



Article

Adenosquamous Carcinomas and Mucinous Adenocarcinoma of the Minor Salivary Glands: Immunohistochemical and Molecular Insights

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Abstract: There is confusion about the diagnosis, histogenesis and taxonomical efforts regarding adenosquamous carcinomas (ASCs) and mucinous adenocarcinomas (MACs), especially with calls for reconsidering the nature of *high-grade* mucoepidermoid carcinoma (MEC). This study aims to compare the genetic profiles of ASCs and MACs that have been previously reported in the literature and investigate if either ASC or MAC is closer in genetic mutations to high-grade MEC. Systematic searches in the NCBI, Web of Science, and Scopus databases were performed between January 2000 and August 2022. The retrieved genetic mutations were processed and annotated. Protein–protein network analysis was conducted for each neoplasm. The results were viewed and discussed in terms of molecular oncogenesis of ASCs and MACs at different topographies. Molecular profile mapping was conducted by annotating all the retrieved genes for each neoplasm using genetic network analysis (Cytoscape software program). The genetic profile of each lesion was compared to that of *high-grade* MEC. To conclude, both genetic profiles do not tend to intersect specifically with high-grade MEC, except for the generic mutations commonly detected in all high-grade head and neck tumors. However, the availability of data on the molecular profile of each lesion limits the generalizability of the findings of this study.

Keywords: adenosquamous carcinoma; mucinous adenocarcinomas; network analysis



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1. Introduction

Adenosquamous carcinomas (ASCs) of the minor salivary glands elude all taxonomical efforts because their diverse morphologic features, disparate molecular involvement, and histogenesis remain controversial. Mucinous adenocarcinomas (MACs) pose the same challenge because they have no specific immunohistochemical profiles and are diagnosed by excluding other salivary-type mucin-producing carcinomas.

Controversy about the proper classification of these lesions is fierce, especially since they show a strong predilection for affecting minor salivary glands. It has been found recently that ASCs of the lung resemble pulmonary adenocarcinomas genetically; both harbor an EGFR mutation [1]. Additionally, the KRAS mutation characterizes pancreatic ASCs, causing confusion about the impact of topography on the cytogenetic profile of ASCs as a whole. EGFR and KRAS mutation, both characteristic of adenocarcinoma, have been reported in adenosquamous carcinoma (ASC) of the lung. Using microdissection molecular analysis has shown identical mutations in both morphologic components of ASC, leading to a phenotypically heterogeneous but genetically clonal tumor [2–4].

The ASC profiles of the oropharynx [5], salivary glands [6], intestines [7], and cervix [8,9], among others [10], are also distinct. The diverse adnexal and parenchymal profiles of ASCs pose fierce taxonomical controversy, especially head and neck ASCs. Like well-differentiated squamous cell carcinomas (SCCs), ASCs tend to affect the surface epithelium

more than the glandular epithelium and are often associated with keratin pearl formation and carcinoma in situ [11]. Histologically, ASCs of lung and minor salivary glands show similar morphologic features, as both originate from the surface mucosa and reveal mixed components, separate areas of adenocarcinoma, and squamous cell carcinoma arising from the surface epithelium. Similar to ASC of the lung, the prognosis of ASCs of the minor salivary glands is poor. Furthermore, ASCs express DeltaNp63 and mucin markers differently [12–14]. ASCs have even been considered variants of SCCs [5,15].

On the other hand, salivary-type MACs have not been well defined. Their blurry conceptualization relates to the frequently changing taxonomy and to the blurry characterization of their morphologic features. Although the World Health Organization (WHO) has finally officialized a histologic and molecular description of MACs, the reported cases in the medical literature rarely align with the WHO's definition [16]. Complicating the matter, the expression of mucin markers has confused ASCs with mucoepidermoid carcinomas (MECs), especially MAML2-negative high-grade MECs, mucinous adenocarcinomas, and other mucin-rich carcinomas [17–20], which demonstrate a remarkable basal component with a squamoid basophilic pattern [21]. This study aims to compare the genetic profiles of ASCs and MACs that have been previously reported in the literature and investigate if either ASC or MAC is closer in genetic mutations to high-grade MEC.

2. Materials and Methods

2.1. Reviewing the Literature

Systematic searches in the PubMed (Medline), Web of Science, and Scopus databases were performed between January 2000 and August 2022. The retrieved genetic mutations were processed and annotated. Protein–protein network analysis was conducted for each neoplasm. The results were viewed and discussed in terms of molecular oncogenesis. The retrieved genetic mutations were processed and annotated. Protein–protein network analysis was conducted for each neoplasm. The results were viewed and discussed in terms of molecular oncogenesis.

Search strategy

The selected databases were searched using a string query, which consisted of “head and neck * carcinoma,” AND “gene”, AND/OR “molecular”, AND/OR “adenosquamous”, AND/OR “adenocarcinoma” AND “mucin*” as medical subject headings.

Criteria of Inclusion

The search results were manually filtered to include the following.

1. All research papers must be original research articles that explore cases empirically.
2. All articles must be published in English.
3. All articles must investigate the diagnosed case molecularly.
4. All articles must justify the diagnosis of the lesion.
5. All published cases must include adequate clinical and histologic descriptions.
6. All published cases must report information about the patient survival.
7. Reporting molecular or immunohistochemical investigations, or both, is recommended.

Criteria of Exclusion

The scope of this review does not include the following:

1. Articles that include an abstract only.
2. Studies that reviewed previous works without reporting new cases.
3. Studies that investigated major salivary gland lesions or extra-salivary neoplasms.

2.2. Collating Molecular Findings in Non-Salivary ASCs and MACs

Molecular profile mapping was conducted by annotating all the retrieved genes to create for each neoplasm using genetic network analysis (Cytoscape software program). The number of molecularly investigated cases of non-salivary ASCs is much greater than that of the ASCs of minor salivary glands. Both of these cases show similar histologic features and diverse molecular profiling. The same holds true with non-salivary and

salivary MACs. Therefore, we create a genetic profile for each lesion to infer implications concerning the salivary-type MACs. After conducting the genetic network analysis, we relate the retrieved genes to the corresponding pathways. Finally, the genetic profiles of salivary-type lesions are compared to those of high-grade MECs, which were previously reported by Wang et al. [22].

3. Results

3.1. Immunohistochemical and Molecular Findings in Salivary ASCs and MACs

From previously published 34 articles [5,12,15,23–53], we retrieved the previously reported results on the ASCs and MACs of the minor salivary glands (Table 1). The reported results demonstrate that the diagnosis of ASCs discovered the existence of a neoplastic adenocarcinomatous component in the stroma underlying a surface SCC. However, the depth level of this component, the immunohistochemical findings, and the molecular investigations are not consistent in the reviewed studies. Several authors diagnosed ASCs based on their morphology without further investigations [25,26], while others used a panel of immunohistochemical markers (mainly CEA, CK7, CK20, EMA, CDX2, and CAM5.2) [32]. Less often, findings generated from next-generation sequencing (NGS), fluorescence in situ hybridization (FISH), and cytometry were reported [5,53].

Table 1. Summary of the reviewed case of ASCs and MACs of the minor salivary glands.

Author, Year	Refs.	Dx	Cases	Morphology	Mucin	Positive IHC	Molecular	Exclusion
Fukuda et al., 2002	[23]	ASC	4	AC + SCC	Y	CK14	No	Not Adenoid SCC
Keelawat et al., 2002	[24]	ASC	5	AC + SCC	Y	No	No	Not Adenoid SCC, not MEC
Sheahan et al., 2003	[25]	ASC	1	AC + SCC	Y	CK7 CAM5.2	No	Not given
Alos et al., 2004	[12]	ASC	5	AC + SCC	Y	CEA, CK7 CAM5.2	Aneuploid ASCs	Not MEC
Morita et al., 2005	[26]	ASC	1	AC + SCC	Y	No	No	Not given
Shinhare et al., 2008	[27]	ASC	1	AC + SCC	Y	No	No	Not given
Masand et al., 2011	[28]	ASC	4	AC + SCC	Y	No	For HPV	Adenoid SCC included
Fonseca et al., 2012	[29]	ASC	1	AC + SCC	Y	CEA, CK7/8/18	No	Not given
Pandilla et al., 2013	[30]	ASC	1	AC + SCC	Y	β -catenin	APC c.4315delC mutation	Not given
Ishida et al., 2014	[31]	ASC	1	AC + SCC	Y	CEA, HCK, CK7, CA19-9	No	Not given
Bhattacharyya et al., 2015	[32]	ASC	2	AC + SCC	Y	No	No	Not MEC, not SCC with mucoserous invasion, not adenoid SCC
Kass et al., 2015	[5]	ASC	42	AC + SCC	Y	No	-ve for MAML2	Not MEC
Magalhaes et al., 2015	[33]	ASC	1	AC + SCC	Y	CEA, CK7/20, EMA, CDX2 CAM5.2	No	Not AC, NOS
Sravya et al., 2016	[34]	ASC	1	AC + SCC	Y	34 β E12	No	Not MEC, not basaloid SCC, not adenoid SCC
Miura et al., 2017	[35]	ASC	1	AC + SCC	Y	34 β E12, CK7, CAM5.2	No	Not given

Table 1. Cont.

Author, Year	Refs.	Dx	Cases	Morphology	Mucin	Positive IHC	Molecular	Exclusion
Satomiet al., 2017	[36]	ASC	1	AC + SCC	Y	CEA, CK7	No	Not given
Kikuta et al., 2018	[37]	ASC	1	AC + SCC	Y	CK7/CK20	No	? Cribriform AC *
Rawal et al., 2018	[38]	ASC	1	AC + SCC	Y	CEA, CK7, CAM5.2	No	Not given
Eguchi et al., 2019	[39]	ASC	1	AC + SCC	Y	CEA, CK7, p53	No	Not given
Prabhakar et al., 2020	[15]	ASC	1	AC + recurrent SCC	Y	Pancytokeratin	No	Not adenoid SCC
Gao et al., 2002	[40]	MAC	1	MAC + features	Y	CK7	No	Not given
Notani et al., 2002	[41]	MAC	1	Classic MAC	Y	CK7	No	Not given
Abecasis et al., 2004	[42]	MAC	2	Classic MAC	Y	CK7, CK20, synaptophysin;	No	Not given
Shumway et al., 2007	[43]	MAC	1	Classic MAC	Y	CK7	No	Not given
Ide et al., 2009	[44]	MAC	1	Classic MAC	Y	CEA, HCK, CK7/20, EMA	No	Not given
Seoane et al., 2010	[45]	MAC	1	Classic MAC	Y	CK AE1/AE3/CK8, CK18, S100	No	Not given
Uchida et al., 2010	[46]	MAC	4	Classic MAC	Y	No	MDM2 AURKA	Not given
Slova et al., 2012	[47]	MAC	1	Colonic type adenocarcinoma + mucin	Y	AE1/AE3, CAM5.2, CK7, CK20, EMA	No	Not given
Bhat et al., 2014	[48]	MAC	1	MAC	Y	No	No	Not given
Mezmezian et al., 2015	[49]	MAC	1	MAC + eosinophil	Y	CK7, CK19, EMA, CEA	No	Mucinous metastatic carcinoma
De Benedittis et al., 2017	[50]	MAC	1	MAC + features	Y	CK7/8	No	Not given
Petersson et al., 2020	[51]	MAC	1	In a hybrid tumor	Y	Mammaglobin	ETV6 RET	MASC dominant
Aoki et al., 2020	[52]	MAC	1	Classic MAC	Y	CK7, CEA	No	Not given
Rooper et al., 2021	[53]	MAC	4	MAC + features	Y	CK7	AKT1 E17K	Not intraductal papillary mucinous ca.

(*) should be viewed with caution.

We retrieved the genetic data corresponding to 13 cases of ASCs and 15 cases of MACs of minor salivary glands. The histologic features of ASCs and MAC are shown in Figure 1. Figure 2 shows the genetic analysis of ASCs. What characterized the genetic profile are mutations in *BCOR*, *CDH1*, *CEP57*, *ERCC4*, *GEN1*, *KLF4*, *LAMA5*, *MAC*, *MET*, *MN1*, *MTOR*, *NF2*, *PCLO*, *PRDM1*, *RB1*, *RELN*, *RIK3R1*, *SMARCB1*, *SOS1*, and *TP53* genes. Figure 3 shows the genetic network analysis for the possible interrelations between these genes. Cases of MACs showed mutations in *AKT1*. Regarding the immunohistochemical profile of ASCs, the squamous component stains with p63, p40, and cytokeratin 5/6.

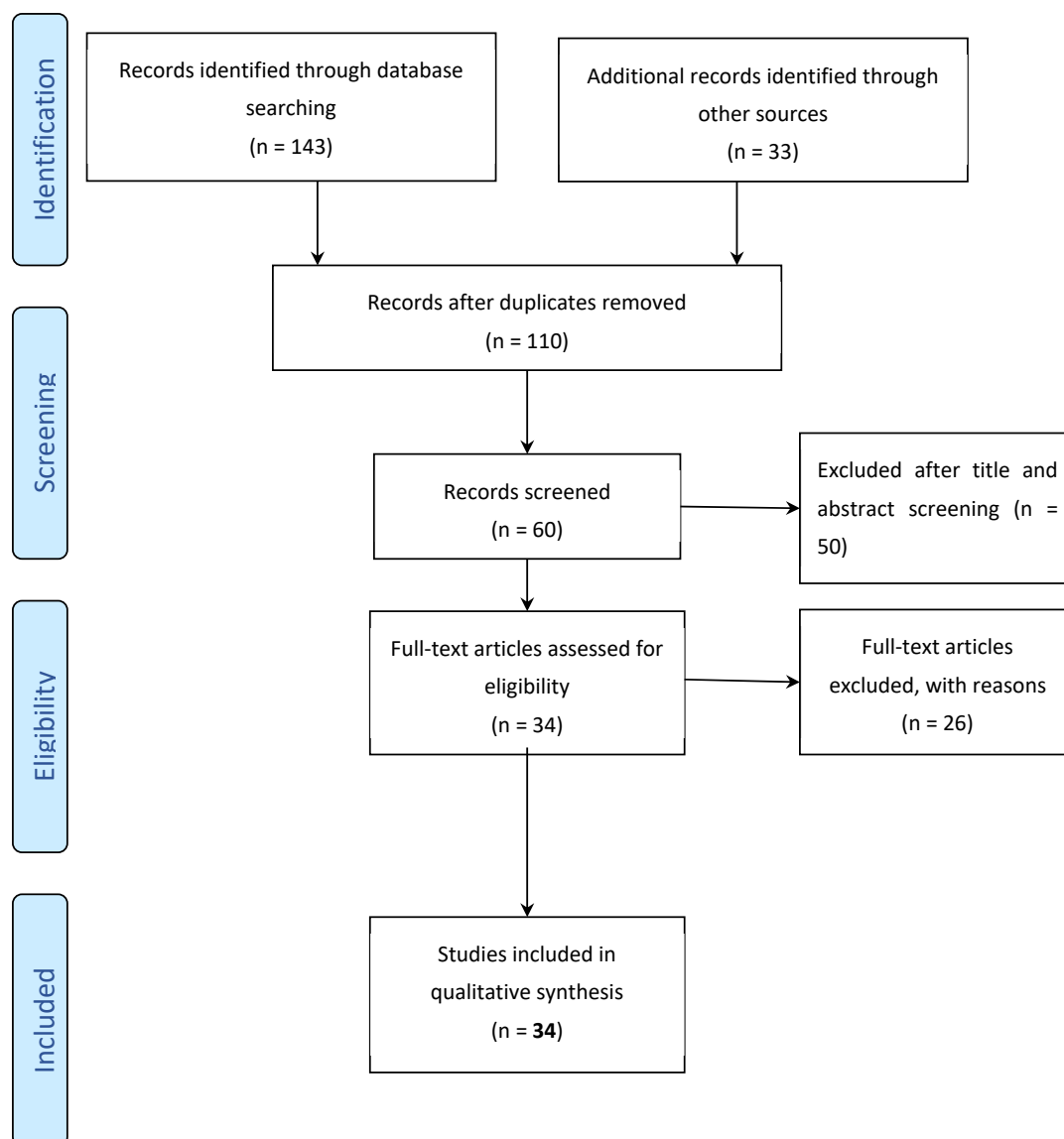


Figure 1. PRISMA flowchart showing the search method.

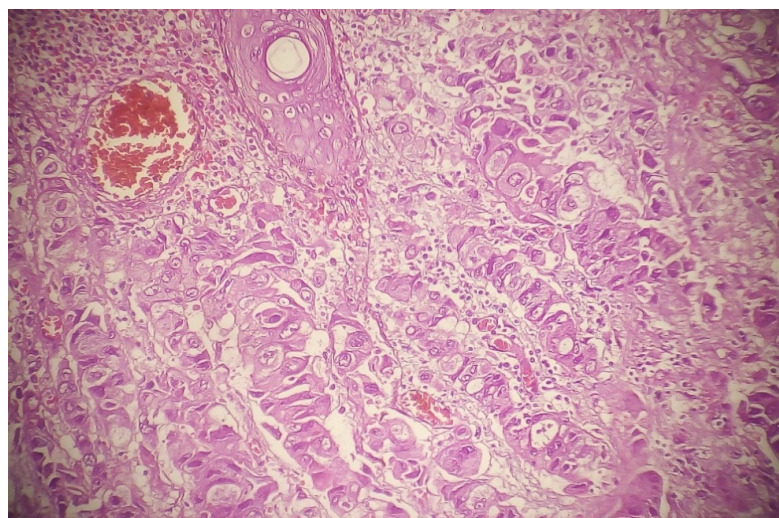


Figure 2. ASC of minor salivary gland.

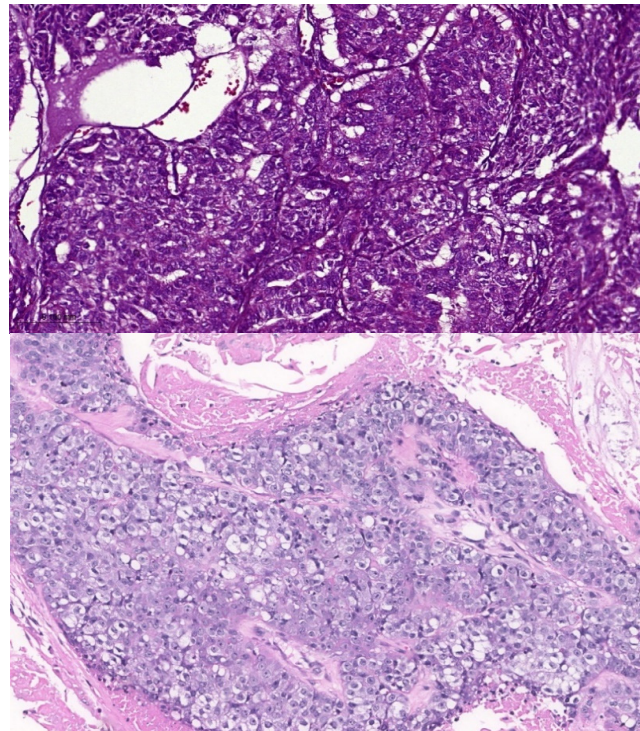


Figure 3. (Top) MAC of the minor salivary gland. (Bottom) MEC of the minor salivary gland.

3.2. Morphologic Difference in Different Sites

Most of the reported ASCs contained dense squamous congregations intermingled with true duct structures that showed cellular atypia. The stromal adenocarcinomatous component must be neither too superficial and inconspicuous (so as not to be considered an adenoid squamous cell carcinoma) nor very deep (so as not to be considered invasive SCC) (Figure 2). These cases are always considered high-grade. MACs are considered ASCs without an overlying SCC. For example, adnecarcinomatous lesions that secrete mucin and do not align with a particular recognized morphology (e.g., HG-MEC or high-grade mucinous cystadenomacinoma) are considered MACs. The indicated diagnostic immunohistochemical panel is rarely investigated. Figure 4 compares a case of MACs with a high-grade MEC of the minor salivary gland. Figure 5 shows a case of low-grade MAC of the lung. On the other hand, the ASCs of breast show both low-grade and high-grade features (Figure 6).

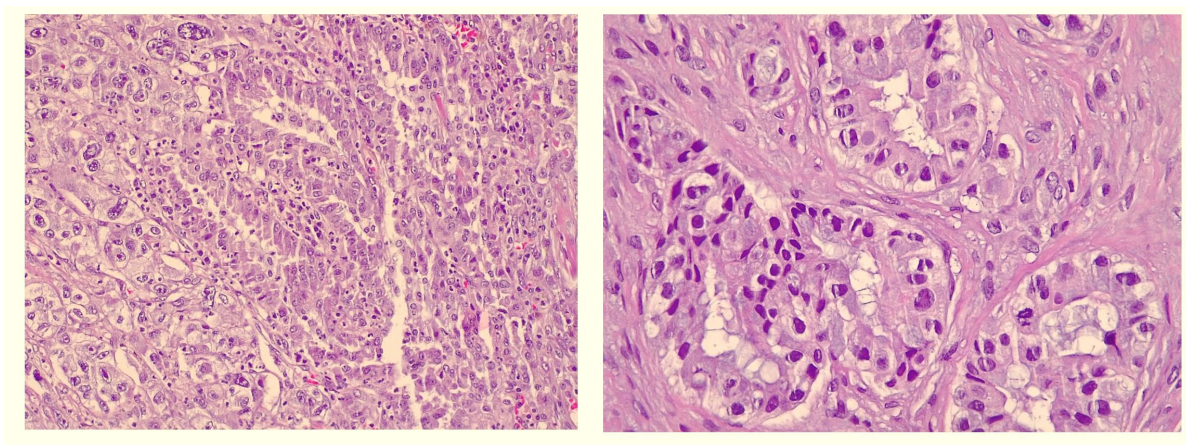


Figure 4. MAC of the lung.

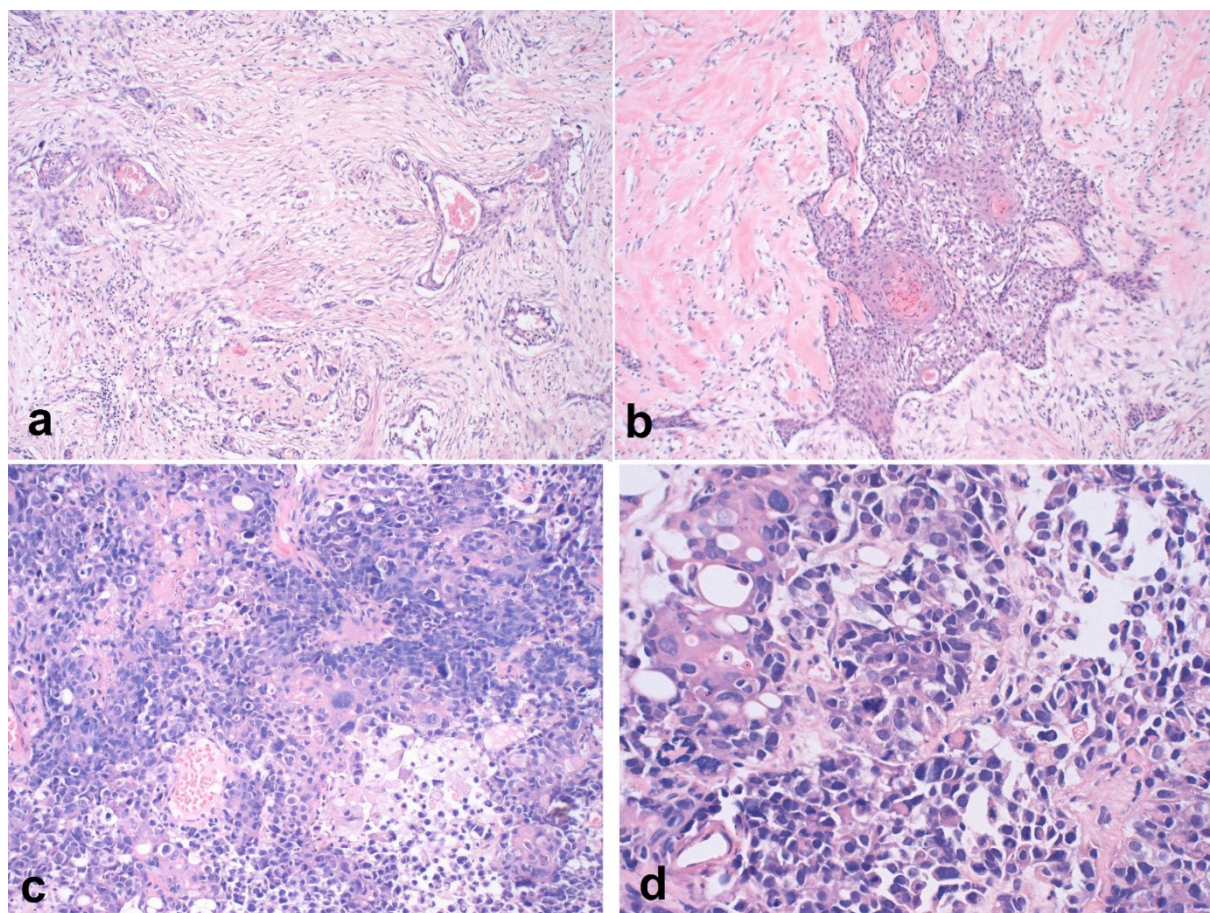


Figure 5. (a,b) Low-grade ASC of breast; (c,d) high-grade ASC of breast (for illustrative purposes).

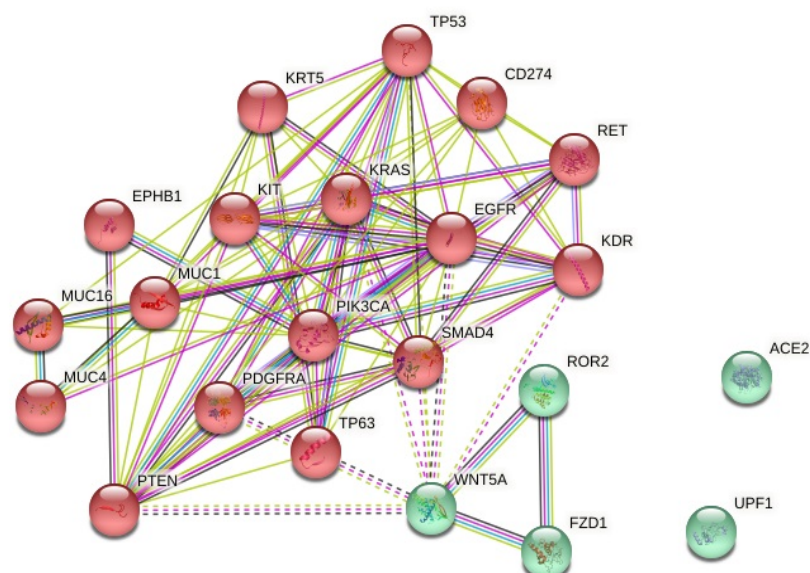


Figure 6. Genetic network analysis of ASCs.

3.3. Molecular Profiling of ASCs and MACs and Relevant Pathways

The genes in Figure 6 were retrieved from the previously reported cases and the PubMed gene library. The green color encodes higher sensitivity. The continuous and dashed lines indicate that there are previously reported links between these genes. As shown in Figure 4, *MAML2* rearrangement is never detected in salivary or non-salivary ASCs.

In Figure 7, *AKT1* is shown to have the highest affinity and to be connected to several other genes in MACs. Table 2 relates the involved genes in each lesion to the corresponding pathway(s).

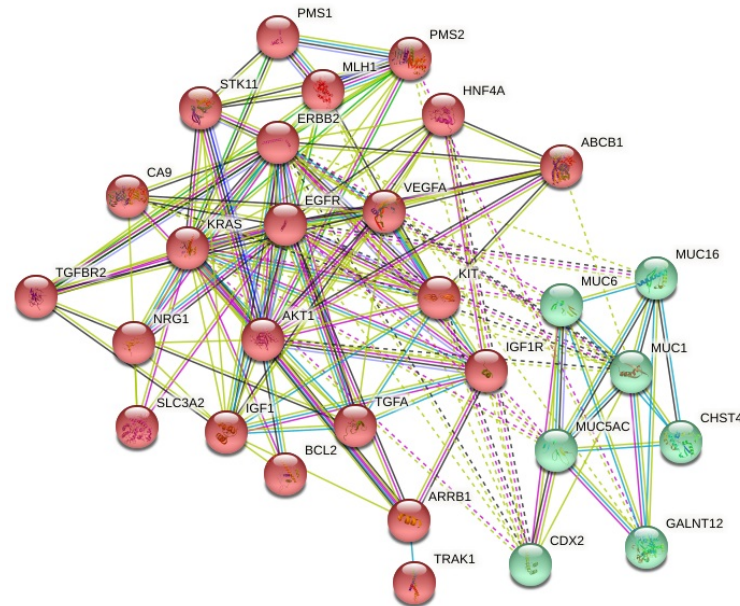


Figure 7. Genetic network analysis of MACs.

Table 2. ASCs, MACs, and HG-MEC mutated genes and corresponding pathway(s).

	ASC	MAC	HG-MEC	Corresponding Pathway
<i>ABCB1</i>		+		Energy Metabolism
<i>ACE2</i>	+			A-beta Uptake and Degradation
<i>AKT1</i>		+		Energy Metabolism; PI3K/Akt Signaling
<i>ARRB1</i>		+		Tyrosine Kinases; Wnt/Hedgehog/Notch
<i>BCL2</i>		+		Apoptosis Signaling Pathway
<i>CA9</i>		+		Angiogenesis
<i>CD274</i>	+			NF-kappaB Signaling
<i>CDX2</i>		+		Wnt/Hedgehog/Notch
<i>CHST4</i>		+		O-linked Glycosylation of Mucins
<i>EGFR</i>	+	+		Akt Signaling Pathway; Jak/STAT Signaling Pathway; MAPK Signaling; Mitogens; mTOR Signaling
<i>EPHB1</i>	+			ErbB2-ErbB3 Heterodimers Pathway
<i>ERBB2</i>		+	+	Akt Pathway Apoptosis Pathway MAPK Pathway NF-kappaB Pathway
<i>FZD1</i>	+			Neural Stem Cells and Lineage-Specific Markers; Wnt Signaling Pathways
<i>HNF4A</i>		+		TGF-beta Signaling Pathways
<i>IGF1</i>		+		IGF1R Signaling Cascade
<i>IGF1R</i>		+		IGF1R Signaling Cascade
<i>KDR</i>	+			Akt Pathway Apoptosis Pathway NF-kappaB Pathway VEGF Pathway
<i>KIT</i>	+	+		NF-kappaB Signaling; Tyrosine Kinases
<i>KRAS</i>	+	+	+	PI3K-Akt-mTOR Pathway TGF-beta Pathway Insulin Pathway
<i>KRT5</i>	+			Cytoskeletal Signaling
<i>MIR205</i>		+		miRNA-Mediated Gene Silencing
<i>MIR373</i>		+		Endoderm Differentiation Pathways
<i>MLH1</i>		+		Cell Cycle/DNA Damage

Table 2. Cont.

	ASC	MAC	HG-MEC	Corresponding Pathway
<i>MUC1</i>	+	+		EGF Pathway; ILK Signaling
<i>MUC16</i>	+	+		O-linked Glycosylation of Mucins
<i>MUC2</i>		+		NTHi-Induced Signaling
<i>MUC4</i>	+			Cell Adhesion
<i>MUC5AC</i>		+		Mucin Expression in CF
<i>MUC6</i>		+		C-type Lectin Receptors (CLRs)
<i>NRG1</i>		+		Apoptosis and Survival Role of CDK5 in Neuronal Death and Survival
<i>PDGFRA</i>	+			Akt Pathway; Apoptosis Pathway
<i>PIK3CA</i>	+		+	EMT Pathway PI3K-Akt-mTOR Pathway TLR Pathway
<i>PMS1</i>		+		DNA Mismatch Repair
<i>PMS2</i>		+		DNA Mismatch Repair
<i>PTEN</i>	+		+	Cytoskeleton Remodeling FAK Signaling; Apoptosis Pathway PI3K-Akt-mTOR Pathway
<i>RET</i>	+		+	G-protein Signaling_H-RAS Regulation Pathway
<i>ROR2</i>	+			Wnt Pathway
<i>SLC3A2</i>		+		Energy Metabolism
<i>SMAD4</i>	+			TGF-beta Signaling Pathways; Th17 Differentiation
<i>SMARCB1</i>		+		AMPK Enzyme Complex Pathway; BRCA1 Pathway; Chromatin Remodeling (Acetylation); Glucocorticoid Receptor Signaling
<i>STK11</i>		+		mTOR Signaling
<i>TGFA</i>		+		Angiogenesis; Tyrosine Kinases
<i>TGFBR2</i>		+		Akt Pathway Apoptosis Pathway NF-kappaB Pathway TGF-beta Pathway
<i>TP53</i>	+			Akt Pathway Apoptosis Pathway MAPK Pathway mTOR Pathway
<i>TP63</i>	+		+	Development Notch Signaling Pathway; DNA Damage
<i>TRAK1</i>		+		O-linked glycosylation
<i>UPF1</i>	+			Translational Control
<i>VEGFA</i>		+		Cell adhesion_Plasmin Signaling; Cytoskeleton Remodeling FAK Signaling; VEGF Signaling and Activation
<i>WNT5A</i>	+			EMT Pathway; Wnt Pathway; GSK3 Signaling

4. Discussion

Histogenetically, ASCs are considered a transitional stage between classical MACs and SCCs, given that they reveal intermediate expressions of miR-205 [54]. However, they have also been suggested to be a separate entity, based on their different thymidylate synthase protein profiles [55]. Immunohistochemically, the squamous component expresses p63, which is helpful in identifying squamous differentiation in ASCs with an acantholytic growth pattern [56]. ASCs are also positive for 34β12, CEA, CAM5.2, Ki-67 (up to 60%), AE1/AE3, CK18, Glut 1, EMA, E-Cadherin, CK19, CD138, and CK7 [57] but negative for CDX2 and CK20 [12].

In our analysis, ASCs differed remarkably from MACs. When compared to the genetic mutations of high-grade MEC, which were reported by Wang et al. [21], ASCs were similar to high-grade MECs, on the one hand, in expressing *BRCA2*, *EPHB1*, *ERBB2*, *FGF3*, and most importantly, *PIK3CA*. On the other hand, *MET* and *MTOR* were sporadically detected in both MACs and high-grade MECs. *TP53* and *EGFR* mutations were detected in the three tumors.

MECs are epistemically known for their mucinous (goblet) cells and epidermoid components. With varying degrees of intermediate cells, mucin-rich carcinomas are often confused with different grades of MECs. Although MECs lack intercellular bridges and

squamous pearls, the wide morphologic spectrum they show between their three grades poses questions about the inclusion of *MAML2*-negative high-grade invasive MECs [58], especially since, in one study, 147 pancreatic ASCs were natively negative for the *MAML2* mutation [1]. In another study, the analysis of 106 head and neck ASCs (salivary-type) revealed their tendency toward affecting the major salivary glands of elderly males, with poor prognosis [59]. ASC tumors have harbored mutations of *EGFR* [60], *KRAS*, *ERBB2*, *STK11*, *PI3KCA* [61], and *HER2* [62]. Furthermore, eight cases of pancreatic ASC showed *KRAS2* gene mutations and homozygous deletions in the *p16/CDKN2a* gene [56]. These genetic mutations have also been detected in high-grade MECs. Notably, ASCs frequently demonstrate a positive genetic mutation in *ALK* [63]. In this regard, ASCs resemble MACs. However, MACs lack acinar, myoepithelial, and neuroendocrine phenotypes, and minor salivary gland MACs tend to recur frequently, cause lymph node metastasis, and demonstrate a poor prognosis [44]. Microsecretory adenocarcinoma and mammary analog secretory carcinoma of minor salivary glands resemble MACs morphologically. However, the former lesions show consistent molecular genetic mutations (*SS18* [64] and *ETV6*, respectively [65,66]).

Based on the molecular heterogeneity among the studied tumors, it is difficult to consider ASCs, MACs, or high-grade MEC a subvariant of another tumor. There are sensitive markers for each lesion. Additionally, ASCs and high-grade MECs share more genetic mutations than do MACs and high-grade MECs. However, there is no specific marker that can distinguish each. Moreover, ASCs demonstrate a diverse genetic profile according to the involved site (e.g., breast, lung, pancreas, salivary glands, or gallbladder). The tendency to consider ASCs and high-grade MEC synonymous based on the clinical behavior of both is insufficient. Low-grade and high-grade ASCs were previously diagnosed (Figure 4). Panaccione et al. [67] detected a molecular involvement of *FAT1*, *KDM6A*, and *KMT2D* in studying metastasizing MAC. Kikuchi et al. [68] reported a case of intestinal-type adenocarcinoma of the buccal mucosa, which showed mucinous growth and negative immunoreactivity for *CDX2*. Our mining revealed that *AKT1*, *ARRB1*, *BCL2*, *CDX2*, *MUC1*, *MUC16*, *MUC2*, *MUC5AC*, *MUC6*, and *CHST4* are actively involved in the oncogenesis of MACs.

5. Conclusions

We retrieved genetic data corresponding to 13 cases of ASC and 15 cases of MAC of minor salivary glands. Both genetic profiles do not tend to intersect with high-grade MEC except for the generic mutations commonly detected in all high-grade head and neck tumors. However, the availability of data on the molecular profile of each lesion limits the generalizability of the findings of this study.

Questions around the different molecular markers of ASCs and MACs according to the site involved remain unanswered. Furthermore, it is unclear if ASCs, SCCs (superficial or invasive), and solid *MAML2*-negative MECs of the minor salivary glands that are natively composed of squamoid/squamous cells are different lesions.

The immunohistochemical expression of some duct structures in SCC and the detection of mucin in adenocarcinomatous lesions should not be considered sufficient for the diagnosis of ASCs and MACs, respectively. This raises the following questions: Are high-grade transformations in salivary gland neoplasia attributed to a particular genetic deletion (e.g., *STK11*, *INI-1*, *KRAS*, *AKT1*, *ROR2*, *FZD1*, *PTEN*, or *CD274*)? Are MACs over-reported? Should high-grade MECs be reconsidered with MACs or ASCs? Are low-grade and high-grade ASCs confined to the breast? Are pancreatic ASCs different from other ASCs? Large-scale studies involving high-quality multi-institutional cohorts with adequate molecular descriptions are required for further investigating these queries.

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