

Genome dynamics and phylogenetic tracking in paired diagnostic Cancer Research and relapsed neuroblastomas

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Key Terms MYC-N amplification – Myc-n is a gene that regulates the expression of many other genes that affect the hallmarks of cancer, and in high risk neuroblastoma this gene is often overexpressed.(1) Copy number abnormality (CNA) – a type of structural variation where sections or entire chromosomes exist in multiple copies, and this can affect prognosis of disease. Copy neutral loss of heterozygosity (CNLOH) - two copies of the same chromosome are inherited from one parent with no copy from the other parent, so total number of chromosomes appears norma Chromothripsis – a single event during which thousands of rearrangements at one time in certain regions of a single chromosome, which has been indicted in some cancers. Variant/ single nucleotide polymorphism (SNP) – a change in a

gene that is not prevalent within the majority of the population, and may be associated with disease or predisposition to disease. <u>Gene cluster – A group of genes that are responsible for producing</u> similar proteins that together complete a generalised function.

Neuroblastoma

Neuroblastoma is a cancer of the sympathetic nervous system, and so tumours are found in various regions of the body where certain nervous tissue grows. Tumours are often found in the adrenal glands, neck, chest, abdomen or spine. Symptoms can involve bone pain, abdominal or other site swelling, constipation, weakness due to spinal cord compression, bruising around the eyes, and anaemia.



Methods

Tumours obtained from Children's Cancer & Leukaemia Group (CCLG) Tumour Bank. Aliquots were cut prior to extraction in the lab.

Case 2

High dose chemotherapy and post chemotherapy tumour

<u>P28</u>

11/1997

04/1998

07/1998

obtained

05/2009

paraesthesia and unsteady gait

Induction chemotherapy treatment began

•Surgical resection of primary tumour

Existing genetic data (whole exome sequencing and SNP arrays) was analysed using specialised software (Nexus and IGV) and results were

Tumour samples selected due to clinical interest in the atypical relapse(s). Comparative analysis was undertaken to identify novel or confirm known variants/copy number aberrations.

Case Findings

- Cases showed many chromosomal abnormalities that were present at diagnosis and at relapse
- Case 1 showed three new genetic variants at relapse that may be of importance; IGFN1, NBPF1 and NBPF10. All three were missense variants on chromosome 1, NBPF genes are in the neuroblastoma
- break point family of genes, which have been previously indicated in the cancer.
- Case 2 also showed missense mutations in IGFN1 and NBPF10 and NBPF20. NBPF10 was a variant detected throughout every time point, and IGFN1 was detected post chemo and at both relapses. KMT2B, ATP11B and RORA genes were relapse specific.
- Case 3 showed relatively fewer variants of note, including PCDHB6 and KMT2C missense variants, both of which were relapse specific.
- Both cases for which CNA data was available showed substantial chromosomal abnormalities present from diagnosis that then persisted through to relapse. Both cases showed 1p loss, 7q gain, 11q loss and 17q gain from diagnosis to relapse.

blue cells with Homer-Wright rosettes that indicate neuroblastic tumour cells

Characteristic round

http://www.pathologyoutlines.com/topic/adre nalneuroblastoma.html

 Neuroblastoma (NB) is the 2nd most common solid tumour in children, though in comparison to other childhood cancers, it disproportionately accounts for 15% of paediatric cancer deaths(1).

Introduction

- ▶ Risk stratification informs treatment, and high risk features include: >18 months of age, unfavourable genetics and pathology, metastatic or unresectable disease due to proximity to major structures. ▶ High risk groups have survival rates as low as 50%, and relapse is
- frequent, often occurring in 1-2 years after treatment and rarely >5 years later. Relapse is associated with poor prognosis, and survival beyond 1-3 years is rare.
- ▶ For this study, particular cases have been selected for genetic analysis due to their atypical relapse time, some of which have occurred up to 18 years later to better understand the changes that may lead to late relapse.

Aims

- extract, quantify and analyse genetic data from frozen ► To tumours and combine the quantitative data with clinical notes to develop a timeline of genetic events.
- To determine the genetic differences between diagnostic and relapsed tumours to identify potential variants and CNAs that



Time point Location D, PC, R1, Chr1:145297661 Missense R2 D chr19:36,208,921 Missense 36,229,779 •Presented age 4 years with polyuria, back pain, perineal PC, R1, R2 chr1:201178660 **IGFN** Missense R1, R2 Chr1:148344644 Missense Thoracic tumour found and diagnostic sample obtained R2 chr3:182554200 ATP11 Missense R2 chr15:60793202 Missense

> As the table shows, these variants are genes that showed at particular time points that may be targetable in the future

> > •This image of the Nexus Biodiscovery software shows the patient's copy number aberrations, at diagnosis and relapse 1, which can be compared with the Venn diagram.



+1q

-14p

Relapse specific CNAs were also prevalent, both cases showing changes to 1q, 13p and 14q. However, there were no specific gains or losses shared by both.

Conclusions and discussion

Copy number abnormalities were similar to those documented in literature, though it is interesting that certain abnormalities such MYC-N amplification which is as associated with relapse and high risk disease (2), were not seen in high frequencies in the cohort. This could indicate that late or atypical relapse may not have the same pathophysiology as the relapse often associated with MYC-N amplification, which could be explored to inform treatment of a potential new sub

- ▶ 11q deletion which is associated with high risk disease was found in both cases for which CNA data is available.
- ► *NBPF* gene variants were identified in 2

may have lead to atypical/late relapse(s).

cases to have persisted from diagnosis to relapse. Variations in this gene family have only been briefly described in literature, so this could be a potential target for new targeted therapies (4)

- Chromothripsis and CNLOH events have been identified from diagnosis to relapse in many cancers (3) and these events were identified within this cohort. This may suggest further exploration into the pathophysiology these events in of neuroblastoma.
- Cases for the study were collected due to the availability of their genetic data and so the patterns and variants identified may not be representative

) Katherine K. Matthay, J.M.M., Gudrun Schleiermacher, Akira Nakagawara, and Crystal L. Mackall, L.D.a.W.A.W. 2016) 'Neuroblastoma', Nature Reviews Disease Primers, 2, 1-21. al, S.e. (2015) 'Mutational dynamics between primary and relapse neuroblastomas', Nature Genetics, 47(8), 872-878.) Rode A, M.K., Willmund KV, Lichter P, Ernst A (2016) 'Chromothripsis in cancer cells: An update.', International ournal of Cancer, 15(138), 2322-2333.) Vanessa Andries, K.V., Katrien Staes, Geert Berx, Pieter Bogaert, Gert Van Isterdael, Daisy Ginneberge, Eef arthoens, Jonathan Vandenbussche, Kris Gevaert and Frans van Roy (2015) 'NBPF1, a tumor suppressor candidate in roblastoma, exerts growth inhibitory effects by inducing a G1 cell cycle arrest', BMC Cancer, 15(91).



CANCER RESEARCH

Case 1

<u>P29 JW</u>

<u>08/2008</u>

 Suspected typhoid fever at home, later on holiday presented with pallor, abdominal mass, on CT left

suprarenal tumour

•Referred to UK hospital with week history of back pain

•Unresectable neuroblastoma, non-MNA with no bony

metastasis or bone marrow involvement

On biopsy poorly differentiated tumour

10/2008

2 courses of chemotherapy

<u>11/2008</u>

 Surgical resection of primary tumour sho necrosis with large proportion of poorly di •Relapse 1/post chemo sample obtained Chemotherapy and radiotherapy planned

<u>05/2009</u>

•Prior to 3rd cycle - abdominal pain, fever

lethargy

 USS: relapsed neuroblastoma, MIBG post unresectable, no tumour available for bio

•High dose chemo begun

<u>09/2009</u>

Extreme blood loss during resection, relation

obtained

Admitted into PICU

2 weeks post op: back pain - suprarenal mass, MIBG

showed active recurrent NB

<u>12/2009</u>

03/2010 •Spiking temperature and abdominal/back pain with

distension •Tumour recurrence, but difference in CNA data to original data on diagnosis.

 Palliative radiotherapy 04/2010

Died at home

	Gene	Time point	Locatio	Variant				
wed 20%			n					
ifferentiated								
d	IGFN1	R1	chr1:201178660	Missense				
>40 and	NBPF 1	R1	chr1:16890604	Missense				
ositive, psy	NBPF 10	R1, R2	chr1:145368499	Missense				
•As the table shows, these variants are genes that showed at particular time points that may be targetable in the future.								

	chr1:201178660	Missense	<u>11/2015</u>
			 MIBG scan shows faint uptake with
			High dose chemotherapy started
	chr1:16890604	Missense	<u>01/2016</u>
			Radiotherapy begun
			02/2016
2 chi	chr1:145368499	Missense	Anti-GD2 antibody immunotherapy
			08/2016

Palliative chemotherapy recommended

06/2017

point chr5:140,529,683 Missense PCDH R2

Presented with cervical lymphadenopathy, tumour recurrence

MIBG scan positive, after high dose chemotherapy

-140,532,868 R2 chr7:151,832,010 Missense KMT2 -152,133,090

•As the table shows, these variants are genes that showed at particular time points that may be targetable in the future.



+1q relapse 1 and 2

14 Chromothripsis

+2p relapse 2

-13p relapse 2

-18q relapse 2

+2q

+5q

+6q

+8q

+9q

-11q

+20g

+7q relapse 1

+17q relapse