Pathogenic germline variants identified in patients with lung cancer

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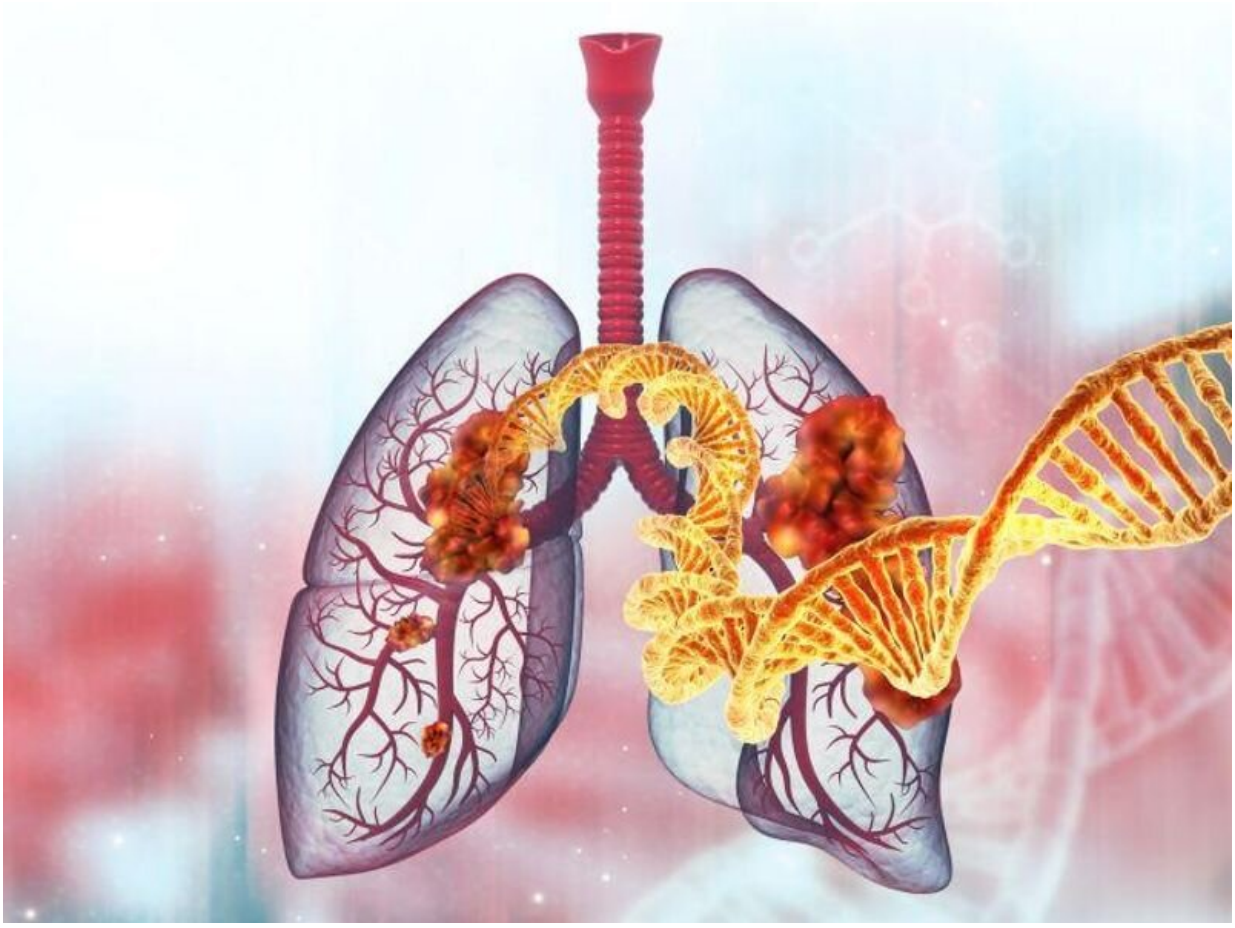

A total of 14.9 percent of patients with lung cancer have pathogenic

germline variants (PGV), most of which are potentially clinically actionable, according to a study presented Aug. 16 as part of the American Society for Clinical Oncology Plenary Series.

Steven Sorscher, M.D., from the Wake Forest School of Medicine in Winston-Salem, North Carolina, and colleagues retrospectively reviewed deidentified data for 7,788 individuals diagnosed with lung cancer for whom germline DNA sequencing and exon-level copy number analysis was performed between 2014 and 2022. Clinically actionable PGVs were defined as those associated with clinical management recommendations or eligibility for trials based on current standard-of-care guidelines.

The researchers found that a median of 79 genes were tested (range, one to 159). In 1,161 patients (14.9 percent), testing identified 1,503 PGVs in 81 known cancer-risk genes. A single PGV in a gene associated with autosomal recessive inheritance was identified in an additional 229 patients (2.9 percent). PGVs were most common in BRCA2, CHEK2, ATM, TP53, BRCA1, and EGFR (2.8, 2.1, 1.9, 1.3, 1.2, and 1.0 percent, respectively). Overall, 61.3 percent of the 1,161 individuals had a PGV in a DNA damage-repair/homologous recombination-repair gene and were therefore potentially eligible for a clinical treatment trial; 95.1 percent of the 1,161 patients had a PGV that was potentially clinically actionable.

"Lung cancer patients should not be deprived of the opportunity to learn of their risks for other cancers, to help family members determine their risks, and to benefit from the management and the potential therapeutic implications of finding PGVs in DNA repair pathways," a coauthor said in a statement.

Several authors disclosed financial ties to the biopharmaceutical industry.

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