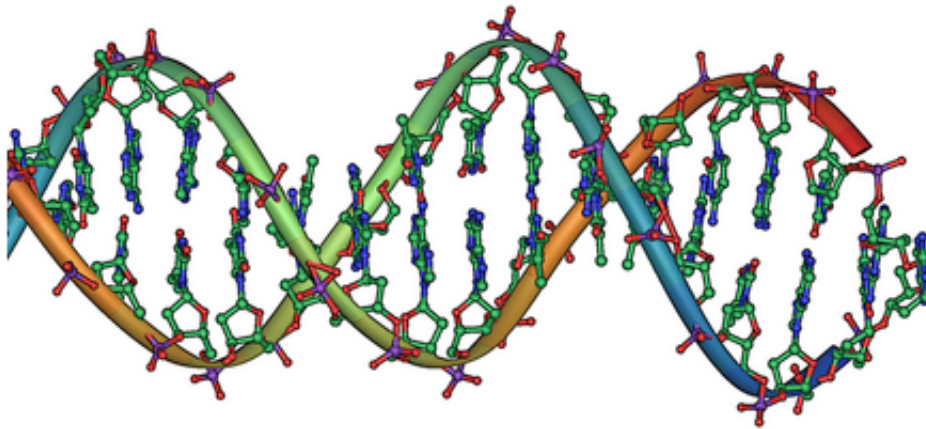


Researchers show that genetic background regulates tumour differences

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DNA double helix. Credit: public domain

Researchers from Uppsala University, Sweden, and the Broad Institute, USA, have identified both similarities and differences between a single tumour type in multiple dogs breeds; a finding they believe parallels the situation in the cancer of human patients.

This novel finding could lead to a better understanding for how varied genetic background influences the differences which occur in [lymphoma](#) tumours. The results were published today in *Genome Research*.

Lymphoma is the most common blood-borne cancer in the Western world. The different types of lymphoma span from the aggressive to those that have a relatively mild outcome. Dogs also develop lymphoma. In terms of genetics, dogs are very similar within, but diverse across breeds, and so they offer a unique possibility to study genetic factors driving inherited diseases. Different dog breeds have varying risk levels for developing different types of lymphoma, even though they live in the same environment. This shows that there are genetic causes for the type of lymphoma a dog develops. This study is the first to show that the genetic changes in a tumour - mutations - are influenced by what breed the dog is, i.e. their genetic background.

"We were surprised to see how much the dog's genetic background affects the mutations. It is known that the genes that accumulate the most mutations are linked to the tumour type, and we found this too, however we showed that the mutational spectrum of a tumour is determined by breed type", says Dr. Ingegerd Elvers, a researcher with Professor Kerstin Lindblad-Toh at both Uppsala University and Broad Institute.

The research team selected three different dog breeds, all with an increased risk of developing lymphoma, but with differential risk for lymphomas arising from either B- or T-cells. Together with veterinarians they collected tumours and healthy control tissue from family dogs. They then performed careful genetic detective work to identify the mutations in each individual tumour. Intriguingly, in two breeds it appeared that the genes that accumulated the most mutations were the same in B-cell lymphomas, whilst for T-cell lymphomas it differed between genes for two breeds. Most of the key genes that the researchers identified were already known to be important in human lymphoma. However, novel genes uncovered by this research may open up for new treatment options for humans.

"There are many different molecular subtypes in humans. We believe that each dog breed may correspond to one type of B- or T-cell lymphoma and so studies within and between [breeds](#) gives us a unique possibility to understand how the [genetic background](#) affects what type of tumour develops, and how its progression is regulated", says Ingegerd Elvers. "We hope that this can enable more individualized treatment options for cancer in both dogs and humans in the future."

More information: "Exome sequencing of lymphomas from three dog breeds reveals somatic mutation patterns reflecting genetic background."

Genome Res. 2015. doi:
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Provided by Uppsala University

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