Immunohistochemical expression of lipoxxygenase-5 (LOX-5) in canine normal urinary bladder, cystitis and transitional cell carcinoma

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OBJECTIVES

Canine transitional cell carcinoma (TCC) mimics human invasive TCC. Human TCC overexpress lipoxxygenase (LOX)-5 and the use of target inhibitors has been proved effective. In this study, we investigated the immunohistochemical (IHC) expression of LOX-5 in normal canine urinary bladder, cystitis and TCC. LOX-5, cyclooxygenase

(COX)-1, COX-2 IHC expression and their relationship among the different groups were investigated.

METHODS

Biopsies of cystitis and TCC were reviewed (2012–2016). Dogs were excluded if had received steroids, non-steroidal antiinflammatory drugs (NSAIDs) and/or chemotherapy prior to tissue collection. Samples of histologically normal bladder were retrieved from the necropsy archive. Representative sections were submitted for anti-LOX5, COX-1 and COX-2 IHC. Distribution and intensity were assessed semi-quantitatively and an IHC score was obtained for each marker. Immunohistochemical results were compared among normal epithelium, cystitis and TCCs. Correlations between variables were analysed with Spearman and Mann Whitney.

RESULTS

Twenty-nine TCCs, 13 cystitis and 10 controls were included. All TCCs were diagnosed as invasive and histologically high-grade. Cystitis were characterised by similar lymphoplasmacytic and occasionally neutrophilic infiltrates. LOX-5 was expressed in 95% of TCCs, 23% of cystitis and 10% of controls. LOX-5 and COX-2 IHC scores were significantly ($P < 0.01$) higher in TCCs vs cystitis and normal bladders.

STATEMENT (CONCLUSIONS)

TCC is the most common canine urinary-tract tumour. Chemotherapy is commonly advised, but responses are poor to modest. Results of this study place the rationale for the investigation of new agents such as tepoxalin, an NSAID with anti COX-2 and LOX-5 effect.

Genome-wide analysis of canine oral malignant melanoma (OMM) metastasis-associated gene expression

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OBJECTIVES

Melanoma of the oral cavity is the most common melanocytic neoplasm in dogs and has a high metastatic potential. The study objective was to identify a canine primary OMM pro-metastatic gene expression signature.

METHODS

Canine Gene 1.1 ST Arrays were employed for comparative genome-wide expression profiling of formalin-fixed paraffin-embedded biopsies of 18 canine primary OMM that metastasised and 10 canine primary OMM that did not metastasise. Results were validated by RT-qPCR.

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