Study links 23 microRNAs to laryngeal cancer

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A Henry Ford Hospital study has identified 23 microRNAs for laryngeal cancer, a discovery that could yield new insight into what causes certain cells to grow and become cancerous tumors in the voice box.

The role of microRNA (miRNA), the small, non-coding RNA molecules that regulate human genes, has recently come into greater focus as researchers continue to understand the cellular mechanics of cancer development, says Kang Mei Chen, M.D., the study's lead author.

"While they may be small, miRNAs are no longer being viewed as just molecular noise," says Dr. Chen, a research investigator in the Department of Otolaryngology – Head & Neck Surgery at Henry Ford Hospital.

"We now recognize miRNAs as bigger players with increasing prominence in theories about cancer."

Findings from the Henry Ford study – supported by a NIH grant – will be presented Tuesday, Sept. 13 in San Francisco at the American Academy of Otolaryngology–Head & Neck Surgery Foundation Annual Meeting.

MiRNA may help cancer researchers unravel the complexities of what happens at the genomic level of cell evolution. It's estimated that there are at least 800 human miRNAs.

Since miRNAs are differentially expressed in various types of cancers compared with noncancerous tissues, researchers believe that they may play a crucial role in the production or formation of tumors.

"By gaining insight into laryngeal cancer, it gives us another level to understand what goes wrong and when cells decide to embark on a tumor genesis journey. From there, it's possible for researchers to look at how to control cancer growth and improve treatment," says co-author Maria J. Worsham, Ph.D., director of research in the Department of Otolaryngology-Head & Neck Surgery at Henry Ford.

The goal of the Henry Ford study was to discover miRNAs specific to laryngeal squamous cell carcinoma – a form of head and neck cancer that starts in the voice box.

Led by Dr. Chen, the researchers performed global miRNA profiling on stored laryngeal squamous cell carcinoma samples, as well as non-cancerous tissue samples from the larynx.

The team then used quantitative real-time polymerase chain reaction – a fast and inexpensive technique used to copy small segments of DNA – to verify miRNAs in the laryngeal cancer samples.

Of the 800 human miRNAs, 23 were found to be different between the cancerous and normal laryngeal tissue samples.

Among the 23 miRNAs tied to laryngeal cancer through the Henry Ford study, 15 had yet to be reported in head and neck cancer.

With the field narrowed to 23 miRNAs in laryngeal cancer, it presents researchers with the opportunity to quantify each piece of RNA and further study miRNAs in head and neck cancer, notes Dr. Chen.

The NIH-funded head and neck squamous carcinoma cohort for Detroit, with over 1,000 primary patients, includes more than 200 laryngeal sites, giving Henry Ford researchers the opportunity to look at miRNA expression in a larger group of laryngeal cancers as well as in other head and neck cancer sites.

Provided by Henry Ford Health System