



How do ACVR1/ALK2 mutations cause childhood brainstem tumours?

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Diffuse intrinsic pontine glioma (DIPG) is a paediatric brain stem tumour characterised by infiltrative growth. Diagnosis occurs on average at 6 years of age and the median overall survival time is 9-15 months¹. Survival has not improved in decades due to the impossibility of complete surgical resection, only temporary response to radiotherapy, and a lack of an effective targeted therapies².

20% of DIPG cases carry missense ACVR1/ALK2 mutations³, which lead to increased activation of BMP signalling, as well as responsiveness to activin A,

Project aims

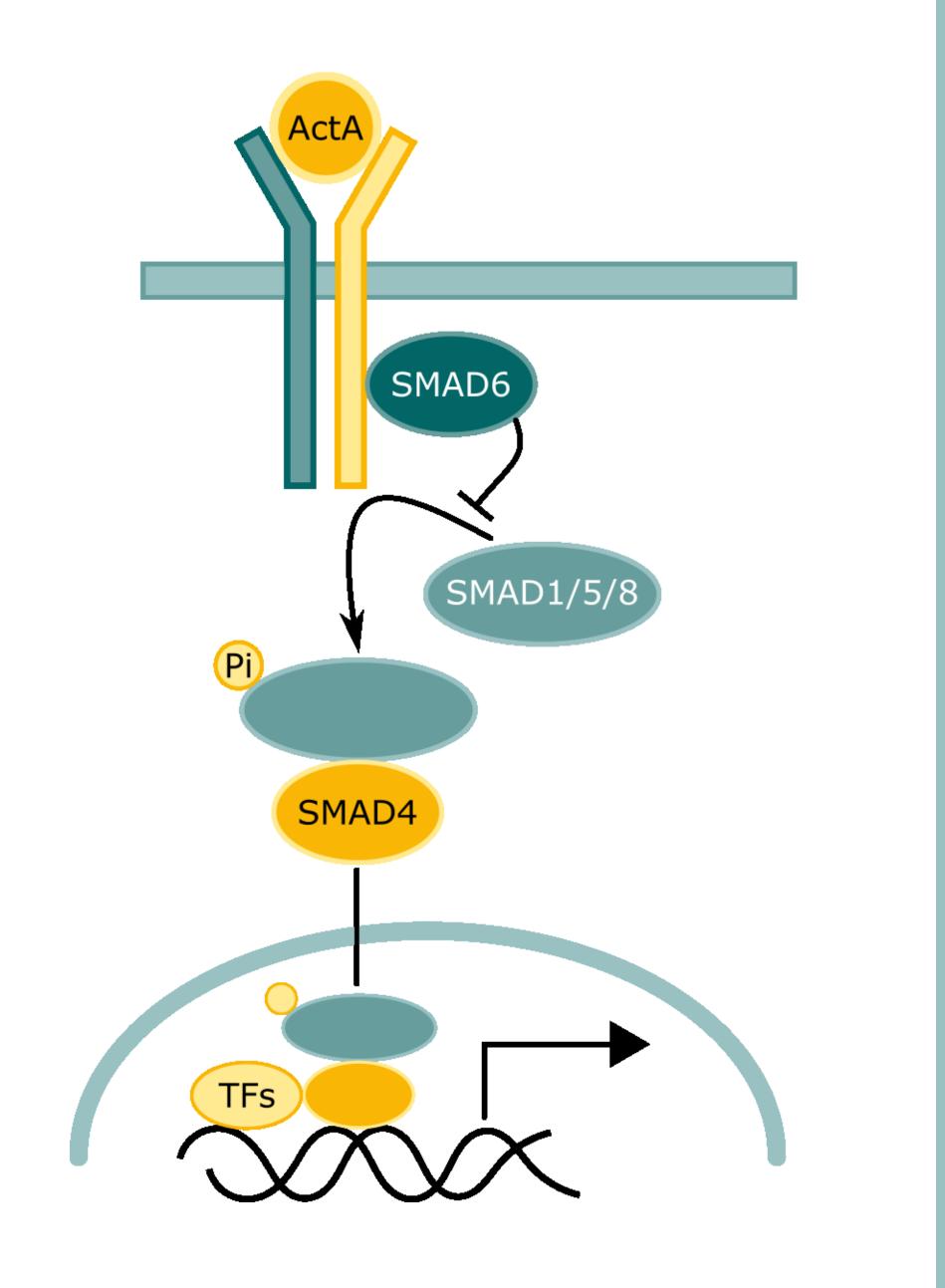
Development of stereotactic biopsy techniques and controlled autopsy protocols have allowed the generation of patient derived DIPG cell lines. I will use these cell lines to investigate:

- Changes in intracellular signalling caused by the mutation
- The link between ACVR1/ALK2 and histone H3K27M mutations

in addition to the normal BMP ligands⁴. Thus, the ALK2/BMP signalling pathway is a promising new target for DIPG therapeutics.

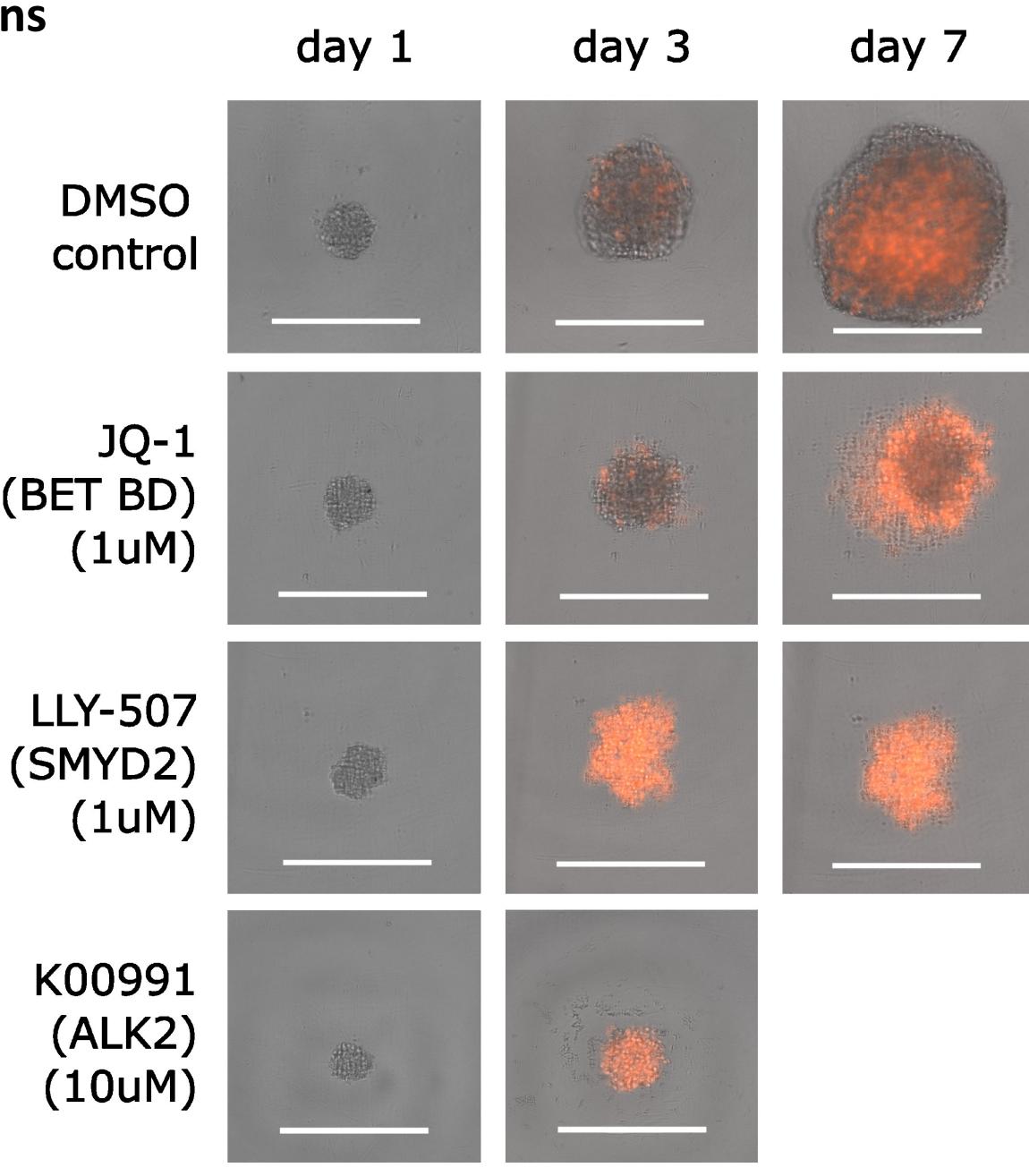
Efficacy of SGC synthesised ALK2 inhibitors

ACVR1/ALK2 mutant signalling



The link to histone mutations

Almost all DIPG cases contain histone H3.3 or H3.1 K27M mutations⁵ indicating the importance of epigenetic regulation in this cancer and over the aberrant ALK2/BMP signalling pathway. I aim to screen the effects of a comprehensive panel of epigenetic probes⁶ on DIPG cell line viability and migration, and BMP signalling responsiveness.



Treatment of DIPG tumour spheres with a test panel of epigenetic probes

Are DIPG cells dependent on the ACVR1 mutation?

Knockdown of ALK2 in DIPG cell lines reduces cell viability^(unpublished), but this does not indicate whether WT ACVR1 or mutant ACVR1 is the necessary gene. I will disentangle these possibilities using the CRISPR-Cas9 technique to introduce a tetracycline dependent knock-down cassette in the mutant allele only of DIPG cell lines.

First transformation:



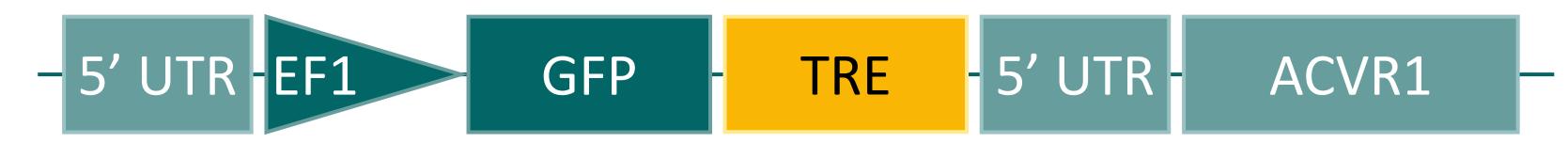
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Second transformation:





As part of the Structural Genomics Consortium's extreme open science initiative most of my work will be pre-published on the Zenodo database and https://opennotebook.thesgc.org/

By publishing data and working protocols as quickly as possible we aim to reduce redundant work and accelerate research progress

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