# Specialised molecular profiling could allow more accurate prognosis and treatment of brain tumours

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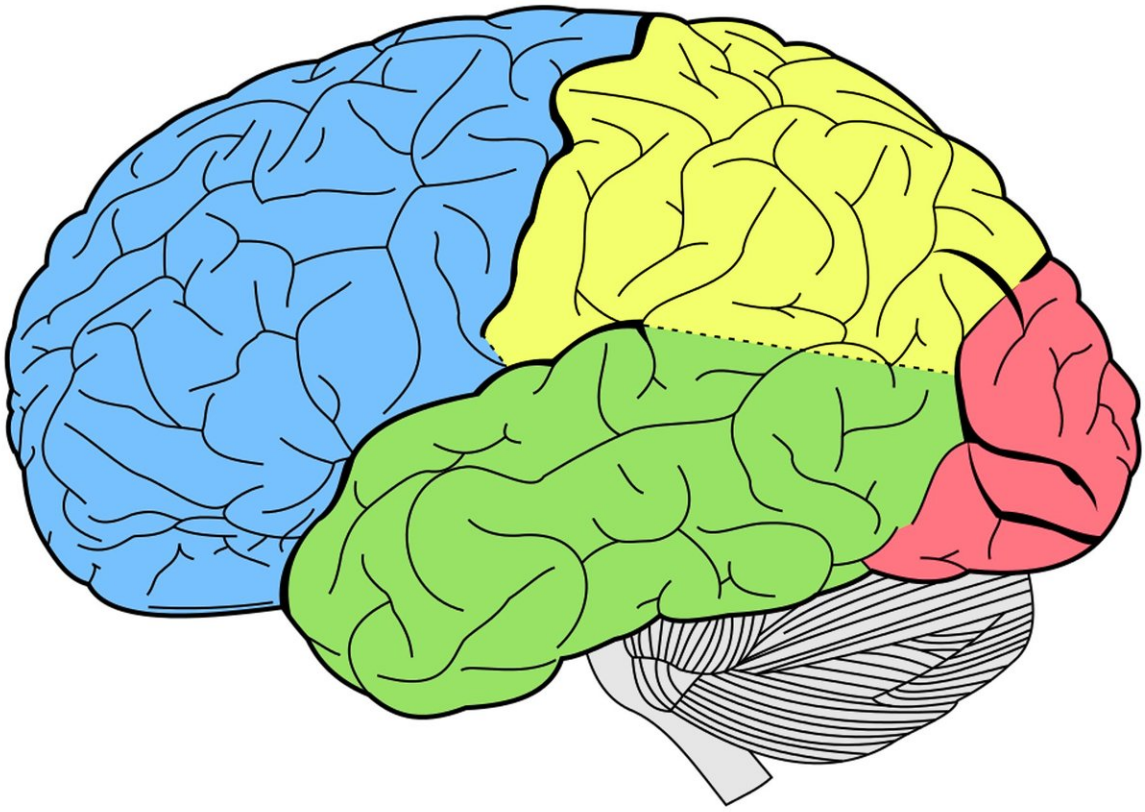

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Meningiomas, a type of brain tumour, are usually easy to treat. However,

there are a few subtypes that follow a very aggressive course and have high recurrence rates, i.e. there is a high risk of them coming back after treatment. These subtypes need to be treated using a specific treatment concept. Researchers from the Comprehensive Cancer Center (CCC) of MedUni Vienna and Vienna General Hospital have now demonstrated that, in addition to conventional tissue analysis (histology), a specific type of molecular DNA analysis can help to identify the subtype of the meningioma, thus facilitating more accurate prognosis and allowing more effective treatment planning.

Meningiomas are among the rarest types of cancer, affecting approximately 500 people a year in Austria. However, they are among the commonest intracranial brain tumours, that is to say tumours that occur inside the cranial cavity. They develop on the meninges, membranes covering the brain and spinal cord, and are largely benign, i.e. they grow slowly and do not metastasise. In most cases surgical removal suffices but there are also some very aggressive subtypes, which are associated with a poorer prognosis and require a different treatment approach. In such cases, surgical removal is often followed by radiotherapy. Hitherto, drug-based treatment has played a subordinate role in the treatment of meningiomas but would be an important extension of the treatment options in aggressive cases.

## International results confirmed

Recent international studies, in which MedUni Vienna has participated, have attracted attention with a method that significantly improves the diagnosis of subtypes. It involves comparing certain genetic mutations, changes in the hereditary material, against so-called DNA methylation patterns. Methylation is used to activate or deactivate particular DNA segments, in other words cell behaviour is controlled without changing the hereditary material itself.

In a recent study, the research group led by Matthias Preusser, oncologist at the Department of Medicine I of MedUni Vienna/Vienna General Hospital and Head of the Central Nervous Tumor Unit (CCC-CNS), has now checked these findings against its own data and validated them. The requisite tissue samples come from the neuro-biobank of the Institute of Neurology at MedUni Vienna/Vienna General Hospital.

Anna Sophie Berghoff, Division of Oncology of MedUni Vienna and Vienna General Hospital, who is a member of the CCC-CNS Unit and lead author of the study, says: "We were able to confirm that genetic analyses, such as determining and comparing mutations and methylation patterns, constitute a reliable way of identifying the subtype of a meningioma. This enables us to make a more accurate prognosis than with the conventional histological classification. The fact that the International Society for NeuroOncology has invited us to present our results at their annual conference in San Francisco in November shows the importance of our work."

## Next step: personalised treatment plans

Based on the results of their recent study, Preusser and his team are now organising an international clinical trial. This will investigate whether genetic analysis and the resulting molecular profiles can also offer a basis for targeted drug treatments. Says Preusser: "Drug-based therapies currently play a subordinate role in the treatment of meningiomas. Identification of target structures for targeted drugs could therefore open up new therapeutic approaches in this disease."

Provided by Medical University of Vienna

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