

# Sniffing out lymphoma by turning dogs into humans

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Researchers at North Carolina State University are narrowing the search for genes involved in non-Hodgkin lymphoma – by turning dogs into humans.

Humans and [dogs](#) don't just share companionship and living space, they also share a similar genetic makeup. Additionally, they share the same types of cancer, including lymphoma. Dr. Matthew Breen, professor of genomics at NC State, uses canines as a genetic model for studying lymphoma because purebred dogs of the same breed have less genetic variation among them than humans do, making it easier to pinpoint areas on canine chromosomes that may be involved with cancer.

In a paper published in the journal *Leukemia and Lymphoma*, Breen's team took the genetic information from dogs with non-Hodgkin lymphoma, and then rearranged or "recoded" the genomes of the dogs so that, genomically speaking, they were human. The researchers then compared the recoded canine genomes with those of humans with non-Hodgkin lymphoma, to see which chromosomes were involved with the cancer in both humans and canines.

"This is the first time that we were able to compare this information from dogs with lymphoma directly with existing data from human patients diagnosed with the equivalent cancer and using the same technique," says Dr. Rachael Thomas, research assistant professor of molecular biomedical sciences at NC State and lead author of the paper.

The data revealed that there were only a few [genes](#) involved with lymphoma that were shared by dogs and humans. This is in contrast to current research into human lymphoma, where numerous genes have been identified as possibly having a relationship to the cancer. Breen and his colleagues hope that this data will point researchers toward the most likely genetic culprits.

"In essence, we stripped the background noise from the human data," Breen says. "[Lymphoma](#) genomics is a lot more complex in human patients than in dog patients. This study tells us that while both humans? and dogs? have comparable disease at the clinical and cellular level, the genetic changes associated with the same cancers are much less complex in the dog. This suggests that maybe there is a lot of genetic noise in the human cancers that are not essential components of the process. While [human](#) studies have been looking in numerous places in the genome, the dog data indicate we need to focus on what's shared, and these are very few regions."

**More information:** Refining tumor-associated aneuploidy through 'genomic recoding' of recurrent DNA copy number aberrations in 150 canine non-Hodgkin lymphomas, *Leukemia & Lymphoma*, 2011

Provided by North Carolina State University

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