

## **BATTLE researchers identify new biomarkers for EGFR inhibition**

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Scientists are continuing their work on the Biomarker-integrated Approaches of Targeted Therapy for Lung Cancer Elimination trial — known more commonly as the BATTLE trial — and presented updated results at the AACR 102nd Annual Meeting 2011, held here April 2-6.

John Heymach, M.D., Ph.D., associate professor of thoracic, head and neck medical oncology at The University of Texas MD Anderson [Cancer Center](#), said this update details the "discovery phase" of the ongoing program.

"Last year, we presented results on pre-specified markers to determine how effective they would be at predicting response to EGFR inhibition. This year we worked in the other direction to try to discover and test novel gene markers that hadn't been pre-specified," said Heymach.

Researchers performed gene expression profiling and core needle biopsies on 101 patients in the BATTLE trial. They found that the presence of an EMT (epithelial-to-mesenchymal signature) and the presence of a novel five gene signature including LCN2 were predictive of response to erlotinib, including patients with wild-type EGFR, as measured by disease control rate and progression-free survival.

Heymach said thus far new markers were identified retrospectively in the BATTLE protocol. The upcoming BATTLE 2 protocol will test the predictive value of these gene signatures prospectively.

"The hope is that we'll be able to predict who will respond to EGFR inhibition with erlotinib, particularly among patients who do not have an EGFR mutation. We currently don't have any predictive markers for this group of patients. We also think a similar approach can be applied to other drugs," he said.

The first results of BATTLE, which were presented at the AACR 101st Annual Meeting 2010, are published in Cancer Discovery, the newest journal of the American Association for Cancer Research, debuting at this year's Annual Meeting on Sunday, April 3.

Provided by American Association for Cancer Research

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