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1. RNA-Seq. 2. Cão. 3. Co-cultivo. 4. Miofibroblastos. 5. Matriz extracelular. I. Título.	

RESUMO

PULZ, L. H. **Isolamento e caracterização de Fibroblastos Associados ao Câncer provenientes de Mastocitomas caninos e sua influência sobre a malignidade de células neoplásicas:** uma abordagem molecular, patológica e *in vitro*. 2019. 112 p. Tese (Doutorado em Ciências) – Faculdade de Medicina Veterinária e Zootecnia, Universidade de São Paulo, São Paulo, 2019.

Os mastocitomas cutâneos (MCTs) são neoplasias comuns em cães e são considerados potencialmente malignos. Diversas pesquisas tentaram identificar biomarcadores para melhor predizer o comportamento biológico deste tumor. Além disso, estudos envolvendo o cultivo primário de MCTs caninos podem ser uma ferramenta valiosa para a análise das propriedades funcionais das células. O objetivo deste estudo foi identificar vias moleculares ligadas a características de malignidade histopatológicas, menor tempo de sobrevida e pior prognóstico associados ao MCT. Além disso, objetivamos investigar o comportamento de mastócitos *in vitro* obtidos a partir de MCTs de diferentes graus histopatológicos e determinar o tipo de interação com os fibroblastos estromais. Realizamos análises de expressão gênica em MCTs únicos obtidos de 15 cães e identificamos dois subtipos distintos de tumor – alto risco e baixo risco - associados a diferenças nos graus histológicos, tempos de sobrevida, índices Ki67 e ocorrência de morte devido a doença. Análises comparativas de perfis de sequência de RNA revelaram 71 genes diferencialmente expressos entre MCTs de alto e baixo risco. Ademais, examinamos redes de co-expressão gênica para explorar as funções biológicas dos genes identificados. A construção da rede revelou 63 módulos gênicos, dos quais 4 foram significativamente associados ao grupo mais agressivo. Dois dos módulos gênicos positivamente correlacionados com MCTs de alto risco também foram associados à proliferação celular e à matriz extracelular. No topo do módulo de matriz extracelular, foram identificados genes com funções diretamente relacionadas àqueles de fibroblastos associados ao câncer (CAFs). Análises imuno-histoquímicas também revelaram um maior número de CAFs em MCTs de alto risco. Os experimentos de cultivo foram feitos imediatamente após a ressecção cirúrgica e as células foram cultivadas em DMEM-F12 completo por 4 a 7 passagens. Os mastócitos foram evidenciados por coloração com Romanowsky e azul de toluidina com perda progressiva de seus grânulos em cultivo. A confirmação de fibroblastos como células aderentes foi feita por qRT-PCR para o gene da Proteína Específica de Fibroblastos 1 (FSP1). A caracterização dos fibroblastos

cultivados como miofibroblastos foi realizada por imunofluorescência para α -actina de músculo liso (SMA) e vimentina. A percentagem de células viáveis no sobrenadante foi determinada a cada passagem. Durante as 4-10 semanas de cultivo sem adição de fatores de crescimento ou citocinas, a população de mastócitos vivos diminuiu progressivamente e os fibroblastos e miofibroblastos continuam a crescer até a senescência. Amostras de MCTs de alto grau foram viáveis por períodos mais curtos ($P = 0.0442$) e menor número de passagens ($P < 0.0001$). Examinamos também os efeitos a curto prazo dos fibroblastos estromais na viabilidade dos mastócitos neoplásicos em diferentes condições de culturas. O contato célula-célula foi a melhor condição em que maior proporção de mastócitos neoplásicos permaneceu viável em comparação com todas as outras condições, isto é, utilizando-se de inserto e no cultivo de mastócitos isolados ($P < 0.05$). Verificamos também que os mastócitos neoplásicos não ficam viáveis por mais de 4 dias na ausência de fibroblastos ou de seus fatores solúveis. Estes resultados indicam uma importante interação entre os mastócitos e os fibroblastos, que podem ocorrer no microambiente tumoral.

Palavras-chave: RNA-Seq. Cão. Co-cultivo. Miofibroblastos. Matriz extracelular.

ABSTRACT

PULZ, L. H. **Isolation and characterization of Cancer Associated Fibroblasts from canine Mast Cell Tumors and its influence on the malignancy of neoplastic cells: a combined molecular, pathologic and *in vitro* approach.** 2019. 112 p. Tese (Doutorado em Ciências) – Faculdade de Medicina Veterinária e Zootecnia, Universidade de São Paulo, São Paulo, 2019.

Mast cell tumours (MCTs) are common neoplasms in dogs and are considered potentially malignant. Several researches have attempted to identify biomarkers to better predict biological behavior for this tumor. In addition, studies with primary culture of canine MCTs could be a valuable tool for the analysis of the cells functional properties. The objective of this study was to identify molecular pathways connected to histopathological malignancies, shorter survival time and poor prognoses associated with MCTs. Moreover, we aimed to investigate the *in vitro* behavior of mast cells obtained from canine cutaneous MCTs of different histopathological grades and the type of interaction with the stromal fibroblasts. We performed genome-wide gene expression analyses on tissues obtained from 15 dogs with single MCTs, and identified two distinct tumour subtypes - high-risk and low-risk - associated with differences in histological grades, survival times, Ki67 indices, and occurrence of death due to the disease. Comparative analyses of RNA sequence profiles revealed 71 genes that were differentially expressed between high and low-risk MCTs. In addition to these analyses, we examined gene co-expression networks to explore the biological functions of the identified genes. The network construction revealed 63 gene modules, 4 of which were significantly associated with the more aggressive tumour group. Two of the gene modules positively correlated with high-risk MCTs were also associated with cell proliferation and extracellular matrix-related terms. At the top of the extracellular matrix module category, genes with functions directly related to those of cancer-associated fibroblasts (CAFs) were identified. Immunohistochemical analyses also revealed a greater number of CAFs in high-risk MCTs. Culture experiments were made immediately after surgical resection and cells were cultured in complete DMEM-F12 for 4 to 7 passages. Mast cells were stained with Romanowsky and toluidine blue and showed progressive loss of their granules in culture. The presence of fibroblasts as adherent cells was confirmed by use of qRT-PCR for Fibroblast-specific Protein 1 (FSP1) gene. The characterization of cultured fibroblasts as myofibroblasts was performed by immunofluorescence for α-smooth

muscle-actin (SMA) and vimentin. The percentage of viable cells in the supernatant was determined in each passage. During 4–10 weeks of culture without any addition of growth factors or cytokines, living mast cell population decreased progressively and adherent fibroblasts and myofibroblasts continue to grow until senescence. High-grade MCTs samples were viable for shorter periods in culture ($P=0.0442$) and lower number of passages ($P<0.0001$). We also have examined the short-term effects of stroma fibroblasts on neoplastic mast cells in different cultures conditions. The cell-cell contact co-culture was the best condition in which canine neoplastic mast cells remained viable in highest proportion during the experiment compared to all other conditions, i.e. with the transwell condition and mast cells isolated cultures ($P<0.05$). We also found that isolated neoplastic mast cells are not viable for more than 4 days in the absence of fibroblasts or their soluble factors. These results indicate an important interaction between mast cells and fibroblasts, which may also occur in the tumor microenvirnomental setting.

Keywords: RNA-Seq. Dog. Co-culture. Myofibroblast. Extracellular matrix.

1. GENERAL INTRODUCTION

In view of the variable biologic behavior of canine cutaneous mast cell tumors (MCT), development of appropriate prognosis and treatment for individual affected dogs can be very difficult. Advances in human molecular medicine have sought to understand the molecular underpinnings of cancer development, metastatic pattern, and response to treatment. In canine oncology, over the past decades, much evidence has emerged indicating that a substantial part of the variability in tumor behavior is genetically determined, with age, breed, tumor location, environmental conditions, and concurrent therapy playing important contributory roles.

A profile of the gene variations of canine MCTs could guide more precise prognosis, and even allow the selection of drugs or treatment protocols that could minimize harmful side effects or ensure more successful outcomes. Additionally, molecular studies could indicate individual's susceptibility to diseases, allowing veterinarians and owners to design a plan for prevention and early diagnosis.

Another point to consider is the success in the treatment of several human cancers related to the development of targeted therapies. However, in order to develop more effective therapies for canine MCTs, it is necessary to learn about the cells that comprise the tumor, their characteristics, functionality, and interactions with the tumor microenvironment. Little is known about the different mast cell populations in dogs and the requirements for canine neoplastic mast cells culture remain poorly defined.

The objective of this work was to approach the canine cutaneous MCT in several aspects: *in vitro* characteristics, cell interactions and molecular signatures of malignancy. In the present research, we have characterized different RNA expression profiles using high-throughput sequencing (HTS) and compared with survival time and significant prognostic markers for canine cutaneous MCTs, including histologic grading and proliferation activity. In addition, *in vitro* studies have provided information for the understanding of the dynamics of neoplastic mast cell growth, suggesting an important role for cancer-associated fibroblasts in this disease.

2. GENERAL CONCLUSION

The aim of this study was to investigate mechanisms to understand the canine MCT malignant behavior beyond morphological characteristics. First, we found differentially expressed genes in high risk tumors related to the extracellular matrix. Changes in gene expression that mediate invasion and metastasis may not reflect histopathological alterations that could be evaluated in the microscopic examination. The differences in gene expression displayed by the cutaneous MCTs that had high grade of malignancy, high proliferation and short survival time appear to reflect the requirements of the extracellular stimuli. The available literature particularly documents the connection between stromal cells as CAFs and poor prognoses, and this was also verified in the present study. In addition, to highlight the importance of this tumoral compartment, we identified selected emerging genes affecting the malignant MCTs phenotype.

Then, we demonstrated the interaction between tumor cells and stromal fibroblasts *in vitro*. It seems clear that stromal fibroblasts and CAFs can influence neoplastic mast cell activity in culture condition. Future studies, are necessary to investigate several stroma-specific factors associated with canine mast cell tumor and elucidate the specific mechanisms of action of these molecules.

Cell migration is facilitated by reduced cell-cell and cell-ECM adhesion and cell softening achieved through cytoskeletal reorganisation. Some of these altered features mediate canine cutaneous MCT invasion and metastasis and may be potential targets for novel therapies directed toward the microenvironment. Furthermore, controlled studies are necessary to assess the real effect of chemotherapy protocols. Thus, *in vitro* experimental investigations will be required to demonstrate the effects of antineoplastic drugs and/or to clarify the role of strmoal cells derived molecules (e.g. on cell adhesion, deformability and motility) on neoplastic canine mast cells. The need for an improved understanding of the progression and treatment responses of MCTs has pushed for increased relevance of canine MCT *in vitro* tumor models.

Finally, we believe that further studies are necessary to identity stromal cell derived factors and their mechanisms of action to provide new tools for the establishment of more accurate prognosis or to predict tumor response to chemotherapy.

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