



# Comparative oncology genomics between canine and humans and its utilization for diagnosis and therapy of human tumors

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## Introduction

There have been few major advances in the treatment of brain tumors in decades. Considering the significant morbidity and mortality from these cancers, a more correlative biologic approach to investigating pathogenesis and effective therapies is needed. With this effort, we validate a unique canine brain tumor model for translational studies.

## Methods

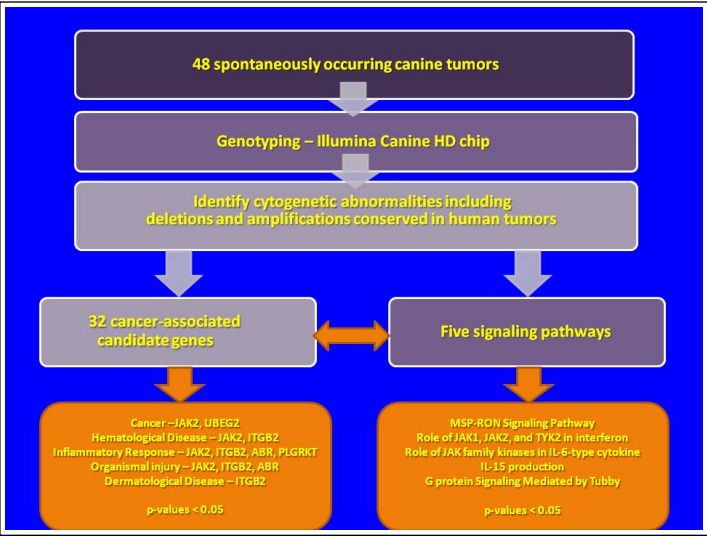
By studying spontaneously occurring canine brain tumors in veterinary patients, we have identified and correlated unique histologic, imaging, and genomic findings associated with human intracranial neoplasms. Genetic mapping was performed on 48 canine meningiomas using Illumina Canine HD Chip to identify cytogenetic abnormalities conserved in human tumors. With location information (chromosome number, start and stop position), we were able to pinpoint genes involved in the same region. We pooled these genes for further analysis involving gene-gene interaction networks and signaling pathways. Signaling pathways were then examined for usefulness as therapeutic targets.

## Results

48 canine meningioma samples were genotyped. DNA amplification and segmental deletions were identified, and 32 genes were contained in the deleted regions. The percentage of matching identity ranges from 26.2% to 95.3% among human orthologs. Cancer related gene functions were among top biological and molecular changes of the affected genes, including cellular death and survival, assembly and organization, movement, signaling, interaction and morphology. Most frequently affected signaling pathways include MSP-RON signaling and interferon gamma signaling, which play a significant role in cancer development.

## Conclusions

This comparative oncology genomics database is beneficial and permits utilization of the sporadic canine tumor model as a large animal model for diagnostic and therapeutic studies to predict success in human brain tumor patients. It allows for optimization of brain cancer therapy based on tumor genetics and molecular analysis.



## Learning Objectives

By the conclusion of this session, participants should be able to: 1) Describe the importance of comparative oncology genomics, 2) Identify four important genes and most important signaling pathways in development of brain tumors 3) Discuss individualized brain cancer therapy based on tumor genetics