Genetic variations indicate risk of recurrence, secondary cancer among head and neck cancer patients

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Eighteen single-point genetic variations indicate risk of recurrence for early-stage head and neck cancer patients and their likelihood of developing a second type of cancer, researchers at The University of Texas M. D. Anderson Cancer Center reported at the American Association for Cancer Research Frontiers in Cancer Prevention Research Conference.

The team examined 241 single nucleotide polymorphisms - variations of a single DNA building block in a gene - in eight genes involved in the creation of micro RNA (miRNA), small bits of RNA that regulate genes, and 130 miRNA binding sites on host genes where miRNAs exert their effects on regulating gene expression.

"We focus on miRNA pathways because these small molecules regulate between one third and half of genes," said senior author Xifeng Wu, M.D., Ph.D., professor in M. D. Anderson's Department of Epidemiology in the Division of Cancer Prevention and Population Sciences.

"Genetic variations in miRNA biogenesis genes and miRNA binding sites have been associated with the risk of having multiple solid tumors, so we hypothesized that these variations might be associated with the risk of recurrence or secondary primary tumors in these patients," Wu said.

About 10 percent of patients have a recurrence, and 15-25 percent go on to develop secondary primary tumors.

The team conducted a case-control study of 150 patients with recurrence or a second cancer and 300 patients without either. They found eighteen SNPs to be associated with recurrence/secondary cancer risk, including eleven SNPs in three miRNA biogenesis genes and seven in miRNA binding sites. Eight of the significant SNPs were in RNASEN gene, one of which was associated with a 72 percent increase in risk.

Compared to patients with fewer than four unfavorable genotypes, patients with five to nine unfavorable genotypes have a 2.4-fold increased risk and those with more than ten a 7.7-fold rise in risk.

Additional analysis of gene-gene interaction characterized the study patients into risk groups. The low-risk group had an event-free median survival time of more than 93 months. The highest-risk group had five times the risk of the low-risk group, and an event-free median survival of 35.9 months.

"Our results suggest that genetic variations in the miRNA biogenesis pathway and miRNA binding sites may be used to predict the risk of recurrence or secondary primary tumor in head and neck cancer patients," said first author Xiaofan Zhang, Ph.D., a postdoctoral fellow in epidemiology.

Source: University of Texas M. D. Anderson Cancer Center (news : web)