

Review

## PTEN Deregulation Mechanisms in Salivary Gland Carcinomas

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**Abstract.** Among the tumour suppressor genes that affect critically cell functions and homeostasis, phosphatase and tensin homolog deleted in chromosome 10 (*PTEN*- gene locus: 10q21) regulates the *PI3K/Akt/mTOR* signalling pathway. *PTEN* is deleted, mutated or epigenetically hypermethylated in a variety of human solid malignancies. Salivary gland carcinomas (SGCs) belong to the head and neck carcinomas (HNCs) super category of solid malignancies. Histo-pathologically, they demonstrate a significant diversity

due to a variety of distinct and mixed subtypes. Genetically, they are characterized by a broad spectrum of gene and chromosomal imbalances. Referring specifically to suppressor genes, *PTEN* deregulation plays a critical role in signaling transduction in the corresponding SGC pre- and malignant epithelia modifying the response rates to potential targeted therapeutic strategies. In the current review, we explored the role of *PTEN* deregulation mechanisms that are involved in the onset and progression of SGCs.

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Key Words: *PTEN*, suppressor gene, salivary, gland, mutation, review.

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Concerning the carcinogenic process in normal epithelia, there are two main categories of genes that critically enhance their neoplastic and malignant transformation (1-3). Over activation of oncogenes –such as RAS family members– combined with silencing of tumor suppressor genes negatively influence the cell cycle rhythm and a significant spectrum of signal transduction pathways in solid malignancies of different histogenetic origin (4-6). Among suppressor genes, tumor phosphoprotein 53 (*TP53*, gene locus: 17p13) and phosphatase and tensin homolog deleted in chromosome 10 (*PTEN*-gene locus: 10q21) control crucial molecular pathways (7, 8). They are involved in apoptosis, cell arrest, DNA base repair, signalling transduction down-regulation, and generally in genome stability (9, 10). Specifically, *PTEN* encodes for a lipid phosphatase that

consists of two distinct domains: a C2 and a protein tyrosine phosphatase that provides its enzymatic activity (11). Normally, PTEN protein catalyses inositol dephosphorylation, whereas in neoplastic and cancerous cell this function is lost (12). This biochemical reaction is significant for the inhibition of Akt signalling pathway that regulates cell survival, growth, proliferation, migration, and tissue formation (13, 14). PTEN decreases the nuclear expression and localization of cyclin D1 cell cycle kinase preventing AKT over activation that promotes the cell cycle (15) Somatic mutations, deletions but also epigenetic silencing - due to hyper methylation of the *PTEN* gene promoter- have been detected in a variety of solid malignancies (16-18). For these reasons, *PTEN* functional silencing leads to an aberrant activation of the phosphoinositide 3-kinase/Phosphorylated protein kinase B/mammalian target of rapamycin (*PI3K/AKT/mTOR*) downstream genes that triggers an excessive signal transduction to the nucleus (19). Modern targeted therapeutic strategies based on *PTEN* enhancement combined with PI3K/AKT/MTOR protein pathway inhibition are under development and evaluation in solid malignancies (20-23). In the current review, we describe and analyze *PTEN* gene deregulation mechanisms in salivary gland carcinomas (SGCs) and explore their role in onset, progression, and biological behaviour.

### SGCs: Histo-genetic Subtypes

Salivary gland epithelia are the histological substrates for the onset of a broad spectrum of solid malignancies. SGCs represent a subset of head and neck carcinoma (HNC) super family characterized by distinct histo-genetic profiles (24). World Health Organization (WHO) tumor classification identifies a variety of SGCs including predominantly mucoepidermoid (MEC), adenoid cystic (ADCC) and salivary duct (SDC) carcinomas (25). The first category (MEC) corresponds to well- and moderately-differentiated carcinomas affecting mainly the parotid glands (26). Additionally, ADCC is predominantly a well differentiated neoplasm and affects frequently all major glands. Interestingly, a sub-group of them demonstrates increased recurrence rates following surgical excision combined or not with a radiation-based therapeutic regimen (27). In contrast, SDCs represent high-grade malignancies characterized by local and distant metastases that appear as rapidly formed neck masses (28) Besides the abovementioned main SGC histotypes, there are also other less frequently observed including clear-cell carcinoma (CCC), basal cell adenocarcinoma (BCAD), acinic-cell carcinoma (ACC), cystadenocarcinoma (CADC), polymorphous adenocarcinoma (PADC), sebaceous adenocarcinoma (SADC), secretory carcinoma (CEC), mucinous adenocarcinoma (MADC), and sebaceous lymphadenocarcinoma (SLADC) (29). Furthermore, more ‘exotic’ and rare with increased

biological aggressiveness carcinoma sub-types include epithelial–myoepithelial carcinoma (EMC), carcinoma ex pleomorphic adenoma (CexPAD), intra-ductal carcinoma (INDC), carcinosarcoma (CSC), squamous cell carcinoma (SCC), anaplastic small cell carcinoma (ASCC), and finally undifferentiated carcinomas (UNC) (30).

Differences have been reported, regarding gross chromosomal instability (CI) as aneuploidy/polysomy/ monosomy and related gene imbalances between SGCs histo-variants (31, 32). ADCs demonstrate a tendency for translocations and gene gains in chromosomes X/ 6/8, whereas SDCs are characterized by point mutations and amplifications of chromosome 17 genes (33, 34). BCC cases cytogenetically demonstrate deletions of specific loci on chromosome 16 (35). In contrast, MECs are characterized by translocations and deletions affecting chromosomes 9/11/15/19 (36). Furthermore, rare subtypes, such as CexPAD and PADC are characterized by translocations and amplifications on chromosomes 8/12 and chromosomes X/1/2/14/19, respectively (34, 37). Similarly, gene amplifications and translocations on chromosomes 12/15/22 have been detected in CCCs and SECs (38).

### PTEN Alterations in SGCs

*PTEN* suppressor gene silencing -due to mutations predominantly or deletion- leads to reduction of the corresponding protein expression levels in SDCs. Moreover, these genetic events combined with activation of specific oncogenes is responsible for the biological aggressiveness of the malignancy (39). According to a massive parallel sequencing gene analysis (MSK-IMPACT), a subset of examined SDCs demonstrated *PTEN* point mutations combined or not with mutated or amplified oncogenes including *ERBB2*, *PIK3CA*, *HRAS*, *ALK*, and *BRAF* (40). Interestingly, the combination of *PTEN* mutations and a novel HNRNPH3-ALK rearrangement -the ALK G1202R- was associated with increased resistance to targeted therapeutic regimens in the corresponding SDC and ex pleomorphic adenoma cases. Similarly, a study based on protein analysis by immunohistochemistry revealed loss of *PTEN* expression combined with HER2/neu over expression in a subset of SDCs (41).

Furthermore, the researchers suggested that high-mobility group AT-hook 2 (HMGA2) and *PTEN* should be considered potential targets for applying specific therapeutic strategies in SDCs. In another study, the researchers detected different *PTEN*/HER2/PI3KC/p AKT co-expression patterns in a series of SGCs that modify their biological behaviour (42). Analyzing the same molecules, another study group identified reduced *PTEN* protein expression, specifically in poorly differentiated solid SACCs (43). They also reported a combination of mTOR over activation and *PTEN* loss associated with an increased metastatic potential. According

to another study, combined PIK3CA mutations and PTEN deficiency are responsible for an aggressive SDC phenotype but also targets for specific chemotherapeutic regimens (44). Additionally, *PTEN* silencing leads to an excessive production of the WD repeat containing protein 66 (WDR66), which is involved in the onset and progression of the epithelial mesenchymal transition (EMT). Loss of PTEN functional activity is indirectly responsible for cancer cell proliferation and metastatic invasion (45).

Besides the main SGC histotypes, *PTEN* gene deregulation affects also rare and some “exotic” SGCs variants. A next generation sequencing analysis in a series of aggressive salivary high-grade neuroendocrine carcinomas showed a co-downregulation of PTEN and retinoblastoma 1 (RB1) suppressor genes combined with overexpression of components of the PI3KCA/AKT/mTOR pathway (46). Furthermore, another genetic analysis in a series of apocrine SDCs revealed some cases characterized by PTEN mutation and others with deletion (47). Concerning another rare neoplasm, the murine salivary gland tumour (SGT), a study group detected a Smad and PTEN genes co-deletion that enhances its aggressiveness (48). Additionally, the combination of PTEN loss of expression due to mutations and the AKT/mTOR overactivation has been also reported in salivary gland secretory carcinoma (SSGC) (49). Similarly, PTEN mutations/deletions characterize a subset of the Carcinoma ex pleomorphic adenoma (CXPA). Additionally, hyalinising clear cell carcinoma (HCCC) subtype demonstrate similar genetic signatures (50, 51). In conjunction, another genetic analysis in secretory myoepithelial carcinomas (SMCA) - a very rare, signet ring-like mucinous carcinoma with a myoepithelial component – revealed very specific and unique PTEN mutation and splicing variant (c.655C>T p. Q219\*, and c.1026+1G>A p. K342, respectively) (52). Similarly, a unique PTEN frameshift deletion (p. G36Dfs\*18) has been detected in salivary gland intraductal papillary mucinous neoplasm (SG IPMN), a rare variant of SGC (53). Additionally, another “exotic” variant of SDC, the salivary duct carcinoma with rhabdoid transformation harbors combinations of specific mutations in *TP53* and *AKT* (54).

In conclusion, PTEN suppressor gene silencing plays a critical role in SGCs by enhancing signal transduction to the nucleus. Mechanisms of this deregulation include different point mutations and deletions of this specific gene locus that demonstrate in different SGC histo-types (55). PTEN silencing enhances PI3K/AKT/mTOR overactivation in pre- and malignant salivary gland epithelia. Additionally, PTEN deficiency modifies the response rates to potential targeted therapeutic strategies in SGCs that are based on specific genetic signatures detected by novel multi-gene molecular analyses (56, 57). In addition to *PTEN* down-regulation, differences among SGC histotypes are demonstrated by altered expression of

factor-kappa B (NKkB1/p65), c-Jun N-terminal kinase (JNK1), growth arrest, and DNA damage (58). Finally, *PTEN* mutations are frequently combined with *PIK3CA* mutations, which also include a novel transforming growth factor (TFG)-PIK3CA fusion mechanism in borderline, neoplastic-like entities, such as sclerosing polycystic adenoma (59).

## Conflicts of Interest

The Authors have no conflicts of interest to declare in relation to this study.

## Authors' Contributions

ET, AC, and VP: Design of the study and article writing; DS, DP, VR, NM, and EK: academic advisors; PF, AA, SP, DR, GP, LM, MA, and SM: collection and management of references and published data. All Authors read and approved the final article.

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*Received October 4, 2023*

*Revised November 12, 2023*

*Accepted November 13, 2023*