

Departamento de Ciências da Vida

Transcriptome and proteome profiling of canine mammary tumors

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Objectives

Canine mammary tumors (CMTs) are the most common tumor type in female dogs, with about 50% of them being malignant. In these cases, surgery appears to be the only successful treatment. The main goals of this PhD thesis are:

- 1) Construction of a CMT tumor base with clinical, epidemiological and histopathological information from each animal;
- 2) Establishment of primary CMT cell lines;
- 3) Characterization and quantification of the transcriptome of CMTs by RNA-seq;
- 4) Analysis of the proteomes of CMTs and primary CMT cell lines;
- 5) Primary CMT cell lines susceptibility to novel organometallic compounds developed at CQE-IST;
- 6) Potential new anti-tumoral compounds that will improve CMT treatment and prognosis will be further tested in human breast cancer cell lines.

Methodology

- 1) Matched tumoral and normal mammary tissue are collected from patients, Clinical and histological characterization had been performed for each animal and data stored in a database containing clinical, epidemiological and histopathological.
- 2) Primary CMT cell lines from fresh sample biopsies have been established.
- 3) RNA have been extracted from tumoral and normal samples stabilized in RNAlater and sequenced.
- 4) Two dimensional gel electrophoresis, 2-DE, will be performed for proteins of tumor cell lines and selected tumor samples.
- 5) Selected immortalized CMT cell lines will be used for susceptibility testing to several new organometallic compounds, using common anti-tumor drugs such as doxorubicin as a control.
- 6) New anti-tumoral compounds with promising results in CMT cell lines will be further tested in Human breast cancer cell lines such as MCF-7.

Expected Results

- 1) The CMT tumor base will a source of information and biological material for the present and future work in canine mammary tumor.
- 2) The primary CMT cell lines (Figures 1 and 2) will provide suitable *in vitro* models for oncogenomic and drug screening assays and for scientific dissemination.
- 3) High quality total RNA obtained from the samples (figure 3) will be used for RNA-seq studies that will allow us to obtain a picture of the transcript population (new exons or genes and rare transcripts some of them non-coding). We will also get insights into the miRNA population involved in tumorigenesis or in tumor suppression that could serve as targets for gene therapy in the dog.
- 4) The 2-DE analysis (figure 4) of proteins in CMT cell lines will reveal the main players for the tumoral progression.
- 5) Expectantly novel organometallic compounds will be discovered for cancer therapy in canine mammary tumor.
- 6) These novel organometallic compounds will also be useful in the treatment of Human breast cancer.

Funding: Fundação para a Ciência e Tecnologia, FCT, PhD grant SFRH / BD / 70202 / 2010
CIGMH, Strategic Project PEst-OE/SAU/UI0009/2011;
PTDC/QUI-QUI/112597/2009;
PTDC/CTM-NAN/109877/2009;
Private Funding

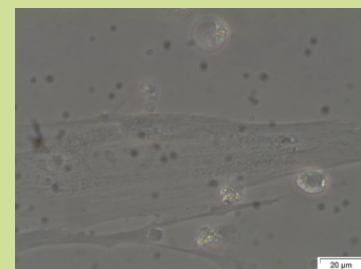


Figure 1 – Cells of a primary culture from canine mammary tumor cells.

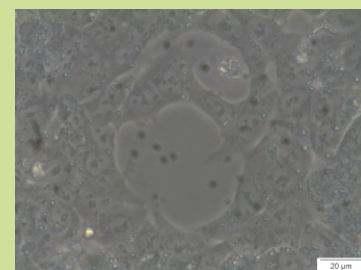


Figure 2 – Cells of a primary culture from canine mammary tumor cells forming a duct.

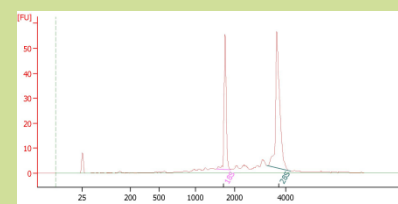


Figure 3 – Electropherogram of a RNA sample from a canine mammary tumor biopsy.

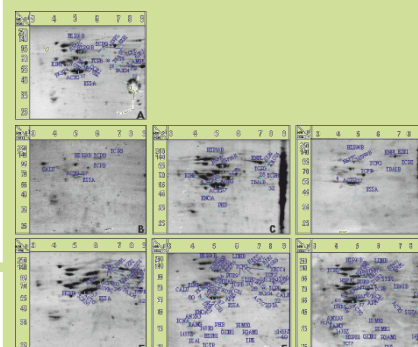


Figure 4 – 2-DE gels of proteins from a human cell tumor line, HCT116.