appears that mechanism-based pharmacological interactions become a reality. Molecular targets can be defined for drug discovery programs and methodological advances, such as molecular diversity strategies including combinatorial chemical libraries and high throughput screening systems have increased the chance to find new lead compounds for more effective cancer therapy.

Drugs, which are meant to restore regulatory pathways in the biochemistry of signal transduction or cell division, will most likely be used as longterm chronic therapies. Therefore, oral bioavailability and high specificity for the target, i.e. low toxicity to normal tissues, will be required. In addition, the pretherapeutic diagnosis of the target in a given patient's tumor will be a prerequisite for adequate treatment. In clinical phase I-studies new pharmacokinetic or pharmacodynamic principles need to be defined as end points. The conversion of malignant tumors from an aggressive and destructive disease to a chronic condition with which the patient can live and age, is becoming a realistic concept. Unfortunately, the translation of new molecular biology concepts into useful cancer therapies is more difficult than the scientific community originally anticipated. One reason for this might be the lack of adequate pharmacological test systems. Human species specific therapies have no reasonable experimental equivalent in which the pharmacological behavior of a potential drug can be characterized. Despite all foreseeable pitfalls in the pharmaceutical development of new molecular targets, the gradual understanding of the fundamental processes opens up new avenues for anticancer drug development.

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NEW DRUG DEVELOPMENT AT THE END OF THE SECOND MILLENNIUM

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A limited number of cancer patients can be cured with currently available chemotherapy. Therefore, the search for and subsequent development of more effective and selective agents for cancer remains one of the major challenges in medicine today. Over the last decade our knowledge on the molecular basis of cellular processes like proliferation, differentiation, and apoptosis and their importance in cancer biology and treatment has increased dramatically. Also specific pathways of neoplastic transformation and processes involved in tumour vascularization have been elucidated. Key proteins involved in such processes are currently investigated as possible targets for therapeutic intervention. Among these the E2F transcription factor family, the cyclin dependent kinases, the tumour suppressor gene P53, the enzyme telomerase and others have attracted enormous interest recently. This is illustrated by the rapid growth of mechanism based screens. The availability of large chemical or natural product collections recently extended by combinatorial libraries and the presence of advanced technology allow high throughput screening of several thousands of compounds per week. Nevertheless, *in vitro* and *in vivo* models exhibiting presence or absence of such mechanisms will remain necessary to demonstrate activity at cellular and tumour level. Moreover, by studying drug activity in relation to the level of expression of different targets in tumour cell line panels, the advantages of both random and mechanism based approaches can be combined. Despite several advantages, the human tumour xenograft model in immunodeficient mice or comparable models cannot be used for such first line testing, because of the high costs and relatively large quantities of drug required. By performing limited "rodent only" toxicological research on potential anticancer agents and careful planning of subsequent steps of the drug development process significant unnecessary time loss up to several years between the discovery of a new drug and its ultimate use in clinical medicine can be avoided. This will certainly lead to an even more rapid clinical evaluation of exciting new concepts in the coming years. Several examples of new drugs already under clinical trial will be presented.

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TAXOTERE: FROM PRECLINICAL TO CLINICAL PHARMACOLOGY

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Taxotere (Docetaxel) (TXT) is the first active hemisynthetic taxane with specific properties in part related to the hydrophobic domain (3′ phenyl group) and the polar functions of the C13 lateral chain. In the purified tubulin test as well as in experimental tumors TXT (1) is 2–12 times more active than paclitaxel (TAX); (2) retains activity in some tumors overexpressing Gp 170; (3) shows only partial cross resistance with TAX. In humans 100 mg/m^2/3 weeks has been defined as the optimal schedule with >80% neutropenia, anaphylactoid type reactions, and cumulative skin toxicity and fluid retention syndrome. The latter are in part prevented by corticoseroid premedication.

A striking activity was observed in patients with advanced breast cancer in pts with prior chemotherapy (CT) for metastatic progression RR was 50%; it was 48% in anthracyclin resistant pts and 39% in anthracyclin refractory pts with a response duration of 25–28 weeks in these studies. In pts with NSCLC whether previously treated or not RR were close to 20%. Other tumors (Head and Neck, pancreatic, NHL) appeared sensitive although confirmation is required. Taxotere appears a promising new agent which should be part of combination regimens in particular for breast cancer patients.

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THE ROLE OF LYMPH NODE DISSECTION IN BREAST CANCER SURGERY

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Axillary dissection has been a routine part of breast cancer treatment to provide accurate staging and information on which decisions about adjuvant treatment can be made and to provide local tumour control. The aim of this paper is to explore the opportunity not to perform an axillary dissection in all breast cancers.

Between 1987 and 1994, 1351 full axillary dissections were performed for five breast cancer subgroups by T category: pT1a, 100; pT1b, 197; pT1c, 574; pT2, 453 and pT3, 27.

Nodal positivity was 11%, 16.7%, 32.6%, 55.0%, 66.7% respectively. The total number of nodes involved and the type of involvement for each T category was compared with the next more advanced T category; interrelationships between clinical and pathologic characteristic were determined.

In conclusion our data suggest that only in selected patients (age, small size lesions, prognostic factors) axilla, performed only as a staging procedure, can be left untouched because of the low rate of lymph node metastasis. In these patients adjuvant systemic treatment can be planned on the basis of other factors.

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DOES EXTENSIVE SURGERY IMPROVE SURVIVAL IN GASTRIC CANCER?

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Experiences from Japan with extensive lymph node removal and much better survival as compared with the results following surgical therapy as it is conventionally performed in Europe has been put forward to support a more aggressive surgical approach to patients with gastric cancer. On the other hand, it has been argued that cancer with spread to distant lymph nodes is unlikely to be cured with techniques that only can provide local cancer control. Furthermore, previous trials from the western world have not been able to support the hypothesis that more extensive surgery prolongs survival. Instead higher post operative morbidity has argued in favour of more conventional techniques. However, a recent large German-Austrian randomized study (Siewert *et al.*, *Br J Surg*, **80**, 1015, 1993) did demonstrate that a subgroup of gastric cancer patients did benefit from more extensive lymph node dissection. The data pros and cons and their potential consequences are discussed.

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RESULTS OF SENTINEL NODE BIOPSY IN CUTANEOUS MELANOMA

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Lymphatic mapping and sentinel node (SN) biopsy is an exciting development that can give better regional tumor control, improve survival and spare patients unnecessary lymph node dissection. Lymphoscintigraphy, intra-operative gamma ray (Neoprobe®) and dye (patent blue) detection as means for SN identification in melanoma were studied in 55 patients with a primary tumor thicker than 1 mm according to Breslow (median 2.2, range 1.1–8). A total of 116 SN's were visualized in

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