

# New genetic findings help explain inherited predisposition to myeloma

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Researchers have identified eight new genetic variations in the human genome that could be linked to an increased risk of developing myeloma. The findings provide additional evidence and build on existing research that suggests myeloma can run in families.

In the largest study of its kind, scientists at The Institute of Cancer Research, London, compared the genomes of [myeloma](#) patients with those of healthy individuals. The team also combined and re-analysed data from similar research undertaken as part of a genome-wide association study (GWAS). In total, the researchers compared DNA from 9,866 myeloma patients with 239,188 healthy adults.

Every year around 5,500 people in the UK are diagnosed with myeloma, a rare and incurable form of cancer affecting the [plasma cells](#) in bone marrow, and around one in 115 men and one in 155 women in the general population will develop myeloma in their life time.

Eight [single nucleotide polymorphisms](#) (SNPs), inherited single letter variations in DNA, were linked to increased susceptibility of developing myeloma.

These SNPs were located in regions of the genome involved in regulating genes linked to cell processes known to go wrong in myeloma development. These included the production of antibodies in plasma cells, as well as the regulation of gene activity and the maturation of these cells.

The ICR research suggests that subtle effects on the activity of key genes could mean that the proper development of plasma cells breaks down, increasing the likelihood of developing myeloma. However, further work would need to be undertaken to fully understand this.

In total 17 risk variants for myeloma have now been identified by the ICR team. It is estimated that the risk variants identified so far account for just 20% of the heritable risk factors connected to myeloma and further GWAS studies of patients are planned.

The research, published online in the journal *Nature Communications* today (Friday), was principally funded by the charities Bloodwise and Myeloma UK, with additional support from Cancer Research UK and Rosetrees Trust.

Study leader Richard Houlston, Professor of Molecular and Population Genetics at The Institute of Cancer Research, London, said: "Our study expands our understanding of how inherited risk factors can influence the risk of myeloma. We know that the inherited risk of myeloma does not come from just one or two major risk genes, as can be the case with breast cancer, but from multiple different genetic variants, each with only a small individual effect on risk. Identifying more of these variants gives us new insights into the potential causes of the disease, and open up new strategies for prevention."

Myeloma UK Chief Executive Eric Low said, "This research allows us to build a greater understanding of the genetics of myeloma and it could play a vital role in the future development of preventative and curative strategies. It is important to note, however, that myeloma accounts for only 2% of all cancers, so whilst this research takes an extremely important look at the familial risk of developing myeloma, the overall risk to the general populace of developing myeloma is small."

Dr Alasdair Rankin, Research Director at Bloodwise, said: "These findings give an insight into the genetic and biological basis of why myeloma can occasionally run in families. It is important to remember that while relatives of patients may have a higher risk of developing myeloma than the rest of the population, their absolute risk is still low. Further studies could help guide the development of new drugs to treat this cancer in the future. With a more complete genetic picture, it may even be possible to identify those family members at an increased risk and find ways to prevent them from developing myeloma."

**More information:** The report is published online in the journal *Nature Communications* on Friday 1st July 2016 under the title, 'Genome-wide association study identifies multiple susceptibility loci for multiple myeloma'.

Provided by Institute of Cancer Research

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