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# New strategies for cancer therapy in the 21st century

Abstract The development of new anticancer drugs, radiation therapy devices, and surgical techniques has improved the survival and quality of life of cancer patients. Despite these advances, many adverse events prevent patients from receiving treatment in comfort, and a majority of patients die from recurrent disease. The limitations of treatment in terms of effectiveness and tolerability have driven researchers to develop new strategies to reduce treatment-related toxicity and improve the survival rates of cancer patients.

**Keywords** Pharmacogenetics · Pharmacogenomics

## **Promising target-based therapy**

The anticancer drugs of the future will be relatively specific and nontoxic at clinically effective doses. Such agents are called target-based drugs because they will be rationally screened based on their molecular targets [7, 15, 18, 26, 33, 36, 40, 44, 46]. They can be classified into cytotoxic and noncytotoxic drugs. Cytotoxic drugs are currently being screened by the same strategy. Some noncytotoxic agents have been demonstrated to possess direct antitumor activity, therefore, making it difficult to differentiate between cytotoxic and noncytotoxic drugs.

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Methodologically, the newer treatments can be classified into small-molecule therapy, antibody therapy, gene therapy, and immunotherapy, some of which are tumor-specific and some nonspecific. Target-based drugs include signal transduction inhibitors such as receptor tyrosine kinase (RTK) inhibitors and farnesyl transferase inhibitors, CDK inhibitors, and angiogenesis inhibitors such as matrix metalloproteinase inhibitors and vascular endothelial growth factor (VEGF) inhibitors (Table 1) [1, 3, 32].

#### Antibodies

Monoclonal antibodies (mAbs) for cancer therapy have undergone the transition from basic research to tools for clinical cancer treatment. In November 1997, the mouse/human chimeric anti-CD20 mAb, rituximab (Rituxan) became the first antibody to obtain approval from the US Food and Drug Administration for the treatment of B cell lymphoma [13, 14, 27]. In October 1998, the antibody product mouse/human chimeric anti-HER2 receptor mAb trastuzumab (Herceptin) was approved for the treatment of HER2-positive breast tumors. A randomized, controlled trial comparing chemotherapy alone vs chemotherapy plus trastuzumab demonstrated the superiority of the combined modality in terms of survival, time to progression, and response rate [4, 5, 9, 12, 31, 39].

The immunoglobulin G2a mAb 17-1A edrecolomab has been approved in Germany for the treatment of colorectal cancer in the adjuvant setting. Other promising antibodies under clinical evaluation include C225 anti-epidermal growth factor receptor (EGFR) mAb [6], anti-VEGF mAb [8, 38], and anti-GM2 or GD2 mAb [16, 20].

#### Tyrosine kinase inhibitors

RTKs, including many growth factor receptors, are transmembrane glycoproteins with a single membrane-

Cytotoxic drug therapy

Target-based therapy in the narrow sense (Small molecules) Tumor-specific noncytotoxic drugs Tumor-nonspecific noncytotoxic drugs

(Macromolecule therapy)

Topoisomerase inhibitors, tubulin binders, minor groove binders, antimetabolites, etc

CDK inhibitors, FTI, TK inhibitor Angiogenesis inhibitors, TK inhibitor, matrix metalloproteinase inhibitors Gene therapy (Ad p53), cytopathic virus (ONYX type) Immunotherapy (peptide Ag) Cytokine

spanning domain and a conserved cytoplasmic tyrosine kinase domain. There are 18 known families in vertebrates, comprising 56 receptors. The subfamilies of RTKs include the receptors for EGF, insulin, plateletderived growth factor (PDGF), VEGF, fibroblast growth factor (FGF), hepatocyte growth factor (HGF), and the neurotropins, as well as a number of orphan receptors for which no ligands have been identified. RTKs and their downstream signaling molecules have emerged as important targets for the development of inhibitors because of their role in positive growth control [24, 25]. The degree of expression of many tyrosine kinases found in different tumor types has been associated with progression of cancer, increasing grade of malignancy, and a poorer prognosis.

SU-101 targets the PDGF signaling pathway, and in clinical trials in patients with glioblastoma multiforme it has been demonstrated to be metabolized rapidly to active compounds [17, 28]. The molecular pathways on which SU-101 acts remain unknown because of the difference in concentrations that inhibit molecular targets and tumor growth.

Sugen Co. (South San Francisco, Calif.) is developing two other compounds, SU-5416 [43] and SU-6668 [41]. SU-5416 is an angiogenesis inhibitor that targets the VEGF receptor, Flk-1, and is undergoing phase I, II, and III evaluations in various tumors. A phase I study of SU-6668 has recently been initiated. It is a more broadly targeted RTK inhibitor and has been reported to cause tumor shrinkage in animal experiments [23, 34].

ZD-1839 targets the EGF RTK. The EGF receptor is considered an important target because it is found in many tumors, including breast, ovarian, renal, and lung, and its overexpression frequently indicates a highly aggressive cancer. During global phase I trials of ZD-1839, at least seven partial responses have been recorded in non-small cell lung cancer among the 173 patients enrolled [11]. ZD-1839 is important because it is active against cisplatin- and/or taxane-refractory tumors. Phase III trials of standard chemotherapy with and without ZD-1839 in non-small cell lung cancer have been initiated in the USA and Europe. Two independent phase II studies of ZD-1839 alone have also been instituted for second- or third-line treatment.

The tyrosine kinase inhibitor STI-571, developed by Novartis (Basle, Switzerland) for the treatment of chronic myelogenous leukemia, is a bcr-abl tyrosine kinase inhibitor. Complete responses have been reported in a phase I study [42]. The concentration of STI-571 required to block tumor growth is much higher than that needed to shut down the target signaling pathways, suggesting that it also works through another unknown pathway.

## **Pharmacogenetics**

Antibody (trastuzumab)

Factors that influence the variability of drug toxicity and response can be divided into two categories: pharmacokinetics and pharmacodynamics. Pharmacokinetics, the relationship between time and plasma concentration, is influenced by: (1) dose, route, and schedule of administration; (2) metabolism (anabolism or catabolism); and (3) protein binding, which strongly influences drug distribution. Pharmacokinetically, metabolism is influenced by genetic factors regulating metabolic enzyme activity. Many anticancer drug doses are usually calculated on the basis of body surface area. However, there is considerable individual pharmacokinetic variation even when the dose is based on body surface area.

Drug metabolism is a major factor in pharmacokinetic variability. Cytochrome P450 (CYP3A4) is the enzyme responsible for the metabolism of a wide variety of compounds [30]. A number of isozymes of P450 are known to exist, and they have been classified into families and subfamilies. CYP3A4 is present in human liver microsomes and plays an important role in the metabolism of many anticancer drugs. It exhibits at least a five- to ten-fold interindividual variability in the disposition of the drugs, and thus it is important to determine its activity before administration to patients.

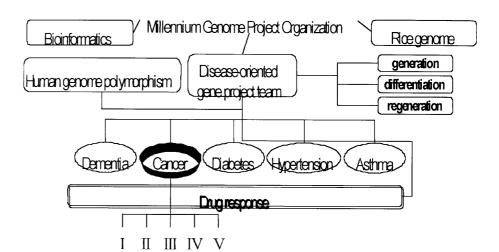
Three major noninvasive in vivo methods for estimation of interpatient variability of CYP3A4 activity have been reported [21, 22, 30]: the erythromycin breath test, the urinary dapsone recovery test, and measurement of the ratio of endogenous urinary 6- $\beta$ -hydroxycortisol (6 $\beta$ -OHF) to free cortisol (FC) (6 $\beta$ -OHF/FC). However, none of these methods provides satisfactory estimates. Measurement of endogenous 6 $\beta$ -OHF/FC is considered the simplest and most practical method, and

while it has been reported to be able to assess intrapatient variability due to enzyme induction and inhibition, for example, estimation of interpatient variability is considered impossible. The reason for the difficulty has not been completely elucidated. One possibility is that the small amount of endogenous substrate does not reflect the actual activity of CYP3A4. We have hypothesized that administration of a large dose of exogenous cortisol would allow more precise estimation of interpatient variability of CYP3A4 activity [45].

A group of 30 patients with advanced non-small-cell lung cancer were enrolled in the study, and urinary  $6\beta$ -OHF and FC were measured after administration of hydrocortisone 300 mg i.v. More than 2 days later, docetaxel 60 mg/m<sup>2</sup> i.v. was administered, followed by pharmacokinetic sampling. The correlation between docetaxel pharmacokinetics and the interpatient variability of CYP3A4 activity estimated by our method was assessed. After cortisol administration, 24-h urinary  $6\beta$ -OHF ( $t6\beta$ -OHF) increased by about 60-fold compared with pretreatment levels to an average of  $12,273 \pm 4,076 \text{ mg/day}$  (mean  $\pm$  SD). Docetaxel clearance (CL) and area under the concentration-time curve  $24.5 \pm 6.4 \text{ l/h/m}^2$ averaged and  $2.66 \pm 0.91$  mg/l, respectively, and an excellent correlation between docetaxel CL and  $t6\beta$ -OHF was observed (r = 0.867). Multivariate analysis revealed that t6β-OHF (P < 0.001),  $\alpha$ -1-acid glycoprotein (P < 0.004), AST (P=0.007), and age (P=0.022) were significantly correlated with docetaxel CL. The interpatient variability of CYP3A4 activity and docetaxel CL were accurately predicted by measuring  $t6\beta$ -OHF after cortisol administration.

Recently, single-nucleotide polymorphisms (SNPs), a molecular technique for the detection of genetic polymorphisms, have become available. The SNPs of the genes encoding drug-metabolizing enzymes are being studied intensively. It is expected that the interpatient variability of drug-metabolizing enzyme activity at the gene level will be determined [10, 19, 29].

# Fig. 1 The disease-oriented Japanese genome project



#### **Pharmacogenomics**

Genome-wide studies of gene expression have become possible due to the availability of all the sequences of protein-coding genes. Genome-wide expression studies are being carried out in various laboratories using DNA microarrays that are being applied for molecular evaluation not only of tumor cell lines but also of tumor tissues. DNA microarrays have shown that gene expression patterns in tumor cells are associated with biological and clinical characteristics [35, 37], and clusters of genes with similar function are regularly found that can be explained by their biological roles. Their patterns of expression are associated with proliferation, cytokine induction, and cell type. In studies using tumor tissue, the patterns of gene expression in tumor cells are also associated with those in nonmalignant cells, such as stromal and infiltrative lymphocytes. Some of these associations have been confirmed by immunohistochemistry using antibodies to the gene clusters. These procedures enable analysis of a much higher level of molecular events.

Specimens obtained by repeated biopsy and from primary and metastatic sites are reported to show a similar expression pattern, suggesting the validity of this technique. We analyzed the expression profiles of genes in lung cancer and neighboring normal lung tissue obtained from three lung cancer patients and found that their expression in cancer tissues was similar to that in normal tissue in the same patient, but there were large differences in lung cancer tissue from different patients. Increased expression of angiogenesisrelated genes was observed in lung cancer tissue compared with normal lung tissue from the same patient [2]. Clustering of expression profiles revealed that angiogenesis-related genes can be classified into three groups. Studies of many tumor tissues may succeed in defining subclasses of tumors in different biological and clinical categories, and application of this technology may lead to an understanding of the function of gene

Table 2 The Japanese Millennium Project

Immortalization of small samples Basic technology for genome research Gene amplifier SNP-based genome research High-throughput SNP typing Construction of clinical and genome databases Guidelines for ethical aspects Informed consent Genetic counseling Protection of privacy Establishing ethics committees Auditing Harmonization with the EU and USA Identification of gene polymorphisms related Expression profiles to disease and clinical applications Somatic mutations Identification of gene polymorphisms related Drugs: taxanes, irinotecan, fluorouracil, etc to PK/PD and clinical applications Genes: metabolism and transporters SNPs: CYP, DPD, etc Expression profiling Sample sources: peripheral lymphocytes immortalized by Epstein-Barr virus, animal models, rat liver cells, human primary hepatocytes Individualization based on genome analysis Lung, pancreas, gastric, colon, and esophageal carcinomas and genetic tumors Known cSNP analysis Whole genome association study Genomic analysis of animal carcinogenesis models

expression, provide a means of diagnosis, and identify targets for therapy.

# Millennium Project in Japan

A disease-oriented genome project called the Millennium Project was inaugurated in Japan in 2000 (Fig. 1). One of the issues addressed under this project is cancer, which is divided into the five projects shown in Table 2. The author's group will work on the fourth project, "Identification of genomic polymorphisms related to pharmacokinetics/pharmacodynamics and their drug-metabolizing applications". Genes encoding enzymes for the taxanes, irinotecan and fluorouracil and drug transporters will be analyzed. Changes in genes, such as in expression and mutations, will be evaluated for their correlation with pharmacokinetics and pharmacodynamics. The samples for genetic analyses will be peripheral lymphocytes, rat liver cells, human primary hepatocytes, etc. The techniques used for pharmacogenetic and pharmacogenomic analyses will be SNPs and cDNA expression arrays. We will use these techniques to try to identify the genes governing drug sensitivity and resistance in the hope of finding new molecular targets for chemotherapy and to develop order-made, tailor-made, customized, individualized, and personalized therapy.

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