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Evaluation of c-*erbB2/neu* Oncogene Status in Canine Mammary Tumors on Tissue Microarray

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Introduction

The c-erbB2/neu oncogene (alias HER2, NEU) encoding a tyrosine kinase receptor protein, the overexpression of which correlates with a more rapid progression and a worse prognosis in human breast cancer [1]. Otherwise, this gene is still poorly investigated in veterinary oncology [2,3]. To gain insight into the patterns of c-erbB2/neu status in canine mammary tumor, we constructed one such mammary tumor tissue microarray (TMA) from 60 tumors from our lab. This enabled the amplification of c-erbB2/neu oncogene of all 60 tumors to be simultaneously analyzed by chromogenic in situ hybridization (CISH). The aim of this study was to evaluate status of c-erbB2/neu oncogene in canine mammary tumors and to correlate this status with the differentiation grade of neoplasm.

Materials and Methods

A total of 60 formalin-fixed, paraffin-embedded mammary tumor samples were arrayed (PETAGEN INC, Korea). After construction of the array blocks, multiple consecutive 4-㎛ sections were cut and placed on charged poly-L-lysin-coated slides for CISH. c-erbB2/neu oncogene status was determined by using FITC labeled canine c-erbB2/neu DNA probe (innogenex, USA). CISH procedure was performed by Zhao et al [4].

Results and Discussion

c-erbB2/neu oncogene amplification detected by CISH was visualized typically as large clusters or by many dots in the nucleus. In the canine mammary carcinoma cases, detection rate of c-erbB2/neu oncogene amplification is higher than that of benign tumors. In this work, we constructed a TMA from 60 canine mammary tumors. TMA techniques enables many tumor samples to be studied simultaneously in a single experiment. So, this will be widely use in veterinary oncology.

References

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