Study finds 231 new genes associated with head and neck cancer

October 4 2009

A Henry Ford Hospital study has identified 231 new genes associated with head and neck cancer, one of the most deadly cancers responsible for 2.1 percent of all cancer deaths in the United States.

Previously, only 33 genes were reported associated with head and neck cancer.

"These new genes should advance selection of head and neck-specific gene targets, opening the door to promising new molecular strategies for the early detection and treatment of head and neck cancer," says study lead author Maria J. Worsham, Ph.D., director of research in the Department of Otolaryngology at Henry Ford Hospital. "It also may offer the opportunity to help monitor disease progression and a patient's response to treatment."

Results from the study will be presented Sunday, Oct. 4 at the American Academy of Otolaryngology-Head & Neck Surgery Foundation Annual Meeting & OTO EXPO in San Diego.

This year alone, more than 55,000 Americans will develop head and neck cancer, which includes cancers of the mouth, nose, sinuses, salivary glands, throat and lymph nodes in the neck; nearly 13,000 of them will die from it.

According to the National Cancer Institute, 85 percent of head and neck cancers are linked to tobacco use. People who use both tobacco and

alcohol are at greater risk for developing these cancers than people who use either tobacco or alcohol alone.

Treatment for head and neck cancer varies based on the location and stage of the tumor, but most often includes surgery, radiation therapy or chemotherapy.

To identify new genes that could ultimately aid in future diagnosis and treatment of head and neck cancer, Dr. Worsham's study used a whole-genome methylation approach to detect genes with altered promoter gene regions due to DNA methylation. DNA methylation - a type of chemical modification of DNA where a methyl group (CH3) can be added (hypermethylation) or removed (hypomethylation) - allows the researchers to look for genetic abnormalities within tumor samples.

Using five DNA samples from tumor tissue, the researchers looked for 1,043 possible cancer genes. Those genes were cross-examined with those already reported in PubMeth, a cancer methylation database. Of the 441 genes in the database, only 33 genes were referenced in connection with head and neck cancer.

In all, the whole-genome methylation approach revealed 231 potential new genes not previously reported in head and neck cancer. Of those, 50 percent were present in three or more of the DNA samples, and 20 percent were represented in all five samples.

"DNA methylation is emerging as one of the most promising molecular strategies for early detection of cancer, independent of its role in tumor development," says Dr. Worsham. "Abnormal methylation can result in shutting off or silencing gene function. However, treatment with more recent drugs can reverse abnormal DNA methylation patterns, reactivating silenced genes, and restoring normal gene function. Therefore, a validated head and neck cancer-specific gene panel is likely

to signify potential demethylation treatment targets."

Source: Henry Ford Health System (news : web)