

# ***In vitro* assays for anticancer drug discovery—a novel approach based on engineered mammalian cell lines**

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Despite decisive progress in understanding the molecular biology of cancer development, cytotoxic anticancer drugs continue to be the cornerstone of modern antitumor therapies. The developmental therapeutics program, initiated by the US National Institutes of Health's National Cancer Institute in the early 1990s, pioneered massive-scale screening for agents able to phenotypically interfere with the growth and viability of neoplastic cell lines derived from a representative panel of human carcinogenic tissues. Capitalizing on advanced knowledge of molecular processes particular for neoplastic cell characteristics, target-specific screening scenarios became since increasingly popular. With drug targets defined, natural and synthetic (combinatorial) compound/peptide/nucleic acid libraries available and the high-throughput screening technology of the systems' biology era in place, the *quo vadis* of anticancer drug discovery seems to be well determined. We review recent

advances in cytotoxic anticancer drug assay design with emphasis on a novel mammalian cell-based anticancer drug finder technology for the discovery of cytotoxic drugs with fewer side-effects on non-dividing cells. *Anti-Cancer Drugs* 16:223–228 © 2005 Lippincott Williams & Wilkins.

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## **Introduction**

The discovery that tumor-derived cell lines proliferate almost indefinitely promoted our present understanding of cancers, and formed the basis of pioneering *in vitro* anticancer drug discovery and testing initiatives [1]. By the early 1990s a large number of human tumor cell lines had been established and the time was ripe for extensive anticancer drug discovery in the newly available 96-well high-throughput (HTS) screening format [2,3]. A massive-scale anticancer drug screening initiative, launched by the National Cancer Institute (NCI) and the National Institutes of Health (NIH), and known as the developmental therapeutics program (DTP; <http://dtp.nci.nih.gov>), profiled large compound libraries for stability and solubility of individual small molecules along with their acute/chronic toxicity and proliferation inhibition on more than 60 cultured tumor-derived cell lines [4]. In current screening programs, tumor-derived cell cultures have been largely replaced by yeast mutants harboring alterations in tumor-associated genes and, by *in vitro* tests, revealing direct compound interference with key cancer targets [5] (Table 1). Although the molecular mechanisms underlying anticancer action remain elusive for most DTP-screened compounds, structure–function correlations are known for a few. Prominent examples include 5-fluorouracil (a DNA antimetabolite) [6], doxorubicin (topoisomerase II inhibitor) [7], etoposide (topoisomerase I inhibitor) [8], mitomycin C (a DNA alkylating agent) [9] and vinblastine as well as vincristine

(inhibitors of microfilament turnover) [10]. All the aforementioned examples of anticancer drugs are among a set of 122 compounds whose drug action is reasonably well known for assembly as a training panel for sophisticated network analysis of drug mechanisms [11,12]. Complementary information as well as data on over 10 000 anticancer agents is available at <http://dtp.nci.nih.gov>. DTP also encourages submission of compounds to be evaluated for their anticancer activities.

Screening formats designed for the discovery of anticancer drugs can be grouped into cell-free and cell-based assays (Table 1 for non-limiting examples [13–27]). Recent advances in our understanding of the molecular basis of cancer development resulted in the discovery of neoplastic cell-exclusive protein targets, for which specific protein or small-molecule inhibitors are either screened *in vitro* and/or developed by rational design [28]. The aim of most prominent target-specific *in vitro* anticancer drug assays was to discover angiogenesis, metastasis and cytoskeleton polymerization inhibitors as well as apoptosis inducers [29–33]. Although promising inhibitors of all the aforementioned targets have emerged from *in vitro* screening initiatives, most of them failed in follow-up cell culture experiments due to undesired side-effects, limited specificity, stability or bioavailability [34,35].

In contrast to cell-free *in vitro* assays where drug–target interaction remains the exclusive readout, cell-based

**Table 1 HTS-compatible anticancer drug screening assays**

Assay type	Target	Readout system	Reference
Cell-free assays	serine/threonine kinase inhibitors	<sup>33</sup> P incorporation	[13]
	protein phosphatase inhibitors	fluorescence	[14]
	inhibitors of microtubule formation	fluorescence	[15]
	protein kinase inhibitors	β-galactosidase complementation	[16]
	protein kinase inhibitors	fluorescence polarization	[17]
	pro-apoptotic determinants	fluorescence polarization	[18]
Cell-based assays	topoisomerase inhibitors in CHO cells	alkaline comet assay	[19]
	HepG2 hepatoma cells	GFP-based fluorescence	[20]
	apoptosis-inducing determinants in lymphocytes	colorimetric assay	[21]
	different mammalian cell lines	fluorescence	[22]
	EGFP-engineered human cell lines	EGFP-based fluorescence	[23]
	topoisomerase inhibitors in mammalian cells	colorimetric assay	[24]
	human tumor cell lines	rhodamine-based fluorescence	[4]
	angiogenesis-inhibiting determinants in glioma cells	luciferase reporter gene	[25]
	differentiation factors (C/EBP α) in U937 cells	luciferase reporter gene	[26]
	inhibitors of the met tyrosine kinase signaling pathway in MDCK cells	chromogenic reporter	[27]

screening scenarios have the potential to score (i) intracellular target specificity, (ii) target-unrelated cytotoxicity, (iii) (metabolic) stability and (iv) bioavailability. Over 90% of drug candidates prevailing in cell-free assays fail to show any effect in follow-up cell culture assays for lack of cell penetration or metabolic conversion prior to reaching their intracellular target site [35]. While early DTP screening cell lines were molecular black boxes providing phenotypic readout limited to growth and viability profiles, latest-generation screening cell lines are transgenic and engineered for state-of-the-art ultra (u)-HTS-compatible read-out technology [36–39] (Table 1).

Cell death profiling has been by far the most popular read-out scenario of modern anticancer screening assays and a variety of different fluorescence- or chemiluminescence-based detection technologies were developed to score mammalian cell death. Examples include green fluorescent protein- and luciferase-based assays. Cell death of EGFP-transgenic reporter cells can directly be scored by HTS-compatible fluorescence quantification [40]. In another configuration, the luciferase reporter gene was placed under the control of a SMAD<sub>4</sub>-specific promoter to signal tumor-suppressor pathway activation by small molecule compounds in human pancreatic cancer cells [41]. As an alternative readout to fluorescence/chemiluminescence-based monitoring technologies, dye-exclusion assays which are based on the exclusive uptake of vital dyes by dead cells have found widespread applications in screening [42–44]. For example, the use of Trypan blue staining for monitoring viability versus cell death profiles is generally accepted [45,46].

Most clinically useful drugs have been isolated from natural sources including plants and microorganisms [47–49]. Microbes like *Actinomycetes* exhibiting rapid generation times are the origin of two of the most potent anticancer drugs ever discovered: doxorubicin and acti-

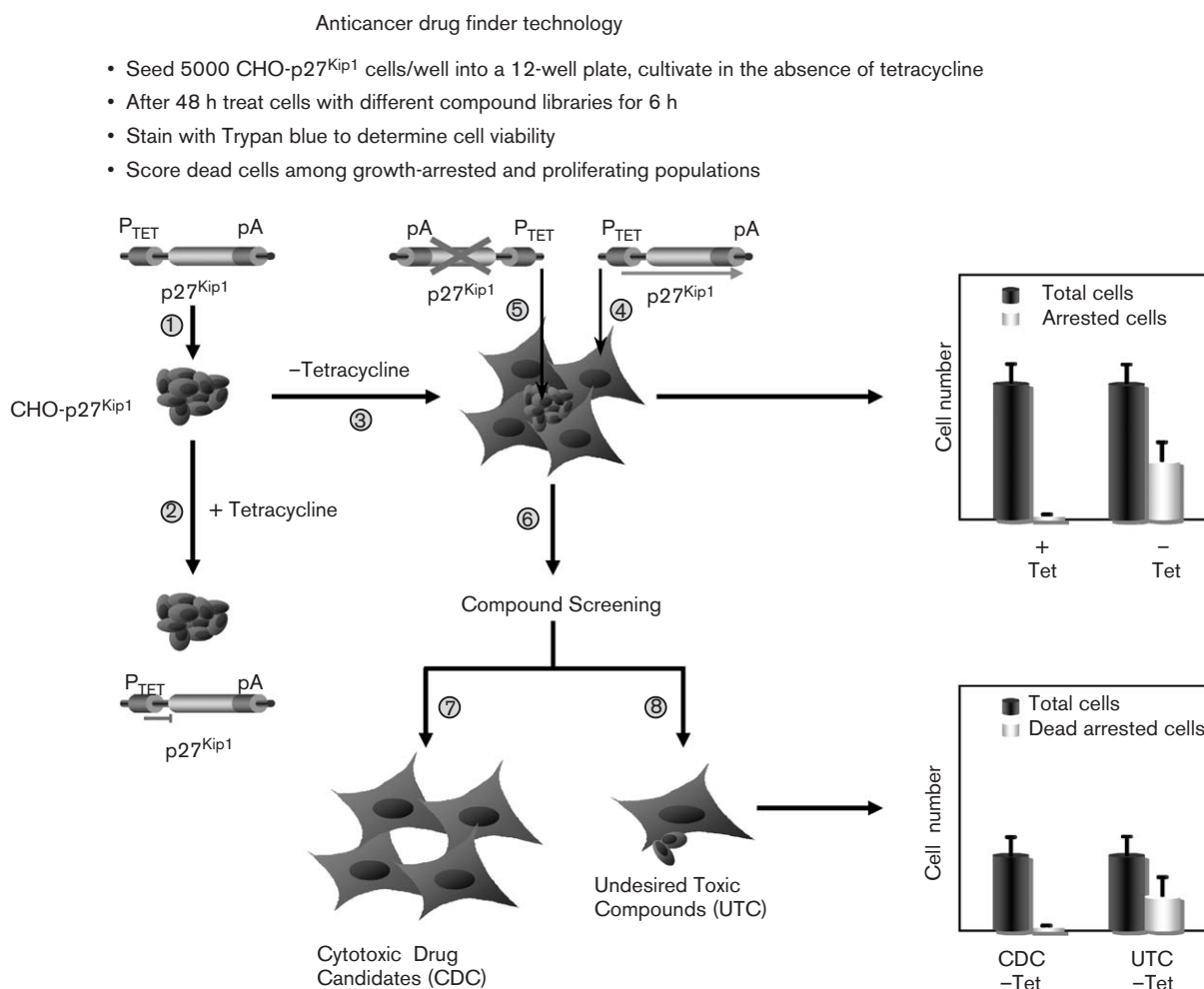
nomycin D [50]. Because of major initiatives in rational drug design, efforts on production of combinatorial chemical, peptide and antibodies libraries as well as automated synthesis of new molecule classes have been dramatically increased [51–53]. Furthermore, HTS complemented by robotic liquid handling systems and newest-generation readout systems are evolving rapidly [54–56].

We have developed a rapid and sensitive technology for detecting novel anticancer drugs. This cytotoxic drug discovery assay is based on a transgenic CHO-K1-derived cell line, which auto-differentiates into equal populations of growth-arrested (mimicking terminally differentiated body cells) and proliferating (mimicking neoplastic cells) cells (Fig. 1) [57].

### Controlled proliferation technology

Genetic reprogramming of mammalian cell lines for conditional growth arrest is essential for gene therapy strategies, biopharmaceutical manufacturing, drug discovery and expansion of feeder-dependent primary cells [57–62]. Different heterologous gene regulation systems (see [63] for a review) responsive to tetracycline [58], estrogen [60] or isopropyl-β-D-thiogalactopyranoside (IPTG [62]) were engineered to reversibly control growth-arresting determinants including the cyclin-dependent kinase inhibitors p27<sup>Kip1</sup> and p21<sup>Cip1</sup> [58,62], the differentiation factor c/ebp-α [58] or the interferon-responsive factor 1 (IRF-1 [61]). In all expression configurations arrested mammalian cells showed up to 50-fold higher specific productivity, which established this metabolic engineering strategy as controlled proliferation technology within the biopharmaceutical manufacturing community [58,64]. The pioneering controlled proliferation technology capitalizes on reprogramming cell-cycle regulatory networks by conditional tetracycline-responsive overexpression of the human cyclin-dependent kinase inhibitor p27<sup>Kip1</sup> in Chinese hamster ovary (CHO-K1) cells [58]. p27<sup>Kip1</sup> is a major

**Fig. 1**



Protocol and schematic representation of the anticancer drug finder technology. (1) CHO-K1 cells are engineered for tetracycline-responsive expression of the human cyclin-dependent kinase inhibitor p27<sup>Kip1</sup> (CHO-p27<sup>Kip1</sup>). p27<sup>Kip1</sup> is driven by the tetracycline-responsive promoter (P<sub>hCMV<sup>\*</sup>-1) and terminated by a simian virus 40-derived polyadenylation site (pA). (2) When cultivated in the presence of the antibiotic tetracycline (+ Tetracycline) P<sub>hCMV<sup>\*</sup>-1-p27<sup>Kip1</sup>-pA is repressed and CHO-p27<sup>Kip1</sup> exhibits wild-type-like proliferation profiles. (3) Following cultivation in tetracycline-free medium (- Tetracycline), CHO-p27<sup>Kip1</sup> evenly differentiates into a G<sub>1</sub>-arrested subpopulation showing high-level P<sub>hCMV<sup>\*</sup>-1-driven p27<sup>Kip1</sup> expression and a particular fried-egg-like cell phenotype (4), and a proliferation-competent subpopulation characterized by reproducible deletion of the p27<sup>Kip1</sup> expression unit and wild-type-like cell morphology (5). (6) Isogenic proliferation-competent/arrested populations are challenged with desired compound libraries and profiled for viability, e.g. using the Trypan blue dye-exclusion method. (7) Compounds with a capacity to preferentially eliminate proliferation-competent cancer-mimicking cells are classified cytotoxic drug candidates (CDC), while substances which indiscriminately kill mammalian cells are scored as undesired toxic compounds (UTC).</sub></sub></sub>

cell-cycle regulator, which binds and inhibits cyclin-dependent kinases managing G<sub>1</sub>/S phase transition in mammalian cells. p27<sup>Kip1</sup> expression is increased in mitotically inactive terminally differentiated cells and downregulated in proliferating ones [65–69].

In its pioneering configuration, the tetracycline-responsive expression system (TET system) was derived from the *Escherichia coli* Tn10 [70] and consists of the tetracycline-dependent transactivator (tTA; TetR repres-

sor fused to the *Herpes simplex*-derived VP16 transactivation domain) and the tetracycline-responsive promoter (P<sub>hCMV<sup>\*</sup>-1; heptameric TetR operator module placed 5' of a minimal human cytomegalovirus immediate early promoter) [71]. In the absence of tetracycline antibiotics tTA binds and activates transcription from P<sub>hCMV<sup>\*</sup>-1, while the tTA-P<sub>hCMV<sup>\*</sup>-1 interaction is abolished by tetracyclines in a dose-dependent manner resulting in graded transgene expression control (see [63] for a review; [71]).</sub></sub></sub>

## Engineered cell-based approach to anticancer drug screening

The ability to screen for cytotoxic drugs which selectively kill proliferating cells while having minimal or no effects on mitotically inert cells remains a major goal in modern anticancer drug discovery. Currently available anticancer drug screening assays are aimed at detecting small molecules, which kill a panel of selected human cancer-derived cell lines (see DTP above). Most of the compounds prevailing in such screens show random cell-killing activities, irrespective of the cell's proliferation phenotype and/or restricted tropism for panel cell lines which result in drug candidates with limited effect or undesired side-effects [72]. We have constructed a double-transgenic CHO-K1-derived cell line (CHO-p27<sup>Kip1</sup>) engineered for constitutive tTA (P<sub>SV40</sub>-tTA-pA) and tTA-driven tetracycline-responsive p27<sup>Kip1</sup> expression (P<sub>hCMV</sub>\*-1-p27<sup>Kip1</sup>-pA) (Fig. 1). CHO-p27<sup>Kip1</sup> typically expands in the presence of tetracycline when expression of cyclin-dependent kinase inhibitor remains repressed and can be switched into proliferation-controlled assay mode by cultivation in antibiotic-free media. Following cultivation for 2 days in a growth-arrested manner the engineered cell line differentiates evenly into G<sub>1</sub>-arrested and proliferation-competent populations owing to reproducible elimination of the P<sub>hCMV</sub>\*-1-p27<sup>Kip1</sup>-pA expression unit in a self-sufficient manner [57,73] (Fig. 1). Proliferation-competent CHO cell revertants lacking ectopic p27<sup>Kip1</sup> expression mimic a neoplastic cell phenotype with a single well-defined mutation. Proliferation-competent/controlled cell populations can be distinguished by their cell morphology when grown in an attachment-dependent manner: while growing CHO cells exhibit a typical cell morphology, G<sub>1</sub>-arrested cells adopt a fried-egg-like shape. p27<sup>Kip1</sup>-specific immunofluorescence microscopy substantiated fried-egg-like cell morphology/G<sub>1</sub>-arrest/p27<sup>Kip1</sup> expression correlations [57]. Furthermore, CHO-p27<sup>Kip1</sup> grown in the presence of tetracycline proliferates without any signs suggestive of G<sub>1</sub> arrest, indicating that the transgenic cyclin-dependent kinase inhibitor is tightly regulated.

Scoring relative viabilities of arrested/proliferating cell populations following exposure of CHO-p27<sup>Kip1</sup> to chemical or metabolic libraries will reveal drug candidates

with the potential to selectively kill proliferating cell phenotypes (Fig. 1).

## Screening performance

In order to establish CHO-p27<sup>Kip1</sup>'s potential for the discovery of anticancer drugs, we cultivated this cell line under tetracycline-free conditions and challenged it by administration of top-prescribed cancer therapeutics. Table 2 exemplifies the cytotoxic impact of 5-fluorouracil, doxorubicin, etoposide and mitomycin C treatment on CHO-p27<sup>Kip1</sup> populations grown in the presence (proliferating cells only) and absence (approximately a 1:1 ratio of growing and growth-arrested cells) of tetracycline. Comparative scoring of relative viability profiles of arrested/proliferating populations indicated preferential killing of the proliferating subpopulations by established anticancer drugs. As assessed using a Trypan blue-based dye-exclusion assay, 43–61% of all cells were eliminated, which correlated with almost the entire proliferating cell population. In contrast, less viability interference on the G<sub>1</sub>-phase-arrested subpopulation was observed: 5-fluorouracil, 13% of G<sub>1</sub>-arrested cells, doxorubicin, 11%, etoposide, 12% and mitomycin C, 25% (Table 2). These data substantiate the selective killing of proliferating cells by clinically licensed anticancer drugs and confirm that the CHO-p27<sup>Kip1</sup>-based anticancer drug finder technology is ready to apply in HTS of chemical as well as metabolic libraries to discover novel cancer therapeutics with reduced cytotoxicity on terminally differentiated cells [57]. Moreover, the anticancer drug finder technology also enables comparative analysis of established drugs or drug candidates. Table 2 shows viability profiles of CHO-p27<sup>Kip1</sup> incubated in tetracycline-free media prior to treatment with a particular drug. Arrested dead cells were scored as the percentage of total dead cells, which revealed significant differences in today's top anticancer drug's with respect to undesired cytotoxicity against proliferation-inert G<sub>1</sub>-arrested cells. For example, mitomycin C was more toxic for non-growing cells than doxorubicin. Such differences may reside in the molecular mechanisms underlying cell killing. Doxorubicin as well as etoposide inhibit topoisomerases, which eventually results in DNA damage and apoptosis. 5-fluorouracil is an antimetabolite interfering with DNA replication leading to DNA damage as well as apoptosis. However,

**Table 2 Cell-death profiling of CHO-p27<sup>Kip1</sup> cultivated in the presence (+) and absence (–) of tetracycline**

Tetracycline		Anticancer drug (% cell death)			
		5-Fluorouracil	Doxorubicin	Etoposide	Mitomycin
+	proliferating cells (100%)	72.4	67.2	72.0	66.8
–	proliferating cells (50%)	48.8	61.0	49.4	42.7
–	arrested cells (50%)	13.3	10.8	12.0	25.0

CHO-p27<sup>Kip1</sup> cultivated in the presence of tetracycline form a homogeneous proliferating population (100%) since cyclin-dependent kinase inhibitor expression is repressed. CHO-p27<sup>Kip1</sup> cultivated in the absence of tetracycline evenly differentiates into arrested (50%; p27<sup>Kip1</sup> expressed) and proliferating (50%; p27<sup>Kip1</sup> expression unit lost) populations. CHO-p27<sup>Kip1</sup> cultures were treated with 5-fluorouracil (200 µg/ml), doxorubicin (800 ng/ml), etoposide (60 µg/ml) or mitomycin C (60 µg/ml). Cell death was determined using the Trypan blue dye-exclusion method.

mitomycin C-induced cell damage causes necrosis and apoptosis [9]. The anticancer drug finder technology has the potential to enable (i) detection of novel anticancer drugs, (ii) profiling of cytotoxic activities against proliferating cells as well as (iii) scoring of undesired side-effects on proliferation-inert cells. Furthermore, since human p27<sup>Kip1</sup> is a universal cell-cycle regulator, conditional growth control could likely be engineered into any human cell line in order to provide test and screening opportunities for novel anticancer therapeutics specific for particular cell types and tissues.

## Outlook

Target-specific *in vitro* drug discovery assays provide only limited information on the potency, specificity and side-effects of drug candidates, because isolated drug targets fail to score off-target impact and miss the cellular scope of drug action. Therefore, target-specific uHTS strategies typically result in increased numbers of poorly qualified compounds being approved for expensive toxicology and animal studies where they fail at a high rate. Phenotypic cell-based assays, which offer a maximum amount of information along with first-step screening including specificity, cytotoxicity and bioavailability, are expected to increase the success rate of future drug discovery initiatives and will dramatically reduce from-discovery-to-market timelines and costs. Furthermore, it remains an ongoing challenge, associated with the treatment of polygenic diseases such as cancer, that small-molecule drugs are expected to selectively eliminate tumor cells of completely different genotypes, while leaving healthy terminally differentiated body cells unaffected. Our cell-based anticancer drug finder technology enables target-independent discovery/validation of small-molecule drugs, which selectively kill proliferating cells, a key phenotype common to all neoplastic cells irrespective of their underlying genetic profile. The CHO-p27<sup>Kip1</sup>-based anticancer therapeutic screening and validation system is expected to be compatible with all of the currently available dye-exclusion assays and, thus, suitable for large-scale applications including DTP.

We believe that the CHO-p27<sup>Kip1</sup>-based anticancer drug finder technology has the potential to significantly speed up the discovery and validation of highly efficient anticancer therapeutics resulting in fewer side-effects.

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