evident at the protein but not the RNA level. We describe several which are druggable and suggest certain therapeutic modalities e.g. specific combinatorial chemotherapy, Hematology, Immunology, Pathology, Developmental Biology, and Genetics.

METHODS: We performed whole-genome CRISPR/Cas9 screening we describe functionally essential SMARCB1 dependent pathway/membrane biomarkers, evident at the protein but not the RNA level. We describe several which are druggable and suggest certain therapeutic modalities e.g. specific combination chemotherapy.

RESULTS: Our analysis of the single nuclei obtained from the various single cell clusters and the data derived from single nuclei sequencing, found an OPC-like gene signature in ATRT-SHH. In contrast, ATRT-MYC and ATRT-TYR showed a profile consistent with glioblastoma with a high degree of intratumoral heterogeneity and the information on cellular subpopulations currently remains largely an unexplored territory. To explore the transcriptional landscape of ATRT, we performed single nuclei RNA sequencing for 16 ATRTs representing all three molecular subgroups (5 ATRT-TYR, 7 ATRT-SHH, 4 ATRT-MYC). By performing tSNE cluster analyses of all the single cell data (~50,000 cells) that were sequenced, we were able to gain unprecedented insights into the phenotypic composition of ATRTs and unravelled substantial differences between the three groups.

Integrating transcriptomic information from non-neoplastic brain cells and the data derived from single nuclei sequencing, we found an OPC-like gene signature in ATRT-SHH. In contrast, ATRT-MYC and ATRT-TYR showed a profile consistent with glioblastoma with a high degree of intratumoral heterogeneity and the information on cellular subpopulations currently remains largely an unexplored territory. To explore the transcriptional landscape of ATRT, we performed single nuclei RNA sequencing for 16 ATRTs representing all three molecular subgroups (5 ATRT-TYR, 7 ATRT-SHH, 4 ATRT-MYC). By performing tSNE cluster analyses of all the single cell data (~50,000 cells) that were sequenced, we were able to gain unprecedented insights into the phenotypic composition of ATRTs and unravelled substantial differences between the three groups. Integrating transcriptomic information from non-neoplastic brain cells and the data derived from single nuclei sequencing, we found an OPC-like gene signature in ATRT-SHH. In contrast, ATRT-MYC and ATRT-TYR showed a profile consistent with glioblastoma with a high degree of intratumoral heterogeneity and the information on cellular subpopulations currently remains largely an unexplored territory. To explore the transcriptional landscape of ATRT, we performed single nuclei RNA sequencing for 16 ATRTs representing all three molecular subgroups (5 ATRT-TYR, 7 ATRT-SHH, 4 ATRT-MYC). By performing tSNE cluster analyses of all the single cell data (~50,000 cells) that were sequenced, we were able to gain unprecedented insights into the phenotypic composition of ATRTs and unravelled substantial differences between the three groups.
with residual disease at diagnosis, 5 (36%) and 7 (50%), respectively, exhibited complete and partial response to induction. Three patients progressed on therapy, and six progressed after completion of therapy at a median of 9.7 months. In all, 18 patients completed RT (16 focal/4 CSI and 6 pre/12 post-consolidation). Three died of therapy-related toxicity (two in primary therapy and one in relapse therapy), and 8 died of disease. Sixteen patients (59%) are alive at a median follow up of 53 months (range 9–114). Of 17 with disease (47%) had thrusted predisposition syndrome whom of three are alive. At the time of presentation, data for approximately 50 patients is expected, and we will compare outcomes to soon-to-be-published data from ACNS0333.

ATRT-31. SUCCESSFUL MULTIVARIATE MODULARITY OF ATRT OF THE LOWER DORSAL SPINE WITH SPINAL DROP METASTASIS
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A 6 year old boy presented with low backache for the last 5 months. MRI of the spine showed a 1.5×1.5×7cm intradural mass extending from D10-D12, causing compression of the conus medullaris. With a preoperative diagnosis of intradural ependymoma, a gross total resection (GTR) of tumour was performed. Post-operative histopathology showed a markedly cellular, malignant tumour with frequent mitotic figures. To demonstrate its origin originating from the spinal cord, cells were subjected to polyclonal with vesicular nuclei, prominent nucleoli and were immunopositive for CK,EMA,p53 and immunonegative for MIC2,desmin,SMA,GFAP,NF1-p1 (MB1 labeling index:35–40%). The overall impression was spinal atypical teratoid rhabdoid tumour(AR/RT). Post-operative neuraxis MRI revealed post-operative changes(D10-D12) with a 9 mm enhancing lesion at L5-S1 junction suggesting drop metastasis. There was no brain lesion. CSF cytology did not show any malignant cell. The metastatic work-up was negative. He was started on chemotherapy with ICE regimen (etoposide-250mg/m2IVD1–D3,Carboplatin-500mg/m2IVD1, Etoposide-100mg/m2IVD1–D3q3weeks). Subsequently he received craniospinal irradiation (CSI)-36Gray/2fractions/4weeks→ focal boost to primary tumour bed and spinal drop metastasis-14.4Gray/8fractions/1.5 weeks. Thereafter he received 3 more cycles of ICE regimen. End-of-treatment MRI spine showed post-op changes(D10-D12) and 38.9% reduction of the L5-S1 lesion suggesting partial response. Six monthly spinal MRI showed serial reduction of the metastatic lesion, leading to complete resolution of the lesion on MRI. On follow up after 30 months from initial diagnosis, he was neurologically intact and in CR. Multimodality management comprising GTR,CSI followed by focal boost and multivariant chemotherapyc(ICE) can lead to successful outcome in patients with this rare and aggressive spinal tumour.

ATRT-32. GENOME-WIDE CRISPR AND SMALL-MOLECULE SCREENS UNCOVER TARGETABLE DEPENDENCIES IN AT/RTS
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Brain tumors are the leading cause of cancer-related deaths in children and adolescents. Embryonal brain tumors are a group of high-grade neuroepithelial tumors which primarily affect young patients, and atypical teratoid rhabdoid tumors (AT/RTs) are the second most common type of tumor within this group. In spite of intensive research efforts and the knowledge of molecular mechanisms driving subgroup-specific heterogeneity within ATRTs, survival estimates stay relatively low as compared to other tumor entities with a median survival of around 17 months. More efficacious and durable therapies are urgently needed to improve the situation of patients. We here used a combination of genome-wide CRISPR dependency screens and small-molecule drug assays to identify genetic vulnerabilities and novel therapeutic targets for this tumor entity. Here, we successfully generated a chemical library that shows preferential activity in AT/RT cell lines, thereby validating our CRISPR assay against a well-established TCGA gene expression dataset. Of note, non-viral reprogrammed rhabdoid tumors from patients had cell lines which were classifiable by methylation-based method. We are presenting here a rapid and accurate ATRT subclassification assay for clinical usage that is compatible with archived ATRT tissues.

COVID-19 AND PEDIATRIC NEO-ONCOLOGY

COVID-01. VINBLASTINE MONOTHERAPY INDUCTION FOR LOCALISED CNS GERMINOMA DURING THE COVID-19 PANDEMIC
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INTRODUCTION: Patients with localised CNS-germinoma have excellent survival. More recently, intensive inpatient chemotherapy (carboPEI=carboplatin/etoposide/dosfamide in Europe) has been employed to reduce radiotherapy fields and/or dose. Current research priorities focus on reducing treatment burden and long-term sequelae. Of note, outpatient-based single-agent carboplatin chemotherapy is associated with excellent outcomes in metastatic testicular seminoma (an identical pathology) [Altfrang,JCO,2020]. Recently, successful vinblastine monotherapy was reported in localised CNS-germinoma [Murray,Neurooncol-Adv,2020]. METHODS: Due to the COVID-19 pandemic, adapted UK guidelines for germ-cell-tumour management were distributed, including potential non-standard treatment options that would reduce inpatient visits/ admissions. A 30-year-old patient presented with a 32mm×30mm×35mm diameter solid multi- cystic localised pineal CNS lesion, consistent radiologically with a germ-cell tumour with prominent teratoma component. Investigation revealed negative AFP/HCG markers and biopsy-proven pure germinoma. After appropriate consent, the patient commenced 12-week induction with weekly vinblastine monotherapy (low-grade glioma dosing [Lasaleta,JCO,2016]), with wk6&12 MRI re-assessment prior to definitive radiotherapy. RESULTS: Vinblastine was well-tolerated. After initial 4mg/m2 test-dosing (wk1), standard 6mg/m2 was delivered for wk2, but reduced in asymptomatic neutropenia (nadir 0.3×109/l) and missed dosing at wk3. Subsequent doses were 4mg/m2, with no further neutropenia. As expected, MRI showed moderate 40% tumour volume reduction by wk12. Surgical resection of the residual preserved teratoma component was undertaken prior to radiotherapy. CONCLUSION: Patients with CNS-germinoma have excellent outcomes and reduction of treatment-effects remains a priority. The exquisite chemosensitivity of germinoma, excellent results from monotherapy for metastatic testicular disease, and early promise of vinblastine monotherapy lend itself to further exploration for CNS-germinoma.

ATRT-33. ENABLING RAPID CLASSIFICATION OF AT/RT WITH NONOSTRING NCOOUNTER PLATFORM
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In recent years, using gene expression and methylation array platform, multiple research groups have reported the presence of at least three major Atypical Teratoid Rhabdoid Tumor (ATRT) subtypes that exhibit distinct epithelial, transcriptomic and clinical features. Yet, utilizing ATRT subtypes in a clinical setting remains challenging due to a lack of suitable biological markers, limited sample quantities and relatively high cost of current assays. To address this gap between research and clinical practice, we have designed an assay that utilizes a custom 33 signature genes panel for the NanoString nCounter System and have created a flexible machine learning classifier package for ATRT tumour subtyping. We have analyzed 71 ATRT primary tumours with matching gene expression data using the 35 genes panel. 60% of the data was used for models training (10 repeats of 10-fold cross validation with subgroup balanced sample splitting) resulting in overall 94.6% training accuracy. The remaining 40% of the samples were used for model validation and the assay was able to achieve 92–100% accuracy with no subgroup intractability of the workflow, we have tested it against other transcriptome-based methods such as gene expression array and RNAsq. We have also demonstrated its use in samples that were not classifiable by methylation-based method. We are presenting here a rapid and accurate ATRT subtyping assay for clinical usage that is compatible with archived ATRT tissues.

COVID-02. COVID-19 AND CHILDHOOD CANCER CARE - THEMATIC ANALYSIS OF PUBLISHED SCIENTIFIC AND CLINICAL LITERATURE
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INTRODUCTION: The SARS-CoV-2 pandemic has affected modern medicine and healthcare provision profoundly. National and regional ex-