Test helps target glioblastoma patients most likely to benefit from bevacizumab

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A new test may help identify newly diagnosed glioblastoma patients more likely to benefit from bevacizumab (Avastin), according to new research from The University of Texas MD Anderson Cancer Center.

The results of the study were presented today at the annual meeting of the American Society of Clinical Oncology.

This study is associated with RTOG 0825, a large multi-center Phase III trial that evaluated the addition of bevacizumab to standard chemoradiation and maintenance temozolomide in treating newly diagnosed glioblastoma. Half of the participants received bevacizumab while the other half received a placebo.

Glioblastoma is the most frequent and aggressive type of brain tumor. Despite slight gains, tumors pose a high risk of recurrence and are commonly fatal.

"In general, glioblastomas are heterogeneous and no drug has been found that benefits every patient," said Erik Sulman, M.D., Ph.D., assistant professor in MD Anderson's Department of Radiation Oncology and lead author of the study. "We wanted to determine which patients are most likely to benefit from bevacizumab and use that information to develop a diagnostic tool that can predict which patients may be good candidates for the drug."

Does mesenchymal gene expression predict response to bevacizumab?

Bevacizumab is a monoclonal antibody that binds to the protein vascular endothelial growth factor. It is a type of anti-angiogenesis agent and prevents the growth of new blood vessels that tumors need to develop.

Previous studies found some patients with recurring glioblastoma have longer progression-free survival and receive some lessening of symptoms with the drug.

The goal of this study was to investigate the ability of a particular type of gene expression signature to predict response to bevacizumab.

Mesenchymal expression, poor outcomes correlated

As part of RTOG 0825, 637 randomized patients submitted specimens for molecular analysis. The umbrella study data also included molecular stratification that measured the degree of gene enrichment. These genes are known to function in cancer cell invasion and in establishing new blood supply, a function which bevacizumab is designed to prevent.

Researchers observed a significant association between a lower mesenchymal signature and better survival in patients taking bevacizamab.

Based on this association and following the examination of 43 genes in total, researchers modeled a novel gene expression predictor of outcome specific to those in the bevacizumab group.

"One of the key things about this predictor is that it's designed to be used on standard, archival tumors found in most clinical pathology labs,"

Sulman said. "It doesn't require fresh tissue."

Next steps

The group plans ongoing studies to determine the extent to which this gene signature represents a predictive marker for bevacizumab use in newly diagnosed glioblastoma.

"We will use data from the remaining patients on the trial to validate these findings," Sulman said. "We hope the test will be validated and used as a diagnostic tool to select patients for initial treatment with bevacizumab. Then, we plan to look beyond glioblastoma to see if it could benefit other tumor types currently treated or in clinical trials with bevacizumab."

Provided by University of Texas M. D. Anderson Cancer Center