

Unveiling the Molecular Signature of Salivary Gland Neoplasms with Tumor-specific Fusion Oncogenes

Fusion oncogenes (FOs) resulting from chromosomal translocations are linked to the initiation and progression of several human cancers including benign and malignant salivary gland neoplasms.¹ The FO may encode for novel fusion proteins or ectopically expressed normal protein. Studies demonstrating FO in healthy individuals, indicate that the mere presence of FO does not merit tumor formation.²⁻⁴ Several additional factors shift the balance in favor of tumorigenesis. These include the rate of FO formation, degree of penetrance (potential of the individual FO to induce tumor), susceptibility of the tissue/cells and finally other genetic and epigenetic alterations. Double-strand breaks (DSBs) represent the first stage in the formation of fusion oncogenes as most of the DSBs do not undergo DNA repair. Currently, there is no collaborating evidence for any physiologic event causing FO. External factors including ionizing radiation are documented to be the primary cause of DSBs in leukemias and thyroid cancer. Since most of the benign and malignant salivary gland tumors have radiation as one of their etiologic factors, it is safe to presume that DNBs could be a common event in salivary gland neoplasms.¹⁻⁴

Nordkvist et al and Persson et al⁶ have shown a recurrent t(6;9)(q22-23;p23-24) translocation in adenoid cystic carcinoma (ACC). This translocation has in most cases led to the fusion of transcription factor gene NFIB and MYB oncogene.^{5,6} Brill et al⁷ and West et al⁸ noticed MYB–NFIB FO was specific for ACC and was not detected in other benign or malignant salivary gland neoplasms. Nordkvist et al elicited a characteristic t(11;19)(q21-22;p13) translocation causing fusion of transcriptional coactivators MAML2 and CRTC1 in salivary, bronchial, and thyroid glands mucoepidermoid carcinoma (MEC).¹⁰ CGH study on MEC have shown that the presence of MAML2 and CRTC1 FO has a impact on the overall prognosis. Jee et al¹¹ subdivided MEC into three groups based on the presence or absence of FO: (1) FO positive tumors: low grade, favorable prognosis with no, or few genomic imbalances, (2) FO positive tumors: high grade, unfavorable prognosis with multiple genomic imbalances, (3) FO negative non-MEC adenocarcinomas: unfavorable outcome with multiple genomic imbalances.¹¹ Enlund et al¹² demonstrated CRTC1-MAML2 gene fusion in few cases of Warthin's tumor. Winnes et al¹³ Fehr et al¹⁴ suggested that the presence of the CRTC1-MAML2 oncogene could represent either the metaplastic variants of Warthin tumors or the possibility of malignant transformation to MEC or may even represent a misdiagnosed case of MEC. Moller et al noticed a repetitive EWSR1-POU5F1 gene fusion due to t(6;22)(p21;q12) translocation in high grade MECs.¹⁵

FO due to their tumor specificity may also serve as a diagnostic biomarker especially for rare salivary gland neoplasms. Hyalinizing clear cell carcinoma (HCCC) has similar morphology to clear cell variants of epithelial-myoepithelial carcinoma, myoepithelial carcinoma or MEC. Demonstrating the HCCC specific EWSR1-ATF1 FO will serve as a diagnostic biomarker.¹⁶ ETV6-NTRK3 gene fusion has been demonstrated in more than 90% of mammary analogue secretory carcinoma of salivary glands distinguishing it from cell carcinoma and low-grade cystadenocarcinoma.^{17,18} PLAG1 and HMGA2 fusion noticed in most cases of pleomorphic adenoma may serve to distinguish it from diagnostically challenging differentials including adenoid cystic carcinoma, polymorphous low-grade adenocarcinoma.^{19,20} Several cases of carcinoma-ex-pleomorphic adenoma have also shown PLAG1 and HMGA2 fusion in addition to other genetic alterations.²¹

Surgical resection is the primary treatment protocol for salivary gland neoplasms. Treatment for patients presenting with advanced invasion, multiple recurrence, or distant metastasis is mostly palliative in nature as there are no definitive treatment modalities for the same. Studies focussing in disclosing the unique tumor specific FOs may serve as diagnostic biomarkers. The targets for these fusion oncogenes have been responsive to treatment modalities, emphasizing its role in targeted therapy. Unveiling the molecular signatures may also aid to elucidate the pathogenesis behind the difference in aggressiveness among tumors of the same histopathological subtype.

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