

Lay Summary

BRAIN UK Ref: 19/002

Molecular analyses of adult brain tumours by conventional molecular tests and DNA methylation profiling

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In this study we will analyse a range of brain tumours for which no conclusive diagnosis existed, or for types of brain tumours which benefit from a more refined classification using so-called methylation arrays.

The methylation arrays detect small chemical changes in the DNA of the tumour. Such chemical changes also exist in normal tissue but is different from the changes seen in normal tissue in the brain. The pattern of these changes have been used to establish groups of tumours based on this fingerprint on the DNA (also known as epigenetic changes).

The changes of this pattern on individual tumours will be compared with a large comparison group that has previously been identified and has been in-depth characterised.

The study has two purposes: to analyse data of methylation arrays that have previously been performed, as part of the diagnostic procedure. The second purpose is to find out more about tumours that cannot be diagnosed satisfactorily, or where patients had an unexpected clinical development. This way we are trying to better understand what the nature of the tumours were. Eventually, this technique will enable doctors to allocate patients into a risk group and, importantly, make more informed and accurate therapy decisions.

Publications:

Date	Publication title
2019	<u>Methylation array profiling of adult brain tumours: diagnostic outcomes in a large, single centre.</u>
2021	<u>Clear cell meningiomas are defined by a highly distinct DNA methylation profile and mutations in SMARCE1</u>