

thin and is located near the edge of a gyrus. Ammon's horn is displaced and meandering. Subicular-like clusters are profuse. Complex gyri resemble microgyria. White matter forms a subpial border in some gyri. In summary: medial temporal lobe dysgenesis.

This individual also had many autistic features including stereotypies and head banging. The latter could explain another surprising set of brain abnormalities unrelated to the presumed FGFR3-related syndrome.

## LEARNING OBJECTIVES

This presentation will enable the learner to:

1. Summarize current theories on the pathogenesis of FGFR3-related cortical malformation
2. Describe the brain abnormalities in hypochondroplasia
3. Identify the neuropathology resulting from head banging

## ABSTRACT 9

### Area postrema: fetal maturation, tumours, vomiting centre, somatic growth and role in neuromyelitis optica

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The area postrema (AP) in the caudal 4<sup>th</sup> ventricular floor is unique, highly vascular without blood/brain or /CSF barrier. In addition to its function as the vomiting centre, several other important functions are: part of the circumventricular organs for vasomotor and angiotensin II regulation; a role in neuromyelitis optica related to aquaporin-4; contributor to fetal and postnatal somatic growth. Functions are immature at birth.

The purpose of this study was to demonstrate AP neuronal/synaptic/glia maturation in normal fetuses and 3 AP tumours. Transverse sections of the caudal 4<sup>th</sup> ventricle of 18 normal human fetal brains at autopsy, 6 to 40 weeks were examined; also 3 infants 3-18mos; 2 children. A battery of immunocytochemical neuronal and glial markers: MAP2; calretinin; synaptophysin; vimentin; nestin; GFAP; S-100 $\beta$  protein; were applied to paraffin sections. Two children with AP tumours and one with neurocutaneous melanocytosis, all with pernicious vomiting, were studied. In normal fetuses, AP neurons exhibited cytological maturity and well-formed synaptic circuitry by 14wk gestation. Size/volume increase was disproportionately greater than brainstem growth in 2<sup>nd</sup> and 3<sup>rd</sup> trimesters and postnatally. Astrocytes co-expressed vimentin/GFAP but glia were best demonstrated by S-100 $\beta$  protein. Ependyma over the AP in fetuses is simple cuboidal, adjacent to pseudostratified columnar of the 4<sup>th</sup> ventricular floor. Melanocytes infiltrated AP in the toddler with pernicious vomiting; 2 children had primary AP pilocytic astrocytomas. Though AP is cytologically mature by 14wk, growth increases and functions mature into the postnatal months. We recommend that AP neuropathology include synaptophysin and S-100 $\beta$  at autopsy if AP dysfunction suspected.

## LEARNING OBJECTIVES

This presentation will enable the learner to:

1. Explain the maturation of neurons, synaptic circuits and glial elements of the AP
2. List and recognize tumours that can affect the area postrema
3. Describe functions of the area postrema

## ABSTRACT 10

### Human brain atlas: miRNA version

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Human brain is a complex organ comprising multiple cell types of differing function. Although histological evaluation remains the mainstay approach for evaluating tissue, comprehensive molecular characterization is now possible due to advanced -omic approaches. microRNAs (miRNAs) are small (~22 nt) RNA molecules that regulate gene expression and mediate cellular differentiation in normal brain development. miRNAs also make excellent tissue markers due to their abundance, cell-type and disease-stage specificity, and stability in solid/liquid clinical samples. To advance our knowledge of miRNA-mediated gene regulation in human brain, we generated comprehensive miRNA expression profiles from 117 fresh normal brain samples through barcoded small RNA sequencing; tissues included neocortex, allocortex, white matter, cerebellum, olfactory bulb, optic nerve, pineal gland and spinal cord. FASTQ sequence files were annotated using state-of-the-art sequence annotation available through the Renwick lab. Following data pre-processing, high expression analysis of miRNA profiles showed that miR-9 was the highest expressed miRNA in neocortex, cerebellum and olfactory bulb, whereas miR-22 was highest expressed in cingulate cortex, optic nerve and spinal cord; interestingly, miR-29 was the highest expressed miRNA in hippocampus. Our analyses showed a trend towards unique miRNA signatures in different anatomical areas of the brain. Our next step is to perform miRNA fluorescence *in situ* hybridization on formalin-fixed paraffin-embedded tissues using a novel method developed in the Renwick lab. Accurate miRNA characterization of normal tissues will provide a firm basis for understanding miRNA changes in neurological diseases.

## LEARNING OBJECTIVES

This presentation will enable the learner to:

1. Describe the function of miRNAs and their suitability as tissue/cell specific signatures
2. Describe the miRNA expression trends in profiling various anatomical regions of the central nervous system

## ABSTRACT 11

**Image Analysis in Neuropathology: Hue-Saturation-Intensity vs. Colour Deconvolution**

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As image analysis expands into clinical and basic applications it is important that users be aware of opportunities and limitations. A common image analysis workflow involves the digitization of stained tissue sections into a red-green-blue (RGB) colour model for quantitative interpretation. Upstream of the digital image, quality and variability can be degraded at each step (tissue handling, fixation, sectioning, staining, image acquisition). Digital image analysis presents additional steps where variables can affect data quality. Image analysis platforms are not uniform. Aside from interface preferences, some introduce unintended variability due to their processing architecture that may not be obvious to the end-user. One important component of this is colour space representation: hue-saturation-intensity (HSI) vs. colour deconvolution (CD). A potential weakness of analyses within the HSI colour space is the mis-identification of darkly stained pixels, particularly when more than one stain is present. We were interested to discover whether HSI or CD provided greater fidelity in a typical immunoperoxidase/hematoxylin dataset.

Fifty-nine samples were processed using HSI- and CD-based analyses. Processed image pairs were compared with the original sample to determine which processed image provided a more accurate representation. CD proved superior to HSI in 94.9% of the analyzed image pairs. Where the option exists, CD-based image analysis is strongly recommended.

## LEARNING OBJECTIVES

This presentation will enable the learner to:

1. To describe differences between HSI and CD colour spaces
2. To explain limitations in the use of HSI-based analyses
3. To be aware of recent developments in CD-based platforms

## SESSION 3: Tumour neuropathology

## ABSTRACT 12

**NTRK2 Fusion Driven Pediatric Glioblastoma: Identification of key molecular drivers by personalized oncology**Levine<sup>1</sup>, Y Shen<sup>2</sup>, K Mungall<sup>2</sup>, J Serrano<sup>3</sup>, M Snuderl<sup>3</sup>, E Pleasance<sup>2</sup>, SJM Jones<sup>2</sup>, J Laskin<sup>2,4</sup>, MA Marra<sup>2</sup>, R Rassekh<sup>5</sup>, R Deyell<sup>5</sup>, S Yip<sup>1</sup>, S Cheng<sup>5</sup>, C Dunham<sup>6</sup>

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We describe the case of an 11-month-old girl with a rare cerebellar glioblastoma driven by a *NACC2-NTRK2* (Nucleus Accumbens Associated Protein 2-Neurotrophic Receptor Tyrosine Kinase 2) fusion. Initial workup of our case demonstrated homozygous *CDKN2A* deletion, but immunohistochemistry for other driver mutations, including *IDH1* R132H, *BRAF* V600E, and *H3F3A* K27M were negative, and *ATR*X was retained. Tissue was subsequently submitted for personalized oncogenomic analysis, including whole genome and whole transcriptome sequencing, which demonstrated an activating *NTRK2* fusion, as well as high PD-L1 expression, which was subsequently confirmed by immunohistochemistry. Furthermore, *H3* and *IDH* demonstrated wildtype status. These findings suggested the possibility of treatment with either NTRK- or immune checkpoint- inhibitors through active clinical trials. Ultimately, the family pursued standard treatment that involved Head Start III chemotherapy and proton radiotherapy. Notably, at most recent follow up approximately two years from initial diagnosis, the patient is in disease remission and thriving, suggesting favorable biology despite histologic malignancy. This case illustrates the value of personalized oncogenomics, as the molecular profiling revealed two actionable changes that would not have been apparent through routine diagnostics. *NTRK* fusions are known oncogenic drivers in a range of cancer types, but this is the first report of a *NACC2-NTRK2* fusion in a glioblastoma.

## LEARNING OBJECTIVES

This presentation will enable the learner to:

1. Explore the current molecular landscape of pediatric high grade gliomas
2. Recognize the value of personalized oncogenomic analysis, particularly in rare and/or aggressive tumors
3. Discuss the current status of NTRK inhibitor clinical trials

## ABSTRACT 13

**Update on the national survey on molecular diagnostics in CNS tumors**

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There have been significant changes in the diagnostic criteria for diffuse gliomas in the 2016 WHO CNS tumor classification, with the incorporation of molecular criteria into a number of definitions. This has placed a greater emphasis on the availability of key immunohistochemical and molecular tests. In order to determine the effect that these changes have had on