

CANINE CANCER & COMPARATIVE GENOMICS

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(Published in ASTC Barks, Sept. 2010)

[Every effort has been made to ensure accuracy of information. However, this is not a substitute for prompt veterinary care. Any similarity to other publications is unintentional. Published online at Sealyhealthguard.org, 7/2011]

At the last AKC-CHF Parent Club Health Conference, I was pleased to attend a presentation by the world-renowned cancer researcher Dr. Matthew Breen. Dr. Breen completed his PhD in cytogenetics (a branch of genetics which focuses on the structure & function of the cell, especially the chromosomes) then spent two years as a Post Doc in molecular genetics.

His laboratory developed molecular cytogenetics reagents, resources and techniques for use in canine genome mapping, comparative cytogenetics and cancer studies. He is the Treasurer for the Canine Comparative Oncology & Genomics Consortium (CCOGC) sponsored by the AKC-CHF and the Morris Animal Foundation. Dr. Breen currently has a number of active grants from the CHF that are focused on the molecular cytogenetic evaluation of canine tumors.

The CCOGC is a collaboration of veterinary and medical oncologists, pathologists, surgeons, geneticists & molecular & cellular biologists. This group determined that a well-described repository of tissues (tumor and normal) from tumor-bearing dogs was an essential resource needed for advancing our understanding of canine cancer. The biospecimen repository, sponsored by Pfizer, houses tumor tissue, normal tissues, serum, plasma, peripheral blood mononuclear cell preparations, genomic DNA, RNA and urine samples. [In June of last year (2009), the FDA approved Pfizer's Palladia, an anti-cancer drug for dogs. Palladia is for treating recurrent cutaneous mast cell tumors. It prevents formation of new blood vessels in tumors.] The goal of the CCOGC is to obtain 3,000 samples of lymphoma, osteosarcoma, melanoma, hemangiosarcoma, soft tissue sarcoma/histiocytic sarcoma, mast cell tumors and lung cancer.

Advances in genomics technologies over the past decade have been astonishing. New forms of sequencing technology have made the process much faster & less expensive. Comparative genomics is the comparison of the sequence and function of the genomes (a genome includes all the genes of a species) of different species, such as the human & the dog. Since both genomes (human & dog) have been mapped, scientists like Matthew Breen can identify regions of both genomes that are shared and that are associated with disease and determine which genes are playing key roles in a variety of disease processes. They have already found that specific genetic changes are associated significantly with subtypes of canine cancers and have also identified genetic changes that are associated strongly with response to routine therapy.

This information can one day be used to more accurately predict the prognosis and survival time of canine cancer patients.

Currently, the inability to accurately predict response to treatment and survival time is the major reason (in addition to cost) many owners decide not to treat their dogs.

While the CCOGC is building its collection of biospecimens (thanks to the help of hundreds of dog owners), scientists have generated a series of sophisticated molecular cytogenetic reagents and resources that provide a way to examine each tumor specimen for genetic changes that are associated with the corresponding malignancy.

Using these new tools, they have evaluated the tumor genomes of over 500 canine cancer patients. For each cancer type studied, they have demonstrated the presence of numerous cytogenetic signatures that are associated with cancer subtypes and that also correspond to those in humans. If these are so similar, there's a good chance that human-derived therapies will be effective in canine oncology.

As they study these genomic changes, they can begin to determine which are associated with the disease process and which are secondary effects of tumor-associated genomic instability. They are well on their way toward development of more sophisticated molecular sub-classification of canine cancers, a process that should facilitate the emergence of tailored therapies.

Accessibility to new information is becoming easier and faster, and the demands of the public for the latest veterinary care are increasing. It is conceivable that, as with human health, the next decade may bring genotyping and/or whole genome sequencing/analysis of dogs for the purposes of health management.

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