

Scientists Uncover Gene Variation Linked to Melanoma

New gene mutations associated with the development of melanoma have been identified by scientists who conducted what is believed to be the largest DNA-sequencing study of the deadly disease to date.

Melanoma accounts for the vast majority of skin cancer deaths. The main cause of melanoma is excessive exposure to ultraviolet (UV) radiation from the sun.

The Yale Cancer Center team used DNA-sequencing technologies to analyze 147 melanomas originating on both sun-exposed and sun-shielded sites on patients' bodies. They found a large number of UV-induced mutations in sun-exposed melanomas, but most of these are "passenger" mutations that don't have a functional role in melanoma.

"We devised a mathematical model to sort out the relevant DNA alterations from over 25,000 total mutations," lead study author Michael Krauthammer, an associate professor of pathology, said in a Yale news release.

The researchers pinpointed a mutation in the RAC1 gene that speeds growth and movement in normal skin pigment cells, which are where melanoma begins. The mutation likely occurs at an early stage of melanoma development and promotes cancer cell growth and spread to other sites in the body, they said.

The RAC1 mutation was found in about 9 percent of melanomas from sun-exposed skin. It is the third-most frequent mutation after previously identified BRAF and NRAS mutations. Because the RAC1 mutation is so common, it would be worthwhile to develop treatments that target it, the researchers added.

They also identified mutations that disable proteins that suppress tumors.

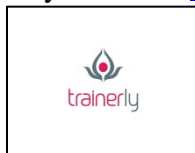
The study was published online July 29 in the journal *Nature Genetics*.

In the United States, about 76,000 new cases of melanoma will be diagnosed this year and about 9,000 people will die of the disease, according to the American Cancer Society.

SOURCE: Yale Cancer Center, news release, July 29, 2012

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