65 lymph node basins. Three SN's were not explored, because of localization in parotid gland (2) and mediastinum (1). Intraoperatively 1 SN could not be found. Gamma ray detection yielded a 99% score (112 SN's identified out of a total of 113). Eighty-six SN's (76%) were blue ($P < 0.01$). Ten patients (18%) had micrometastases in the removed SN's and underwent node dissection. Three of them had a second positive node in the lymph basin specimen.

Conclusion: The SN can be identified in a high percentage of cases and indicates the presence of metastases with a high sensitivity. Gamma detection probe tracing of SN's is superior to the conventional dye method.

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LYMPH NODE DISSECTION IN HEAD AND NECK CANCER—MODALITIES, PROGNOSTIC VALUE

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Radical neck dissection (RND) was first described by Crile in 1906 about 132 procedures. A large variety of modified neck-dissections have been proposed during the past 30 years. The goal of these new procedures was to reduce the sequellae by using functional neck dissections (FND) or selective neck dissections (SND). More than a therapeutic approach the SND are diagnostic tools to know whether the neck is involved or not. In our Institution RND, FND and SND are used depending on nodal status, site and size of the primary. The nodal involvement depends widely on the primary site. The knowledge of the prognostic value of the cervical nodal involvement is based mainly on retrospective studies initiated on a large scale since more than 25 years in our Institution. This is the basis of the well selected use of the different types of neck dissection and of the use or not of elective neck dissection. The histological pattern of node involvement is the better guide for postoperative radiotherapy. The last retrospective study performed at the Institut Gustave-Roussy included 914 patients who underwent a lymph node dissection between 1980 and 1985. The primary tumor sites were oral cavity 287, hypopharynx 249, larynx 247 and oropharynx 131. We defined sentinel nodes as the first area to be involved depending on the site of the primary, either homolateral or bilateral. The prognostic factors studied, using the Cox survival model adjusted on the primary tumor site, surprisingly showed a nonsignificant value for extracapsular spread ($P = 0.09$), and a significant value for the number of positive nodes ($P < 0.001$) and for the positive node in or out of the sentinel node sites ($P < 0.001$). A more accurate approach can be obtained by combining the site and the number of positive nodes. Node location in the upper or lower neck remains a substitute prognostic factor for the site of the positive node in or out of the sentinel node. The involvement of the lower neck drops substantially the survival rate.

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NO ABSTRACT

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NO ABSTRACT

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GENOMIC AMPLIFICATION IN HUMAN BREAST CANCER

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Genomic amplification is a frequent event in human cancer where it parallels the malignancy-related loss of chromosome integrity. It has been proposed to be one of the mutational mechanisms by which cancer cells can adapt to a complex and evolving environment. In breast carcinomas, we have shown that several regions are amplified in $\geqslant 10\%$ tumors: 8p12, 8q24, 10q26, 11q13, 17q11–q12. If *MYC* (8q24) and ERBB2 (17q11–q12) are probably the genes under selection, no obvious candidates have been found in most instances. Our results have unmasked a puzzling picture of the amplification at 11q13 in human cancers: (i) non-overlapping fragments can be amplified separately in different tumors, indicating the existence of several discrete amplifiable regions in the same chromosome band; (ii) amplicons are discontinuous, suggesting either preferential reamplification of certain DNA sequences or counterselection of certain others. The localization, cloning and characterization of the various genes under selection at 11q13 should bring new insights about the precise nature of the *in vivo* selections for amplification in tumor cells.

From a mechanistic point of view, it is striking to note that, in tumor cell lines, the 11q13 amplicons are found often (if not always) on chromosome 11 derivatives. In breast carcinomas, it appears that genomic amplification involves relatively large chromosome portions, and that nonsystemic regions can become intertwined among common chromosome structures ("transplicons"). Since this type of phenomenon seems to happen only *in vivo*, in the very complex and unstable milieu of aggressive tumors, understanding both the significance and the way by which such rearrangements occur places DNA amplification and genomics instability in the prospect of real life cancer.

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CYTOGENETICS AND MOLECULAR GENETICS OF THYROID CARCINOMAS

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In the last few years, we have investigated the molecular features of the tumor derived from the epithelial cells of the thyroid gland. In particular, we have reported an high frequency of tumor-specific rearrangements of the proto-oncogenes RET and TRK, encoding tyrosine kinase membrane receptors, in human papillary thyroid carcinomas. By the combining use of cytogenetic and molecular approaches, we have determined that the oncogenic activation of these genes is accomplished by the fusion of their tyrosine kinase domain with unlinked amino-terminal sequences following chromosomal rearrangements, mostly but not exclusively intrachromosomal, involving chromosome 10 and chromosome 1 in the case of RET and TRK, respectively. We have so far identified and characterized three different versions of RET (designated RET/ptc1, RET/ptc2 and RET/ptc3) and of TRK (named TRK-T1; TRK-T2 and TRK-T3)-derived oncogenes. In particular, RET was found activated in 18 out of 52 cases of papillary thyroid carcinomas, whereas TRK oncogenes were identified in 8 patients of the same series. Finally, we have associated alterations of p53 gene to progression and differentiation of thyroid carcinomas and RAS gene mutations to a high risk of distal metastasis.

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NO ABSTRACT