of Neuropathology, University Medical Center, Hamburg-Eppendorf, Hamburg, Germany

The classification of human brain tumors by global DNA methylation profiling has become an essential part of modern integrated neuropathological diagnostics. It has proven to reliably identify known and novel brain tumor (sub-)types that are biologically and clinically distinct. Therefore, this technique has critically improved diagnostic accuracy and risk stratification of brain tumor patients. Although indispensable for the understanding of tumor biology and for preclinical drug trials, the comparison of genetically engineered mouse models to human brain tumors is still difficult. The assessment of tumor morphology only provides an approximate picture, and transcriptomic data from human brain tumors are sparse and suffer from platform-related technical incomparability. Here, we show array-based DNA methylation profiling of well-established murine brain tumors, such as Wnt and Shh medulloblastoma, YAP and RELA ependymoma, ETMR, and AT/RT. Similar to human brain tumors, unbiased clustering methods revealed distinct methylation profiles and mean methylation levels for mouse brain tumors types. Analyses were possible for fresh-frozen as well as for paraffin-embedded tissue, and copy number alterations could be inferred from methylation profiles. Most importantly, first results suggest that interspecies comparisons allow the classification of brain tumors from known or novel mouse models based on the constantly growing spectrum of human brain tumor types and subtypes with hundreds of thousands of available datasets. As an example, upon DNA methylation profiling, cerebellar tumors arising in *Math1-cre::SmoM2Fl/+* mice display the highest similarity to human SHH medulloblastoma when compared to multiple human brain tumor entities including WNT and Non-WNT/Non-SHH medulloblastoma. These results suggest that global DNA methylation profiling may add another very important level of information to the characterization of genetically engineered mouse models.

PATH-05 CHALLENGE AND CLINICAL RELEVANCE OF A NON-MATCHING CLASSIFIER OUTPUT IN GENOME-WIDE DNA METHYLATION ANALYSIS FOR CNS NEOPLASMS IN PEDIATRIC AND ADOLESCENT PATIENTS

Richard Drexler[1], Alicia Eckhardt[2], Helena Bode[2], Katrin Lamszus[1], Manfred Westphal[1], Ulrich Schüller[2], Malte Mohme[1]; [1]Neurosurgery, Hamburg, Hamburg, Germany. [2]Research Institute Children's Cancer Center, Hamburg, Hamburg, Germany

OBJECTIVE: The molecular classification of CNS tumors has revolutionized our understanding of the biological heterogeneity and diversity of tumor subtypes. DNA methylation-based classification allows to discriminate subtypes. Although DNA methylation-based classification can diagnose tumors with high specificity, there are tumors which cannot be classified. We aimed to gain further insight into these challenging cases. METHODS: Overall, 21 patients with a CNS tumor that was non-classifiable (confidence score <0.3), or had a low confidence score (<0.9) using the DNA methylation-based classifier version 11b4, were included. Tumors were re-classified using version (v12.3), and clinical data were analyzed. RESULTS: A total of 21 pediatric and adolescent brain tumors with a calibrated score below 0.9 in the classifier output were identified. Of these, 11 patients (52.4 %) were assigned to the "no matching methylation class" with a score below 0.3. IDH-wild type glioblastoma (23.8 %), ETMR (14.3 %), and DMG (14.3 %) were the most common histological diagnoses. Surgical and clinicopathological features as well as DNA input and tumor purity did not influence the confidence score. Cases with non-classifiable tumors had a significantly longer time until a decision for adjuvant therapy (p<0.01). Application of the latest classifier version v12.3 led to a re-classification of 9 (42.9 %) cases, of which 5 cases (55.6 %) had an improved calibrated score. CONCLUSION: Our study presents unclassifiable cases and the possible clinical impact when waiting for the accurate diagnosis in these challenging cases. Even though DNA methylation profiling significantly contributes to advanced CNS tumor diagnostics, clinicians should be aware of a prolonged interval to treatment initiation, especially for highly malignant brain tumors. Therefore, we would recommend to schedule adjuvant treatment as early as possible, if surgical and histological results are suspicious for this disease.

PATH-06. MOLECULAR SUBGROUPING OF MEDULLOBLASTOMA VIA LOW-DEPTH WHOLE GENOME BISULFITE SEQUENCING

Dean Thompson[1,2], Jemma Castle[2], Debbie Hicks[2], Ed Schwalbe[1], Steve Clifford[2]; [1]Northumbria University, Newcastle upon Tyne, United Kingdom. [2]Newcastle University, Newcastle upon Tyne, United Kingdom

INTRODUCTION: International consensus recognises four molecular subgroups of medulloblastoma, each with distinct molecular features and clinical outcomes. Assigning molecular subgroup is typically achieved via the Illumina DNA methylation microarray. Given the rapidly-expanding WGS capacity in healthcare institutions, there is an unmet need to develop platform-independent, sequence-based subgrouping assays. Whole genome bisulfite sequencing (WGBS) enables the assessment of genome-wide methylation status at single-base resolution. To date, its routine application for subgroup assignment has been limited, due to high economic cost and sample input requirements. Currently, no optimised pipeline exists that is tailored to handle samples sequenced at low-pass (i.e., <10x depth). METHODOLOGY: Two datasets were utilised; 36 newly sequenced low-depth (10x) and 42 publicly available high-depth (30x) WGBS medulloblastoma samples (n=34), alongside cerebellar control samples (n=8), all with matched DNA methylation microarray data. We applied imputation to low-pass WGBS data, assessed inter-platform correlation and identified molecular subgroups by directly integrating WGBS sample data with pre-existing array-trained models. We developed machine learning WGBS-based classifiers and compared performance against microarray. We optimised reference-free aneuploidy detection with low-pass WGBS and assessed concordance with microarray-derived aneuploidy calls. RESULTS: We optimised a pipeline for processing, QC, and analysis of low-pass WGBS data, suitable for routine molecular subgrouping and reference-free aneuploidy assessment that achieves 96% sensitivity compared to microarray approaches. A pilot study of the suitability of FFPE was promising, and we demonstrate that WGBS data can be integrated into existing array-trained models with high assignment probabilities. Also, WGBS-derived classifier performance measures exceeded microarray-derived classifiers. CONCLUSION: We describe a platform-independent WGBS assay for molecular subgrouping of medulloblastoma. It performs equivalently to array-based methods at increasingly comparable cost ($400 vs $580) and provides a proof-of-concept for routine clinical adoption using standard WGS technology. Finally, the full methylome enabled elucidation of additional biological heterogeneity that has hitherto been inaccessible.

PATH-07. DIAGNOSTIC AND THERAPEUTIC VALUE OF CEREBROSPINAL FLUID BIOPSY IN PEDIATRIC BRAIN TUMORS

Shaoqun Li, Mingyao Lai, Linbo Cai; Guangdong Sanjiu Brain Hospital, Guanghzou, Guangdong, China

BACKGROUND: The application of cerebrospinal fluid (CSF) biopsy in brain tumors is valuable. This paper further explores the diagnostic and therapeutic value of CSF biopsy in pediatric brain tumors. METHODS: In this study, children with primary brain tumor aged ≤18 years old in Guangdong Sanjiu Brain Hospital were enrolled . CSF next-generation sequencing (NGS) tests were required for all included patients. The genetic mutations in these children were analyzed. RESULTS: A total of 12 pediatric brain tumors who underwent CSF NGS were included in this study. 9 patients were brainstem glioma and 3 were pilocytic astrocytoma. The mutated genes were detected in 67% (8/12) patients by CSF NGS. In brainstem glioma, the rate was 67% (6/9), and the most common genes were H3F3A (5/6, 83%) and TP53 (5/6, 83%). Other detected genes included EGFR, CDK4 and NF2. H3F3A mutation is of great significance for the diagnosis and treatment of brainstem glioma, and CDK4 and EGFR are valuable for the treatment. In pilocytic astrocytoma, the deteaction rate was 67% (2/3), and the genes included KIAA1549-BRAF fusion, FGFR1 and PTPN11 mutations. KIAA1549-BRAF fusion is of great value in the diagnosis and treatment of pilocytic astrocytoma, and FGFR is valuable in the treatment. CONCLUSIONS: Fluid biopsy of CSF for pediatric brain tumors may be an important supplement to histological diagnosis, especially when histopathology is not available. The results are significant for the diagnosis and treatment of pediatric brain tumors.

PATH-08. DNA METHYLATION PROFILING IMPROVES ROUTINE DIAGNOSTICS OF PAEDIATRIC CNS TUMOURS: A PROSPECTIVE POPULATION-BASED STUDY

Elizabeth Schepke[1,2], Maja Löfgren[2], Torsten Pietsch[3], Thomas Olsson Bontell[4], Teresia Kling[2], Anna Wenger[2], Sandra Ferreyra Vega[2], Anna Danielsson[2], Sandor Dosa[4], Stefan Holm[5], Anders Öberg[6], Per Nyman[7], Marie Eliasson-Hofvander[8], Per-Erik Sandström[9], Stefan M Pfister[10,11], Birgitta Lannering[12], Magnus Sabel[1,12], Helena Carén[2]; [11]. Childhood Cancer Centre, Queen Silvia Children´s Hospital, Sahlgrenska University Hospital, Gothenburg, Sweden. [22]. Sahlgrenska Centre for Cancer Research, Department of Laboratory Medicine, Institute of Biomedicine, Sahlgrenska Academy, University of Gothenburg, Gothenburg, Sweden. [33]. Department of Neuropathology, DGNN Brain Tumour Reference Centre, University of Bonn Medical Centre, Venusberg-Campus [1], Bonn, Germany. [44]. Department of Clinical Pathology and Cytology, Sahlgrenska University Hospital, Gothenburg, Sweden. [57]. Department of Paediatrics, Karolinska University Hospital, Stockholm, Sweden. [68]. Department of Women's and Children's Health, Uppsala University, Uppsala, Sweden. [79]. Department of Paediatrics, Linköping University, Linköping, Sweden. [810]. Department of Paediatric Oncology and Haematology, Lund University, Skane University Hospital, Lund, Sweden. [911]. Department of Paediatrics, Umeå University, Umeå, Sweden. [1012]. Department of Paediatric Haematology and Oncology, Heidelberg University Hospital, Heidelberg, Germany. [1113]. Division of Paediatric