TGFB1 mutation ups radiation-induced breast fibrosis risk

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(HealthDay)—The C-509T allele in the promoter region of transforming

growth factor β (*TGFB1*) is associated with radiation-induced breast fibrosis risk among patients with early-stage breast cancer, according to study published online July 19 in *JAMA Oncology*.

Aaron J. Grossberg, M.D., Ph.D., from the University of Texas MD Anderson Cancer Center in Houston, and colleagues examined the correlation between the C-509T variant allele in the promoter region of *TGFB1* and breast fibrosis three years after radiotherapy in a cohort study nested in an open-label, randomized clinical trial that compared hypofractionated whole-breast irradiation (WBI) with conventionally fractionated WBI. Two hundred eighty-seven women aged 40 years or older with pathologically confirmed stage 0 to IIA breast cancer treated with breast-conserving surgery were enrolled and observed for a minimum of three years.

TGFB1 genotype and three-year radiotherapy-induced toxicity data were available for 174 patients, 51 percent of whom had at least one copy of C-509T. The researchers found that 13.8 percent of patients with C-509T and 3.8 percent of those without the allele variant had grade 2 or higher breast fibrosis. In multivariable analysis, the only factors significantly associated with breast fibrosis risk were C-509T and postoperative cosmetic outcomes (odds ratios, 4.47 and 7.09, respectively).

"The C-509T allele in *TGFB1* is a key determinant of breast fibrosis risk," the authors write. "Assessing *TGFB1* genotype may facilitate a more personalized approach to locoregional treatment decisions in breast cancer."

Two authors disclosed financial ties to the pharmaceutical and medical device industries.

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