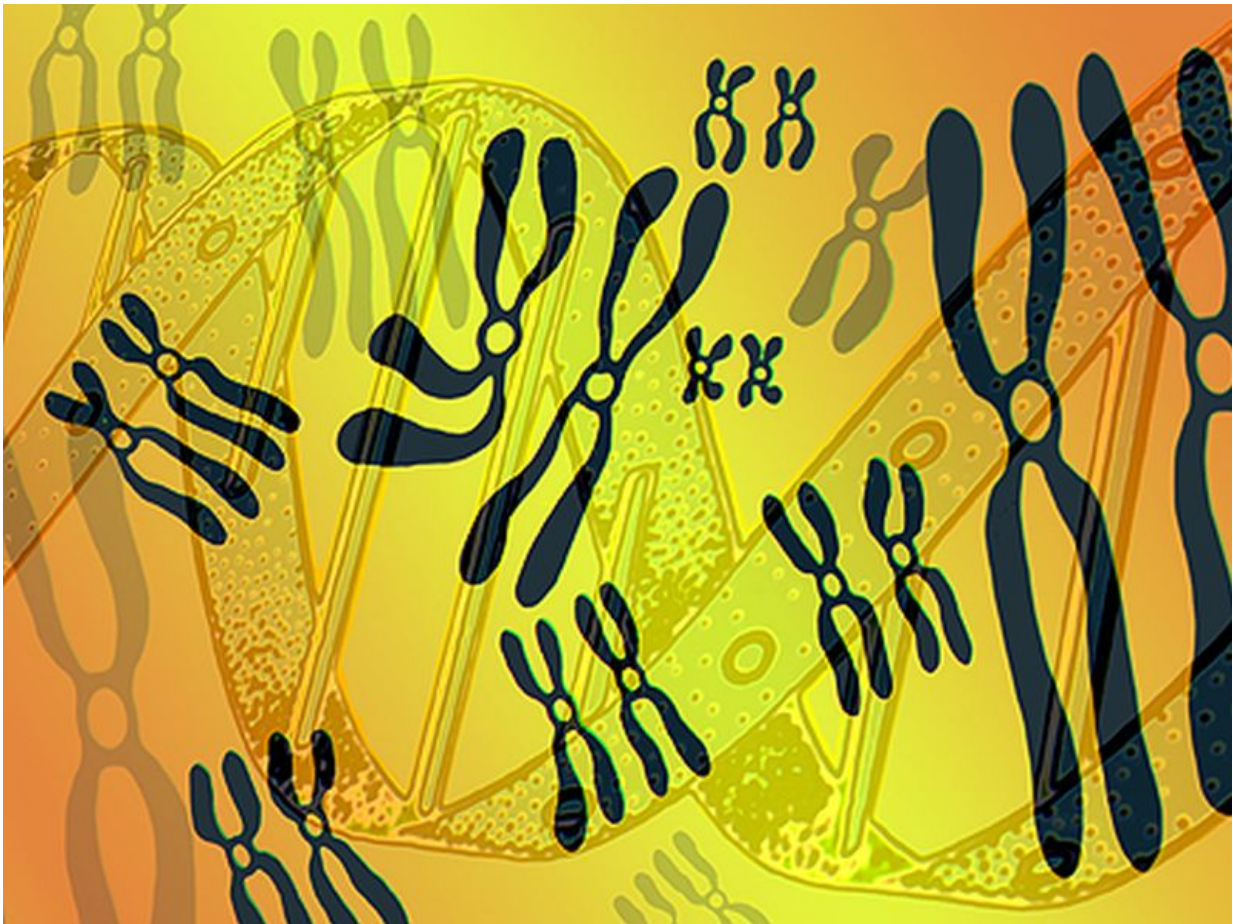


Methylation of gene panel may help predict breast CA survival

November 29 2016



(HealthDay)—Methylation of a gene panel is a strong predictor of

survival outcomes in metastatic breast cancer (MBC), according to a study published online Nov. 21 in the *Journal of Clinical Oncology*.

Kala Visvanathan, M.B.B.S., from the Johns Hopkins University School of Medicine in Baltimore, and colleagues used a new quantitative multiplex assay to predict survival outcomes in MBC. Ten genes were tested in duplicate serum samples at baseline, week four, and first restaging for 141 women. On the basis of six of the 10 genes, a cumulative methylation index (CMI) was generated, and correlations with progression-free survival (PFS), overall survival (OS), and disease status at first restaging were assessed.

The researchers found that women with a high CMI had shorter median PFS and OS (2.1 and 12.3 months, respectively), compared with a low CMI (5.8 and 21.7 months, respectively). Among women with MBC, a high versus low CMI at week four independently correlated with worse PFS and OS (hazard ratios, 1.79 and 1.75, respectively) in multivariable models. A CMI increase from baseline to week four correlated with worse PFS and progressive disease at first restaging (both P

"Methylation of this gene panel is a strong predictor of [survival outcomes](#) in MBC and may have clinical usefulness in risk stratification and disease monitoring," the authors write.

Several authors disclosed financial ties to the biopharmaceutical industry. Several authors are named on patents relating to methylation and cancer.

More information: [Full Text](#)

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Citation: Methylation of gene panel may help predict breast CA survival (2016, November 29)
retrieved 27 April 2024 from
<https://medicalxpress.com/news/2016-11-methylation-gene-panel-breast-ca.html>

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