# Major study links aging gene to blood cancer

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A gene that helps control the ageing process by acting as a cell's internal clock has been linked to cancer by a major new study.

Scientists at The Institute of Cancer Research, London, found a genetic variant that influences the ageing process among four new variants they linked to myeloma – one of the most common types of blood cancer.

The study more than doubles the number of genetic variants linked to myeloma, bringing the total number to seven, and sheds important new light on the genetic causes of the disease.

The research, published in the prestigious journal *Nature Genetics* today, was mainly funded by charities Leukaemia & Lymphoma Research and Myeloma UK, with additional support from Cancer Research UK.

Myeloma affects around 4,700 patients each year, and is caused by genetic mutations in white blood cells, which normally help fight infection and injury. Less than four in 10 sufferers survive the disease for more than five years, and three in 10 die within a year.

One genetic marker found by the researchers is linked to a gene called TERC, which regulates the length of the telomere 'caps' on the ends of DNA. In healthy cells, these caps erode over time – causing tissues to age – but some cancer cells seem able to ignore the ageing trigger in order to keep on dividing. If further studies confirm the link, TERC could be a target for future myeloma treatments.

The team found the new markers by comparing the genetic make-up of a total of 4,692 myeloma patients with DNA from 10,990 people without the disease. A previous UK study led by the team, from The Institute of Cancer Research (ICR) and funded by Myeloma UK, found three genetic variants, or 'spelling mistakes' in DNA, which lead to increased risk of developing myeloma.

The team found the new batch of genetic variants by combining their samples with others from researchers in Germany. The combined results gave the scientists more data and therefore greater statistical accuracy.

All of the four new genetic variants are close to genes which are likely to play important roles in causing myeloma.

Study co-leader Professor Richard Houlston, Professor of Molecular and Population Genetics at The Institute of Cancer Research, said:

"Our study has taken an important step forward in understanding the genetics of myeloma, and suggested an intriguing potential link with a gene that acts as a cell's internal timer.

"We know cancer often seems to ignore the usual controls over ageing and cell death, and it will be fascinating to explore whether in blood cancers that is a result of a direct genetic link. Eventually, understanding the complex genetics of blood cancers should allow us to assess a person's risk or identify new avenues for treatment."

In people affected by myeloma, white blood cells called plasma cells grow uncontrollably in the bone marrow and become stuck there, disrupting normal blood production. It can be very painful, and affects bones in multiple parts of the body.

Professor Chris Bunce, Research Director at Leukaemia & Lymphoma

Research, said:

"The identification of these risk gene variants offers more compelling evidence that susceptibility to myeloma can be inherited. Myeloma remains incurable and the effect on patients' quality of life can be devastating.

"By showing how these specific genes influence the cancer's development, this research could potentially lead to the development of targeted myeloma drugs in the future. In addition we know that a common condition called MGUS predisposes to the development of myeloma. The identification of additional genetic risk factors in these patients could revolutionise their future management and prospects."

Heather McKinnon, Clinical Research Programme Manager for Myeloma UK,, said:

"We are delighted the original study funded by Myeloma UK two years ago into genetic inheritance in myeloma has now led to further important research. The study published today in *Nature Genetics* identifies four more genetic variations in myeloma and for the first time demonstrates an association with ageing. Myeloma UK is committed to supporting this important research and invests in a programme of work at The Institute of Cancer Research."

**More information:** Common variation at 3q26.2, 6p21.33, 17p11.2 and 22q13.1 influences multiple myeloma risk, dx.doi.org/10.1038/ng.2733

Provided by Institute of Cancer Research