**Canine Mammary Tumors: A Microreview**

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**Canine Mammary Tumors (CMTs) spontaneously occurring in unspayed female dogs leads to 3 times higher mortality rate than Human Breast Cancer (Sashid, et al. 1). These two phenomena are very similar in the way they progress and develop, which makes dogs a prime research target in order to better understand mammary tumors in both canines and humans. This is what sparked the start of the research studied in the manuscript “Gene Expression Profiling of spontaneously occurring Canine Mammary Tumors…”. This research paper attempts to uncover more information by profiling genes associated with CMTs. Upregulation and overexpression of certain genes are two of the results that were analyzed and distinguishable between malignant and benign mammary tumors. By utilizing this data, comparisons could be made between the new canine discoveries and human knowledge that has already been discovered, furthering the understanding of mammary tumors in both species. Cancer is an issue that has been studied extensively, however, there is always more to learn. Different cancers act differently, as well as certain cancers act differently between species. This study is a step in the right direction to continue discovering new information that will lead to better prognosis and better treatment of such diseases.**

**Introduction**

Canine Mammary tumors are tumors that develop in the breast tissue of mainly female dogs; it is extremely rare in male dogs. They are much more common in females that have not been spayed, and the sooner the canine is spayed, the less chance of growing a tumor in this part of their body over their lifetime. Mammary tumors are not only found in canines but in breast cancer of humans too, which is part of the reason why this study was performed. Human breast cancer and canine mammary tumors present themselves in the same ways: the age onset, the course of progression, the spontaneously occurring tumor in an otherwise healthy individual, the tumor size and the disease outcome (Abdalmageed, et al. 1). While this article was focused on canine mammary tumors, the hope was to gain new insight into human tumors and possibly identify pathways for treatments to better the prognosis of humans affected by this disease. This profiling included many tests such as 2D Gel Electrophoresis, Microarray Analysis, and Qualitative Real-time PCR. These functionally interpreted the data collected and began to piece together gene networks and pathways that are either unique to malignant CMTs, different than normal CMTs or something that is the same as normal tissue, therefore noncancerous.

**Recent Progress**

Often, mice are used in the laboratory as test subjects for many diseases in order to get an idea of how that disease acts in other species. However, in this study that was not the case. When complete genome sequencing of dogs revealed that the genome of dogs and humans is very similar, that introduced the possibility of utilizing dogs with mammary tumors to better understand the mammary tumor itself in both species. In order to accomplish this, many tests were performed that established connections between benign and malignant tumors in four and six test subjects respectively. In order to establish a control group, three healthy mammary tissues were sampled. These samples were taken from tumors that had been removed or biopsied from consenting patients. The research of Shahid Hussein, et al, discovered that many groups of proteins were up-regulated or down-regulated between benign and malignant tumors. Specific tests such as Microarray Analysis and 2-D Gel Electrophoresis, in that order, narrowed down specific genes that have malignant behavior when up-regulated, or increased their occurrence in the cancer tissue. By comparing malignant and benign mammary tissue cells, it was confirmed that a specific seven differentially expressed proteins were upregulated in the malignant tumor tissue and expressed three times higher. This may be causing the three times higher mortality rates in the unspayed females as stated earlier.

Identification was only one part of this study done on CMTs. By using the information collected from the identification of proteins and genes more common in malignant, benign or healthy tissue respectively, this study hoped to provide insight into prognosis, possible gene target therapy, biomarkers and biological pathways of a Canine Mammary Tumor. The information gathered from this research indicates that different genes are upregulated depending on if the tumor tissue is malignant or benign. This is due to the different ways that these upregulated genes can interfere with the normal pathways of the proteins, which can induce cancerous diagnoses. These upregulated genes in malignant tumors include five genes where at least one of these is known in humans to progress tumor growth as well. These also play a part in the aggressiveness of such tumors. Benign tumors also include upregulation of about five different genes, but different of those presenting in malignant tissue. Overexpression of a certain kind of gene known as Matrix metalloproteinases (MMPs) has a primary function of playing a role in the metastasis of cancer. However, there are many reports that have reported MMP overexpression in Canine Mammary Tumors, meaning that this is an accepted data discovery. And many of the genes that were profiled were found to not only be associated with Canine Mammary tumors but other cancers as well.

**Discussion**

By understanding the concept of CMTs it is possible to compare data that is known about human mammary tumors and canine mammary tumors to establish trends and analyses allowing for a clearer interpretation of the results found. In some cases, new data was found in canines that was not studied in humans, and vice versa. This presented new understandings of the cancerous tissue through overall similarities and differences between the two species. By doing this, this research paper concluded with twice the amount of information than was researched through their methods which does not only benefit canines but humans too.

A problem that may present itself after analyzing this recent research article is that only a total of thirteen different tissues were used from thirteen different canines. This was not a large-scale study by any means. This problem presented that, as the data showed, there was a high overlap between the genes and proteins of the three types of tissues: benign, malignant, and normal. Because of this, the probability of these results matching to those of another set of participants is not incredibly likely. Therefore, a wider range of participants would need to be researched in order to be able to solidify the claims made in this article. These include the top most upregulated genes in both benign and malignant tumors, and the certain genes that are overexpressed leading to malignancy in the tumor. This is an important aspect of any research: having enough representation of the classes being researched to allow the results to be shared by a majority of the presenting population. In this case that would be the canine population who have tumors, which would then translate to humans with breast cancer.

This study “identified several genes which play a diverse role in tumor angiogenesis, cancer onset and pathogenesis (Hussein, et al. 23).” However, in order to act upon the information presented, more understanding needs to be developed. Because of this article, the information has now been collected and presented for other researchers to take advantage of. However, interpretation is a major part of being able to formulate treatments and target gene therapy for these kinds of diseases. So, this research manuscript was a small step in the right direction to helping understand the concept of mammary tumors in both canines and humans.

**References**

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