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Researchers confirm gene variants associated with the most common adult leukemia (w/Video)

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A national team of researchers led by Mayo Clinic has found that patients with chronic lymphocytic leukemia (CLL) are more likely to have similar DNA changes or variants in up to six genes, compared to people who do not have the cancer.

The findings, being presented at the annual meeting of the American Association for Cancer Research, are an independent validation of an earlier European study that found a link to seven different gene variants. Six were replicated in the Mayo Clinic study.

Together, the two studies demonstrate a genetic basis for the development of CLL, the most common adult leukemia in the United States, says the study's lead investigator, statistical geneticist Susan Slager, Ph.D., an associate professor of biostatistics at Mayo Clinic.

"In our study of American patients, we replicated six out of seven gene associations that were linked to this white blood cell cancer in Europeans, and in my field this level of replication is not common," Dr. Slager says. "This is a very exciting finding, and our job now is to investigate these genes to understand how they biologically affect the development of the cancer."

"These findings could potentially lead to new treatments or even

prevention of CLL, but we have a lot more work to do before we can reach that ultimate goal."

Dr. Slager estimates the risk of developing the cancer doubles if a person has any of these gene variants, but overall, that absolute risk is still very small. Four out of every 100,000 people develop CLL, so having the variant genes could increase risk to eight out of every 100,000 people, she says.

Although CLL can be generally controlled, it is considered an incurable cancer, she says.
Researchers from across the country collaborated with Dr. Slager and her team to collect genetic information on 399 CLL patients and 632 participants who did not have the cancer. Within the group of CLL patients, 99 were from high-risk CLL families - defined as two or more relatives diagnosed with CLL.

Using blood samples, investigators performed a genome-wide association study. They combined patients into one group and controls into another and then compared the two groups, looking for differences in genetic variants across the chromosomes. The first analysis of this data focused on the seven single nucleotide polymorphisms (SNPs) that European researchers had found. An SNP is a variation that occurs within a single nucleotide - the structural units of DNA - within a gene, and in most studies like this, the genes in which SNP changes occur are largely known. Analyses of the other genetic variants are under way.

They found that for six of the seven variants examined, CLL patients tended to have the variant more often than patients without the disease. Dr. Slager says these variants are associated with risk of developing the disease, not with prognosis - the outcome of a patient once disease has developed. "We do know that some patients have lost regions of certain genes due to the cancer and this is associated with a poorer outcome.

However, we are looking for changes in the genome that potentially determine who will get the disease in the first place," she says.

"Our general theory is that these changes, which a person inherits, combined with environmental risk factors, can predispose a person to developing CLL," she says. "The more you understand about these gene variants and how they affect risk, it becomes possible to think about ways to treat or even prevent CLL."

The researchers have identified some candidate genes that correspond to the identified SNPs, while other SNPs seem to be located near genes or in regions with no genes, i.e., what scientists call gene deserts.

Source: Mayo Clinic (news : web)