

# Three new lung cancer genetic biomarkers are identified in Dartmouth study

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Both environmental and genetic risk factors contribute to development of lung cancer. Tobacco smoking is the most well-known environmental risk factor associated with lung cancer. A Dartmouth research team led by Yafang Li, PhD, has conducted a study to display that gene-smoking interactions play important roles in the etiology of lung cancer.

In their study, three novel SNPs (single-nucleotide polymorphisms), or variations in our DNA that underlie our susceptibility to developing disease, were identified in the interaction analysis, including two SNPs for non-small cell lung cancer risk and one SNP for squamous cell lung cancer risk. The three identified novel SNPs provide potential candidate biomarkers for lung cancer risk screening and intervention. The team's findings, "Genome-wide interaction study of smoking behavior and non-small cell lung cancer risk in Caucasian population," have been published in *Carcinogenesis*.

The [genotype](#) and phenotype data used in this analysis came from OncoArray Consortium. "Genome-wide interaction scanning remains a challenge as most genome-wide association studies are designed for main effect association analysis and have limited power for interaction analysis," said Li. "This study is by far the largest genome-wide SNP-smoking interaction analysis reported for lung cancer. We also adopted a two-step strategy in the analysis to reduce the power loss from ordinary gene-environment interaction analysis."

The three SNPs, identified in the team's study, stratify lung cancer risk

by smoking behavior. These three SNPs can be potential biomarkers used to improve the precision to which researchers can categorize an individual's risk of [lung](#) cancer disease by smoking behavior, which are helpful for individualized prognosis and prediction of treatment plan.

While this reported study was restricted to a Caucasian population and the results may not be generalized to other ethnicities because of the different genetic backgrounds, the team aims to further test the identified interaction effect using genotype from other populations. "The limited overlap between discovery genotype and replication genotype may have reduced the power in our validation study," says Li. "We believe as more genotype data becomes available in the future we can discover more important gene-smoking interaction in [lung cancer](#) disease."

**More information:** Yafang Li et al, Genome-wide interaction study of smoking behavior and non-small cell lung cancer risk in Caucasian population, *Carcinogenesis* (2017). [DOI: 10.1093/carcin/bgx113](https://doi.org/10.1093/carcin/bgx113)

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