ginal zone lymphomas of mucosa-associated lymphoid tissue (MALT) (Abbondanzo 2001; Ihrler et al. 2000). MALT lymphomas of the salivary glands, similar to their complement in other sites, are clinically indolent lesions (Ellis and Auclair 1996; Harris 1991).

Notable is that primary non-MALT lymphomas of the salivary glands have been described and have a prognosis comparable to nodal lymphomas (Salhany and Pietra 1993). In contrast to non-Hodgkin's lymphoma, Hodgkin's lymphoma of the major salivary glands is most unusual. However, if present the majority of tumors arise in the parotid gland and manifest as either nodular-sclerosing or lymphocyte-predominant variants (Ellis and Auclair 1996; Gleeson, Bennett, and Cawson 1986).

Mesenchymal Neoplasms

Mesenchymal neoplasms make up 2–5% of all neoplasms that occur within the major salivary glands (Seifert and Oehne 1986). The most common varieties of benign mesenchymal salivary gland neoplasms include hemangiomas, lipomas, and lymphangiomas.

Malignant Mesenchymal Salivary Gland Tumors

Malignant mesenchymal salivary gland tumors include malignant schwannomas, hemangiopericytomas, malignant fibrous histiocytomas, rhabdomyosarcomas, and fibrosarcomas, as well as others, and account for ~1.5% of all malignant tumors of the major salivary glands (Luna et al. 1991; Seifert and Oehne 1986). Primary salivary gland sarcomas behave like soft tissue sarcomas in other locations; however, prognosis is governed by cell of origin, histological grade, tumor size, and stage (Auclair et al. 1986; Luna et al. 1991; Weiss and Goldblum 2001). The necessity of establishing a primary salivary gland origin by excluding the likelihood of metastasis and direct extension from other adjacent locations cannot be overemphasized. Furthermore, the consideration of salivary gland carcinosarcoma should be contemplated (Ellis and Auclair 1996).

Malignant Secondary Neoplasms

Malignant neoplasms from primary sites outside the salivary glands may involve the major salivary glands by: (a) direct invasion from cancers that lie adjacent to the salivary glands; (b) hematogenous metastases from distant primary tumors; and (c) lymphatic metastases to lymph nodes within the salivary gland (Ellis and Auclair 1996). It has been estimated that ~80% of metastases to the major salivary glands are from primary tumors somewhere else in the head and neck. The parotid gland is the site for most metastases, followed by the submandibular gland (Seifert et al. 1986). The majority of metastases to the major salivary glands are squamous cell carcinomas and melanomas. More rarely, carcinomas from the lung, kidney, and breast, have been recognized presumably reaching these sites by a hematogenous route (Batsakis and Bautina 1990; Seifert, Hennings, and Caselitz 1986). The peak incidence for metastatic tumors in the salivary glands is reported to be in the seventh decade of life (Ellis and Auclair 1996).

Grading and Staging of Salivary Gland Tumors

MOLECULAR SYSTEMATICS OF SALIVARY GLAND NEOPLASMS

One of the earliest attempts to use molecular systematics was to identify genes with altered expression in salivary adenoid cystic carcinoma (ACC). These studies observed expression of genes indicative of myoepithelial differentiation, including those whose protein products are components of basement membranes and extracellular matrix (Frierson et al. 2002). Other genes that were highly ranked for their expression in ACC were those encoding the transcription factors SOX4 and AP-2γ. Additional genes, which were highly expressed in ACC compared to the other carcinomas, included casein kinase 1, epsilon, and frizzled-7, which are members of the Wnt/β-catenin signaling pathway. More recent studies have indicated that the combination of copy number and gene expression profiling provides an improved strategy for gene identification in salivary gland ACCs (Kasamatsu et al. 2005).

To further relate gene expression profiles with progression and perineural invasion (PNI), laser capture microdissection (LCM) and high-throughput cDNA microarray analyses have been performed to monitor in vivo gene expression pro-