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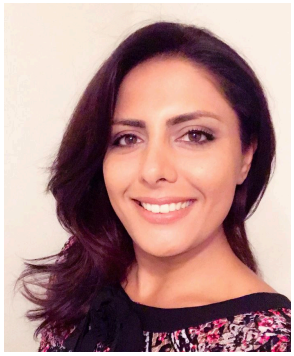

KEYWORDS – Cancer; cancer-associated stroma, canine mammary tumour, gene expression, mammary carcinoma, FFPE-RNA isolation, RNA sequencing, LCM, tumour microenvironment, tumour stroma

MAIN FIELDS OF RESEARCH; ABSTRACT

Cancer-associated stroma (CAS) plays a key role in cancer initiation and progression. Spontaneously occurring canine mammary carcinomas (mCA) are viewed as excellent model of human mCA. Considering the importance of CAS for human cancer, it likely plays a central role in canine tumours as well. So far however, canine CAS lacks characterisation, and it remains unclear whether the biology between CAS from canine and human tumours is comparable. We have successfully established a protocol to specifically isolate CAS and normal stroma from archival, formalin-fixed paraffin embedded (FFPE) canine mCA specimen using laser-capture microdissection (LCM) for analysis by next-generation sequencing (NGS). The possibility to study gene expression in specific sections of archival FFPE tissue unlocks a new dimension of hitherto difficult-to-analyse samples, which now become amenable for investigation.
Using this approach, we have analysed CAS and matched normal stroma from 15 clinical cases of canine simple mCA. We show that, similar to human mCA, CAS in canine mCA clearly differs from normal stroma. Comparative analyses of our dataset with CAS from human mCA reveal significant overlaps between the two species and suggest a significant degree of conservation in the mechanisms underlying CAS. Thus, our approach has the potential to identify novel key candidates that influence CAS biology and cancer progression. This is the first report to provide a comprehensive analysis of CAS in canine simple mammary carcinomas, and further supports validity of the dog as model for human mCA.

SPECIAL TECHNIQUES AND EQUIPMENT

Laser-capture microdissection (LCM), Next-generation sequencing, Immunohistochemistry, qPCR