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Award Number: DAMD17-00-1-0500

TITLE: Novel Histone Deacetylase Inhibitors

PRINCIPAL INVESTIGATOR: Jeannie S. Strobl, Ph.D.

CONTRACTING ORGANIZATION: West Virginia University  
Research Corporation  
Morgantown, West Virginia 26506-6845

REPORT DATE: July 2001

TYPE OF REPORT: Annual

PREPARED FOR: U.S. Army Medical Research and Materiel Command  
Fort Detrick, Maryland 21702-5012

DISTRIBUTION STATEMENT: Approved for Public Release;  
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20011128 226

# REPORT DOCUMENTATION PAGE

Form Approved  
OMB No. 074-0188

Public reporting burden for this collection of information is estimated to average 1 hour per response, including the time for reviewing instructions, searching existing data sources, gathering and maintaining the data needed, and completing and reviewing this collection of information. Send comments regarding this burden estimate or any other aspect of this collection of information, including suggestions for reducing this burden to Washington Headquarters Services, Directorate for Information Operations and Reports, 1215 Jefferson Davis Highway, Suite 1204, Arlington, VA 22202-4302, and to the Office of Management and Budget, Paperwork Reduction Project (0704-0188), Washington, DC 20503

1. AGENCY USE ONLY (Leave blank)	2. REPORT DATE July 2001	3. REPORT TYPE AND DATES COVERED Annual (15 Jun 00 - 14 Jun 01)
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4. TITLE AND SUBTITLE Novel Histone Deacetylase Inhibitors	5. FUNDING NUMBERS DAMD17-00-1-0500
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6. AUTHOR(S)  
Jeannie S. Strobl, Ph.D.

7. PERFORMING ORGANIZATION NAME(S) AND ADDRESS(ES)  
West Virginia University  
Research Corporation  
Morgantown, West Virginia 26506-6845  
E-Mail: [jstrobl@hsc.wvu.edu](mailto:jstrobl@hsc.wvu.edu)

8. PERFORMING ORGANIZATION REPORT NUMBER

9. SPONSORING / MONITORING AGENCY NAME(S) AND ADDRESS(ES)  
U.S. Army Medical Research and Materiel Command  
Fort Detrick, Maryland 21702-5012

10. SPONSORING / MONITORING AGENCY REPORT NUMBER

11. SUPPLEMENTARY NOTES  
Report contains color

12a. DISTRIBUTION / AVAILABILITY STATEMENT  
Approved for Public Release; Distribution Unlimited

12b. DISTRIBUTION CODE

13. Abstract (Maximum 200 Words) (abstract should contain no proprietary or confidential information)  
The research goal is to demonstrate HDAC1 is a new chemotherapeutic target for human breast tumor cells and to identify new HDAC1 inhibitors on the basis of the structure of quinoline antimalarials. The drug screening strategy we used included 8 antimalarial compounds available through the NCI compound library or Sigma Chemical Company (quinidine, quinine, primaquine, chloroquine, hydroxychloroquine, halofantrine, mefloquine), 2 inactive quinolines as negative controls (quinoline, quinolinic acid), and trichostatin acid, a known HDAC1 inhibitor, as the positive control. The antimalarials caused differentiation of breast tumor cell lines and increased histone H4 acetylation. Only halofantrine, a non-quinoline antimalarial may directly inhibit HDAC1 enzyme activity. We published that quinidine, a quinoline antimalarial, acts via a novel mechanism causing differentiation of breast tumor cells following a transient proteolytic degradation of the HDAC1 protein. Our screen has been extended to include 17 additional NCI compounds that possess a quinoline ring; their anticancer mechanisms are unknown, but we have preliminary evidence that several cause breast tumor differentiation. Analysis of these 27 compounds by molecular modeling is not yet complete.

14. Subject Terms (keywords previously assigned to proposal abstract or terms which apply to this award)  
Breast tumor cell lines, differentiation therapy, histone Deacetylase inhibitors, molecular modeling, quinolines

15. NUMBER OF PAGES  
15

16. PRICE CODE

17. SECURITY CLASSIFICATION OF REPORT  
Unclassified

18. SECURITY CLASSIFICATION OF THIS PAGE  
Unclassified

19. SECURITY CLASSIFICATION OF ABSTRACT  
Unclassified

20. LIMITATION OF ABSTRACT  
Unlimited

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## Text Annual Report 01

### INTRODUCTION:

Histone deacetylase (HDAC) enzymatically removes acetyl moieties from the epsilon-amino of L-lysine in histone proteins. Histone modifications such as deacetylation participate in the modulation of gene expression. Drugs that inhibit HDAC activity have anti-tumor activity in transformed cell lines, in animal tumor models and in clinical trial. HDAC inhibitory drugs constitute a potentially important new category of antitumor agents. It is our goal to determine if HDAC inhibitors cause growth inhibition and cell death in human breast tumor cell lines and to identify new HDAC inhibitors for therapeutic use. Our approach is based upon a fortuitous observation that quinidine and quinine, two quinoline antimalarials, caused growth inhibition, differentiation and cell death in MCF-7 human mammary carcinoma cells. We have now undertaken a screen of antimalarial drugs to establish structure activity relationship for HDAC1 inhibition. Additional compounds that possess both antitumor activity in the NCI drug discovery program and a quinoline ring structure have been included in this screen. The significance of this work is that it provides the basis for developing new drug therapies for breast cancer that cause tumor cell differentiation with minimal cytotoxicity to normal tissues.

### BODY:

**Task 1** A total of 27 compounds have been obtained for the CoMFA analysis. Eleven of the 15 compounds described in the proposal were quinolines. Quinacrine proved too toxic and has been dropped. Amodiaquine and hydroxychloroquine were added. Quinone and quinocid were not obtainable from NCI, nor were we successful in multiple attempts to obtain additional antimalarial compounds from Walter Reed Army Medical Center. Instead, additional quinoline compounds were obtained from the NCI, Division of Experimental Therapeutics. A minimum of 25 compounds is required for CoMFA.

The PI completed Pharmacy 491C, Introduction to Molecular Modeling (3CR). This was a computer lab intensive course designed to teach computational chemistry pitfalls and applications. Molecular mechanics and molecular dynamics were covered in Amber; Insight II was used for analyzing protein structure and protein-small molecule docking. The PI has continued to develop skills necessary to perform conformational molecular field analysis, a topic requiring the use of Sybyl. I have used this program, but have not completed the energy minimizations on the 27 compounds we have identified for our screen. I have experienced difficulty converting the chemical structures of these compounds available through the NCI website into a format that is read by the Sybyl program. I have drawn a few compounds by hand in Sybyl, and performed energy minimization; this process is inefficient but workable. I have an excellent starting point for the energy minimizations using the solvated X-ray crystallographic structure of quinidine and quinine that was provided by the Cambridge Crystallographic Data Centre, Cambridge, UK.

The central goal is the development of a molecular model of a new class of HDAC1 inhibitors. The end-point chosen for this analysis is critical to the value of the predictive model, and the following was established as a strategy for end-point analysis. The quinoline compounds were assigned a rank order on the basis of the IC<sub>50</sub> for mitochondrial metabolism of a tetrazolium dye (MTS assay). This assay is usually referred to as a cell viability assay because it is an indirect measure of the ability of a cell to generate ATP needed for cell function. We screened all the compounds in two breast tumor cell lines: the more slowly growing, ER-positive MCF-7 cells and the rapidly growing, ER-negative MDA-MB-231 cell line. Using the MTS IC<sub>50</sub> values compounds were screened for differentiating activity in both cell lines using the Oil Red O lipid droplet stain. Complete data was obtained on 16 of the 27 compounds at the time of this report. These data are described in Table 1. Work on the remaining 11 compounds is in progress.

**Task 2** Compounds that tested positive for differentiation (Oil Red O positive) at or near the MTS IC<sub>50</sub> were screened for direct inhibition of HDAC enzymatic activity in a cell free assay. The original proposal stated that Dr. Jim Davie would conduct the initial HDAC assays, because of his expertise with the radioactive assay. Recently, a fluorescence based cell-free assay kit became commercially available through Bio-Mol. This assay was used to screen the quinoline compounds for inhibition of HDAC1 from

human HeLa cell extracts by an undergraduate summer research student, Mr. Andrew Freeman. Of the 16 compounds tested, only one compound NSC#3852 was a direct HDAC1 inhibitor. Trichostatin Acid (TSA) was used as the positive control (IC<sub>50</sub> = 8.5 nM). This result was not that surprising because earlier work suggested that differentiation in the breast tumor cells by quinidine was the result of a novel mechanism that resulted in histone hyperacetylation without direct inhibition of HDAC enzyme activity (see J.Biol.Chem. publication in the appendix for detail.)

**Task 3** The PI recruited a postdoctoral fellow, Dr. Anna Martirosyan. Dr. Martirosyan began work in this laboratory in August, 2000. Dr. Martirosyan has conducted the MTS and Oil Red O screening of many of the NCI compounds. Two graduate students in the laboratory, Dr. Qun Zhou and Ms. Rayhana Rahim, have also participated in the compound screening.

**Task 4** A nucleosome release ELISA was used as a quantitative index of apoptotic activity. At the MTS IC<sub>50</sub>, only one of nine quinolines (test results to date) caused apoptosis. Etoposide was used as the positive control. In this small subset of compounds that included the antimalarials (quinidine, quinine, amodiaquine, primaquine, chloroquine, halofantrine, mefloquine, quinoline and quinolinic acid), induction of apoptosis required higher drug concentrations than those that affected MTS metabolism or cellular differentiation. We also observed that low concentrations of trichostatin acid (TSA), a classic HDAC inhibitor caused direct inhibition of HDAC activity (IC<sub>50</sub> = 8.5 nM) and inhibition of MTS metabolism (IC<sub>50</sub> in MCF-7 cells = 35nM), but higher concentrations (100-400nM) were required to induce apoptosis by 48 hours in MCF-7 cells. We conclude that apoptosis induction measured using this assay will not be a suitable end-point for our CoMFA analysis.

Task 4 also includes assessment of histone hyperacetylation by drug treatment. We have established qualitatively that quinidine, quinine, amodiaquine, primaquine and chloroquine raise levels of acetylated histone H4 in MCF-7 cells. To use histone H4 acetylation as an end-point in the CoMFA, requires that a quantitative measure of histone acetylation be found. We have worked towards developing methods to quantitatively measure the increase in acetylated H4. There are a number of problems in finding a quantitative way to measure histone acetylation. 1) We found the quality of the histone H4 antibody available varies among commercial vendors and from a single vendor, lot-to-lot. 2) We found that histones do not transfer efficiently from the gel onto nylon filters. 3) We thought we could normalize the signal from the acetylated H4 antibody to total histone on the nylon filter, using antibodies that recognize total histone H4 on the blot (both the acetylated and the non-acetylated form). There appear to be differences in the efficiency of transfer of the unacetylated histone vs. acetylated histone from the gel onto the Nylon membrane or the quality of the antibodies. The signal from the acetylated histones exceeded that of the total histone signal. We are trying other approaches to quantitatively measuring levels of histone acetylation in response to drugs using nitrocellulose membranes, and using the stained membrane as a measure of total histone on the blotting membrane. We are also pursuing a collaborative arrangement to develop a mass spectrometry assay to quantitatively measure histone acetylation.

**New Experiments Proposed for Task 4:** To complete Task 4 we propose to investigate two additional end-points that are representative of drugs that cause differentiation: 1) loss of Ki67 antigen expression which is a marker for cells that exit the cell cycle and enter G<sub>0</sub> (48 hours) and 2) induction of the G<sub>1</sub> cyclin-dependent kinase inhibitor, p21/WAF1/Cip1 using a commercial ELISA kit. Methods for both end-points are straightforward and readily lend themselves to quantitative analysis. These assays may prove to be suitable for the CoMFA if quantitative analysis of histone H4 acetylation eludes us.

**Task 5** We request that task 5 and research goal 2 as originally proposed be eliminated from further consideration. It was brought to my attention that some investigators have had difficulty demonstrating HDAC activity from the baculovirus expressed HDAC enzyme. In addition, most of our data suggest that the quinoline drugs are not direct HDAC inhibitors. Thus, it is possible that the drugs do not directly bind HDAC.

**New Experiments Proposed for Task 5 (Goal 2):** The mechanism of quinidine induction of histone H4 hyperacetylation is sensitive to proteasome inhibitors (JBC publication in the appendix). We therefore propose to examine if HDAC undergoes ubiquitination and whether quinidine regulates this process.

**Task 6** After screening with MCF-7 and MDA-MB-231 cells, we will screen for selective tumor cell toxicity using normal HMEC and immortalized MCF10A cells.

**Task 7** We request that task 7 be dropped from further consideration: quinacrine mustard is too toxic, and we do not think the quinolines are direct HDAC inhibitors.

**Task 8** We are preparing one manuscript describing histone hyperacetylation, cell differentiation, apoptosis in MCF-7 cells by the quinoline antimalarials. We are preparing an abstract for submission August 1 to the American Society for Cell Biology.

#### **KEY RESEARCH ACCOMPLISHMENTS:**

\*Established that quinoline antimalarial agents have differentiating and antiproliferative activity in human breast tumor cell lines.

\*Chloroquine and Hydroxychloroquine (Plaquenil) cause differentiation and inhibition of growth in MCF-7 and MDA-MB-231 human breast tumor cells at concentrations that are non-toxic to immortalized, non-transformed MCF10A human breast cells.

\*Established that quinoline antitumor compounds NSC#4238, 4239, 10010, 2039 and 3852 show promise as differentiating agents in human breast tumor cell lines.

- Identified NSC#3852 as a direct inhibitor of HDAC1 enzyme activity in vitro.
- Using the MTS cell viability assay as an indication of antitumor activity in MCF-7 and MDA\_MB\_231 cells, all of the quinoline antitumor agents examined were more potent than what is reported in the NCI web site (LC50 and IG50).

#### **REPORTABLE OUTCOMES:**

\*One published manuscript, Zhou Q, Melkounian ZK, Lucktong A, Moniwa M., Davies JR and Strobl, JS. *J. Biol. Chem.* 275: 35256-35263 (2000).

\*Research support for 1 postdoctoral fellow and two graduate students.

\*Funded grant application, WVU Research Incentive Competitive Grants Program, \$17,500 to establish an Apoptosis Analysis Facility.

#### **CONCLUSIONS:**

We conclude that the antimalarial quinoline compounds warrant re-investigation of their pharmacologic activity as antitumor agents in breast cancer. Although these compounds show low potency in comparison with some other tumor differentiating agents, our preliminary studies indicate that the antimalarials show selective toxicity to breast tumor cells compared with normal breast epithelial cells. The "antimalarials" have potential both as antitumor and as chemopreventative agents.

We conclude that some of the quinoline antitumor agents listed in the NCI library may act as tumor differentiating agents. A very modest search revealed one compound that was a direct HDAC inhibitor and thus a potential tumor differentiating agent.

Differentiation therapy holds promise as a less toxic alternative to traditional chemotherapeutic regimes and as a mode of chemoprevention. The identification of quinolines as low potency, low toxicity differentiating agents may enable us to develop new agents to control tumors by promoting tumor cell differentiation.

Table 1.		BREAST TUMOR DIFFERENTIATING QUINOLINES							
		Growth End-Points		Differentiation End-Points				Proposed	Proposed
RANK	NSC #	WVU	NCI	ORO	Histone	HDAC <sub>activity</sub>	p21/WAF	Ki67	
		IC50	GI50	Lipid Stain	H4-Acety.	Inhibitor			
		MTS	SRB						
		(uM)	(uM)						
		Cell Line	Cell Line	Cell Line	Cell Line	HeLa X-tract			
		1 2	1 2	1 2	1 2				
1	86372	.14 .17	.12 .16	no		no			
2	4238	.31 .88	1.6 .85	yes		no			
3	4239	.60 .39	2.3 5.9	yes		no			
4	146397	.88 1.8	1.1 2.6	no		no			
5	<b>149765</b>	3.4 >100	16.4 43.7	yes no	yes	no			
6	<b>157387</b>	3.0 nd	nd nd	yes yes		no			
7	85701	2.8 .46	4.2 nd	no		no			
8	10010	6.5 .72	5.4 1.27	yes		no			
9	85700	6.5 nd	7.4 33.2						
10	Amodiaquin	6.9 nd	nd nd	yes yes	yes	no			
11	86371	7.6 nd	nd nd						
12	2039	12.7 7.3	1.7 3	weak		no			
13	86373	13.5 nd	nd nd						
14	69603	14.1 nd	.85 .57						
15	305819	19 nd	12.6 9.4						
16	QuinolinicAcid	28.2 nd	nd nd	weak		no			
17	<b>5362</b>	40.1 nd	60 100	yes yes	yes	no			
18	<b>14050</b>	48.2 51.2	19 16	yes yes	yes	no			
19	<b>305789</b>	58.9 nd	10.2 2.5	yes yes		no			
20	3852	61.2 nd	1.8 6.4	weak		yes			
21	Quinoline	61.5 nd	nd nd			no			
22	Hdrxy/clq	71.2 43.6	nd nd	yes yes		no			
23	249913	102 nd	nd nd						
24	Quinidine	113.6 nd	nd nd	yes yes	yes	no			
25	15783	308? Nd	4.3 16.1						
26	339004	Inactive	45.3 70						
27	124637	Not Tested	13.6 17						

**Legend** Compounds are ranked based on growth inhibition in the MTS (tetrazolium dye assay) and the SRB(sulforhodamine dye assay). Compounds in **bold** are antimalarial drugs. 149765 = Primaquine; 157387 = Mefloquine; 5362 = Quinine; 14050 = Chloroquine; 305789 = Halofantrine  
Cell line 1 = MCF-7 Cell line 2 = MDA-MB-231. nd= not determined  
ORO = Oil Red O Histone H4 Acetylation was measured by Western blot  
HDAC activity was measured using BioMol Fluor d Lys assay kit.

# Rapid Induction of Histone Hyperacetylation and Cellular Differentiation in Human Breast Tumor Cell Lines following Degradation of Histone Deacetylase-1\*

Received for publication, April 12, 2000, and in revised form, August 2, 2000  
Published, JBC Papers in Press, August 10, 2000, DOI 10.1074/jbc.M003106200

Qun Zhou‡, Zaroui K. Melkounian‡, Ann Lucktong‡, Mariko Moniwa§, James R. Davies§, and Jeannine S. Strobl‡¶

From the ‡Department of Pharmacology & Toxicology, Robert C. Byrd Health Sciences Center, West Virginia University, Morgantown, West Virginia 26506 and §Manitoba Institute of Cell Biology, University of Manitoba, Winnipeg R3E 0V9, Canada

**Quinidine inhibits proliferation and promotes cellular differentiation in human breast tumor epithelial cells. Previously we showed quinidine arrested MCF-7 cells in G<sub>1</sub> phase of the cell cycle and led to a G<sub>1</sub> to G<sub>0</sub> transition followed by apoptotic cell death. The present experiments demonstrated that MCF-7, MCF-7ras, T47D, MDA-MB-231, and MDA-MB-435 cells transiently differentiate before undergoing apoptosis in response to quinidine. The cells accumulated lipid droplets, and the cytokeratin 18 cytoskeleton was reorganized. Hyperacetylated histone H4 appeared within 2 h of the addition of quinidine to the medium, and levels were maximal by 24 h. Quinidine-treated MCF-7 cells showed elevated p21<sup>WAF1</sup>, hypophosphorylation and suppression of retinoblastoma protein, and down-regulation of cyclin D1, similar to the cell cycle response observed with cells induced to differentiate by histone deacetylase inhibitors, trichostatin A, and trapoxin. Quinidine did not show evidence for direct inhibition of histone deacetylase enzymatic activity *in vitro*. HDAC1 was undetectable in MCF-7 cells 30 min after addition of quinidine to the growth medium. The proteasome inhibitors MG-132 and lactacystin completely protected HDAC1 from the action of quinidine. We conclude that quinidine is a breast tumor cell differentiating agent that causes the loss of HDAC1 via a proteasomal sensitive mechanism.**

Histone deacetylase (HDAC)<sup>1</sup> proteins comprise a family of related proteins that act in conjunction with histone acetyltransferase proteins to modulate chromatin structure and transcriptional activity via changes in the acetylation status of histones. Histones H3 and H4 are the principal histone targets

\* This work was supported by West Virginia University School of Medicine, the Spurlock Cancer Research Fund, the Susan G. Komen Breast Cancer Foundation, Grants DAMD 17-99-1-9447 and DAMD 17-00-1-0500, and the Medical Research Council of Canada Grant MT-9186. The costs of publication of this article were defrayed in part by the payment of page charges. This article must therefore be hereby marked "advertisement" in accordance with 18 U.S.C. Section 1734 solely to indicate this fact.

¶ To whom correspondence should be addressed: Dept. of Pharmacology and Toxicology, Robert C. Byrd Health Sciences Center, West Virginia University, Morgantown, WV 26506-9223. Tel.: 304-293-7151; E-mail: jstrobl@hsc.wvu.edu.

<sup>1</sup> The abbreviations used are: HDAC, histone deacetylase; DMEM, Dulbecco's modified Eagle's medium; FBS, fetal bovine serum; MG-132, carbobenzoxy-L-leucyl-L-leucyl-L-leucinal; PBS, phosphate-buffered saline; pRb, retinoblastoma protein; SAHA, superoylanilide hydroxamic acid; TSA, trichostatin A; HRP, horseradish peroxidase; HMEC, human mammary epithelial cells; ER, estrogen receptor; MTS, 3-(4,5-dimethylthiazol-2-yl)-5-(3-carboxymethoxyphenyl)-2-(4-sulfophenyl)-2H-tetrazolium; CDK, cyclin-dependent kinase.

of HDAC enzymatic activity, and these histones undergo acetylation at lysine residues at multiple sites within the histone tails extending from the histone octamer of the nucleosome core. The association of HDAC proteins with mSin3, N-CoR, or SMRT and other transcriptional repressors has led to the hypothesis that HDAC proteins function as transcriptional corepressors (reviewed in Ref. 1). The spectrum of genes that show alterations in gene transcription rates in response to decreased HDAC activity is quite restricted (2). Yet, small molecule inhibitors of the enzyme histone deacetylase (HDAC) such as trichostatin A (TSA), superoylanilide hydroxamic acid (SAHA), trapoxin, and phenyl butyrate cause major alterations in cellular activity including the induction of cellular differentiation and apoptosis (3–5). Trichostatin A, SAHA, and trapoxin stimulate histone acetylation by acting as direct inhibitors of HDAC enzyme activity (6). Trichostatin A, SAHA, and trapoxin possess lysine-like side chains and act as chemical analogs of lysine substrates. Molecular models based upon the x-ray crystal structure of an HDAC-like protein indicate that trichostatin A and SAHA can bind within the active site of the HDAC enzyme and interact with a zinc metal ion within the catalytic pocket that is critical for enzymatic activity (7). Trapoxin is an irreversible HDAC enzyme inhibitor (8).

Much remains to be learned about the biochemical events subsequent to HDAC inhibition that lead to cell cycle arrest, cellular differentiation, and apoptosis. However, a spectrum of biological responses characteristic of HDAC inhibitors has emerged, including cell cycle arrest in G<sub>1</sub>, elevated p21<sup>WAF1</sup> expression, hypophosphorylation of retinoblastoma protein (pRb), hyperacetylation of histones, particularly H3 and H4, and apoptosis. Histone hyperacetylation is directly linked to the activation of p21 transcription and is p53-independent (5). This observation provides an important link between HDAC inhibition and cell cycle arrest because p21<sup>WAF1</sup> plays a critical role in causing G<sub>1</sub> cell cycle arrest via inhibition of the G<sub>1</sub> cyclin-dependent kinase family (9). Overexpression of p21<sup>WAF1</sup> has also been associated with apoptosis, but the mechanism of p21<sup>WAF1</sup> induction of apoptosis requires further investigation (10).

Cancer therapy that targets the activity of genes or gene products controlling cell cycle progression, differentiation, and apoptosis is a promising new strategy. Because HDAC inhibitors regulate the cell cycle and cause both cellular differentiation and apoptosis, they comprise an interesting group of compounds with potential for development into a new category of clinically significant anti-tumor agents. Single, key protein targets for "gene-regulatory chemotherapy" are difficult to identify due to the existence of parallel, functionally overlap-

## Histone Hyperacetylation in Breast Tumor Cell Lines

ping signaling cascades. For this reason, use of cancer therapies that target multiple intracellular signaling pathways, such as observed with the HDAC inhibitors, is an intriguing approach that addresses the problem of redundancy in growth signaling pathways. In this regard, the HDAC inhibitor phenyl butyrate was recently shown to have clinical anti-tumor activity (11).

Quinidine is a natural product therapeutic agent originally used as an anti-malarial and as an anti-arrhythmic agent. Previous studies with human breast tumor cell lines demonstrated that quinidine (90  $\mu\text{M}$ ) is an anti-proliferative agent as well. Quinidine arrested cells in early  $G_1$  phase and induced apoptosis by 72–96 h in MCF-7 cells (12), but the biochemical basis for the anti-proliferative effect of quinidine was not well understood. To clarify the molecular mechanisms of the anti-proliferative activity of quinidine, we investigated the effects of quinidine on histone acetylation and cell cycle regulatory proteins. In this report, we show that quinidine causes hyperacetylation of histone H4, down-regulation of HDAC1 protein levels, and cellular differentiation in a panel of human breast tumor cell lines. We conclude that quinidine is a novel differentiating agent that stimulates histone hyperacetylation as a result of HDAC1 protein degradation.

### MATERIALS AND METHODS

**Cell Culture**—Permanent cell lines derived from patients with breast carcinomas were used in these studies. MCF-7 cells, passage numbers 40–55, MCF-7ras (13), T47D, MDA-MB-231, and MDA-MD-435 cells were maintained in Dulbecco's modified Eagle's medium (DMEM) (Bio-Whittaker, Walkersville, MD) supplemented with 10% heat-inactivated fetal bovine serum (FBS) (HyClone Laboratories, Inc., Logan, Utah), 2 mM glutamine, and 40  $\mu\text{g}/\text{ml}$  gentamicin. Experiments were performed in this medium supplemented with 5% FBS. The cells were maintained at 37 °C in a humidified atmosphere of 93% air, 7%  $\text{CO}_2$ . After 6 days, cells became about 70–80% confluent and were passaged at a 1:5 ratio (MCF-7) or at a 1:10 ratio (all others). Normal human mammary epithelial cells (HMEC) were obtained from Clonetics, San Diego, CA, and were grown according to directions of the suppliers. Cells were grown from frozen stocks and used for 1–3 passages. Quinidine, TSA, and all-trans-retinoic acid were purchased from Sigma. The cell-permeant proteasome inhibitors, MG-132 and lactacystin, were purchased from Calbiochem.

**Growth Inhibition Assays**—Growth inhibition by cell numbers was assayed by plating cells in 35-mm<sup>2</sup> dishes ( $1\text{--}1.5 \times 10^5$ ) containing DMEM, 5% FBS plus quinidine (90  $\mu\text{M}$ ). Viable cells were counted using a hemocytometer, and trypan blue (0.02%) exclusion was used as an indicator of viability. Cell growth was also monitored in a 96-well plate format using the One Solution Cell Proliferation Assay (Promega, Madison, WI), which is based upon metabolic bioreduction of a tetrazolium compound (Owen's reagent) to a colored formazan product that absorbs light at 490 nm. The plating density for the 96-well dishes (cells/well) was varied depending upon the relative growth rates of the cell lines as follows: HMEC (2000), MCF-7 (1000), MDA-MB-231 (500), T47D (1500), and MCF-7ras (500). The One Cell Proliferation Assay Reagent was added to each well and incubated for 2 h at 37 °C. Absorbance (490 nm) was read using a Molecular Devices PC340 (Sunnyvale, CA).

**Microscopic Imaging**—Cells were plated ( $1 \times 10^5$ ) on sterile coverslips in 35-mm<sup>2</sup> dishes and grown for 96 h in DMEM, 5% FBS supplemented with either 10  $\mu\text{M}$  all-trans-retinoic acid (in 0.01% ethanol) or 90  $\mu\text{M}$  quinidine (in  $\text{H}_2\text{O}$ ). Control cells were grown in medium containing a final concentration of 0.01% ethanol. The presence of ethanol had no effect upon lipid droplet accumulation compared with cells grown in DMEM, 5% FBS. Cells were fixed in 3.7% formaldehyde/PBS, rinsed in PBS (PBS: 140 mM NaCl, 2 mM KCl, 80 mM  $\text{Na}_2\text{HPO}_4 \cdot 7\text{H}_2\text{O}$ , 1.5 mM  $\text{KH}_2\text{PO}_4$ , pH 7.0), then treated briefly with 0.4% Triton X-100 in PBS. After rinsing three times in PBS, the cells on coverslips were incubated for 30 min at 37 °C with a primary antibody to cytokeratin 18 (1:1 dilution, provided by Dr. Guillaume van Eys, Maastricht University), rinsed, and incubated (30 min/37 °C) with Texas Red conjugated secondary antibody (goat anti-mouse IgG, Sigma). Alternatively, cells were incubated with fluorescein-phalloidin (1:200 dilution of a-5  $\mu\text{g}/0.1$  ml solution, Sigma) in the dark for 40 min at room temperature, rinsed, and incubated for 5 min (room temperature) with the fluorescent lipid stain, Nile Red (1:10,000 dilution of a 1 mg/ml acetone solution, Sigma)

(14–15). All coverslips were rinsed in PBS and mounted with Fluoromount-G containing 2.5% *N*-propyl galate. Images were obtained using a Zeiss Axiovert 100 M confocal microscope ( $\times 63$  objective).

**Immunoblotting**—Cells were harvested from confluent T-75 flasks and subcultured ( $1 \times 10^6$ ) in 60-mm<sup>2</sup> dishes. On subcultivation, this confluent population of cells (85% in  $G_1$ ) synchronously proceeded through the cell cycle. To prepare whole cell lysates, the cells were harvested at the times indicated by scraping into ice-cold buffer (50 mM Tris-HCl, 0.25 M NaCl, 0.1% (v/v) Triton X-100, 1 mM EDTA, 50 mM NaF, and 0.1 mM  $\text{Na}_3\text{VO}_4$ , pH 7.4). Protease inhibitors (protease inhibitor mixture, Roche Molecular Biochemicals) were added immediately. Cell lysates were centrifuged in an Eppendorf microfuge (14,000 rpm, 5 min) at 4 °C, and the supernatants were used in immunoblotting experiments.

Histones were prepared from cells grown at a density of  $1 \times 10^7$ /T-162 flask. To harvest the cells, the flasks were placed on ice, and the growth medium was removed. Following a quick rinse with ice-cold PBS, cells were scraped into 1 ml of ice-cold lysis buffer (10 mM Tris-HCl, 50 mM sodium bisulfite, 1% Triton X-100 (v/v), 10 mM  $\text{MgCl}_2$ , 8.6% sucrose, pH 6.5) and nuclei released by Dounce homogenization. The nuclei were collected by centrifugation (3,000 rpm, 10 min, SS-34 rotor) and washed three times with the lysis buffer. Histones were extracted from the crude nuclear pellets using the procedure of Nakajima *et al.* (16). The pellets were resuspended in 0.1 ml of ice-cold sterile water using a vortex and concentrated  $\text{H}_2\text{SO}_4$  to 0.4 N was added. The preparation was incubated at 4 °C for 1 h and then centrifuged (17,000 rpm, 10 min, Sorvall SS-34 rotor). The supernatant containing the extracted histones was mixed with 10 ml of acetone, and the precipitate was obtained after an overnight incubation at -20 °C, collected, and air-dried. The acid-soluble histone fraction was dissolved in 50  $\mu\text{l}$  of  $\text{H}_2\text{O}$  and stored at -70 °C.

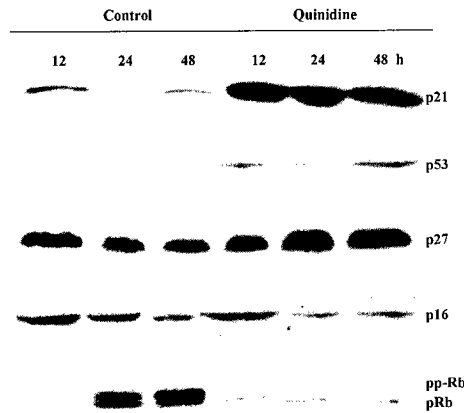
The protein concentration of the whole cell lysate supernatants or histone preparations was determined using the BCA protein assay (Pierce) and bovine serum albumin as a standard. Equal amounts of protein were loaded onto SDS-polyacrylamide gels. Molecular weights of the immunoreactive proteins were estimated based upon the relative migration with colored molecular weight protein markers (Amersham Pharmacia Biotech). Proteins were transferred to polyvinylidene difluoride membranes (NOVEX, San Diego, CA) and blocked at 4 °C using 5% nonfat milk blocking buffer (1 M glycine, 1% albumin (chicken egg), 5% non-fat dry milk, and 5% FBS) overnight. The membranes were incubated with primary antibodies for 3 h at room temperature. The antibody sources were as follows: mouse monoclonal anti-p27 (F-8, SC-1641), rabbit polyclonal anti-CDK4 (C-22), goat polyclonal anti-HDAC1 (N-19, SC-6299), all from Santa Cruz Biotechnology (Santa Cruz, CA); mouse monoclonal anti-pRb (14001A) from PharMingen (San Diego, CA); mouse monoclonal anti-cyclin D1 (NCL-cyclin D1, 113105) from Novocastra (Burlingame, CA); mouse monoclonal anti-p16 (Ap-1), p21 (WAF1, Ap-1), p53 (Ap-6) from Calbiochem; and anti-acetylated histone H4 antibody (rabbit polyclonal, Upstate Biotechnology Inc.). The primary antibodies were diluted at 1:500 in Western washing solution (0.1% non-fat dry milk, 0.1% albumin (chicken egg), 1% FBS, 0.2% (v/v) Tween 20, in PBS, pH 7.3). The antigen-antibody complexes were incubated for 1 h at room temperature with horseradish peroxidase (HRP)-conjugated secondary antibodies (goat IgG-HRP (SC-2020), rabbit IgG-HRP (SC-2004), or mouse IgG-HRP (SC-2005) from Santa Cruz Biotechnology) at a final dilution of 1:3000 in Western washing solution. After washing three times with Tris-buffered saline (10 mM Tris-HCl, pH 7.5, 0.5 M NaCl, and 0.05% (v/v) Tween 20), antibody binding was visualized using enhanced chemiluminescence (SuperSignal West Pico, Pierce) and autoradiography.

**In Vitro HDAC Activity Assay**—Quinidine HCl was added to a chicken erythrocyte cellular extract, which contained HDAC activity, at concentrations of 90  $\mu\text{M}$  (18). HDAC assays were performed as described in Hendzel *et al.* (17). Briefly, the cellular extract was incubated with 500  $\mu\text{g}$  of acid-soluble histones isolated from [<sup>3</sup>H]acetate-labeled chicken erythrocytes for 60 min at 37 °C. Reactions were terminated by addition of acetic acid/HCl to a final concentration of 0.12/0.72 N. Released [<sup>3</sup>H]acetate was extracted using ethyl acetate and quantified by scintillation counting. Samples were assayed three times, and the non-enzymatic release of label was subtracted to obtain the reported values.

### RESULTS

**Hyperacetylation of Histone H4**—Antibodies that recognize acetylated forms of histone H4 have been used as a probe for agents that cause histone hyperacetylation (19). In Western blot experiments, we compared the ability of quinidine to cause

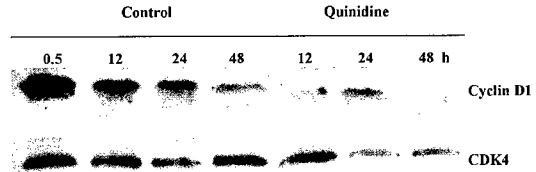
## Histone Hyperacetylation in Breast Tumor Cell Lines



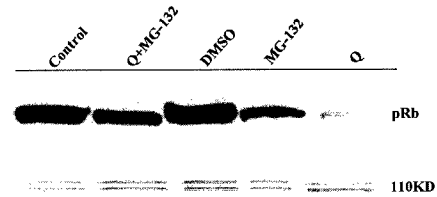
**FIG. 3. G<sub>1</sub> cell cycle proteins in MCF-7 cells.** Cells released from confluency were plated into control medium or medium containing 90  $\mu$ M quinidine. Whole cell lysates were prepared 12, 24, or 48 h after plating and assayed by immunoblotting for the cyclin-dependent kinase inhibitors, p21<sup>WAF1</sup> ( $n = 3$ ), p27 ( $n = 1$ ), p16 ( $n = 3$ ), and p53 ( $n = 3$ ) after electrophoresis of 50  $\mu$ g of protein/lane through 12% SDS-polyacrylamide gels. pRb protein was immunoprecipitated from 500  $\mu$ g of whole cell lysate protein using an antibody that recognizes phosphorylated and non-phosphorylated pRb (56). This entire immunoprecipitate was electrophoresed in a 7.5% SDS-polyacrylamide gel and immunoblotted using this same antibody. Results shown are typical of two independent analyses.

A small, less than 2-fold increase in p27 levels was observed in cells exposed to quinidine for 24–48 h, whereas levels of p16 were unchanged (Fig. 3). Quinidine treatment decreased cyclin D1 and CDK4 protein levels after 12 h of treatment (Fig. 4), indicating that the cyclin-dependent kinase inhibitor, p21<sup>WAF1</sup>, as well as an important G<sub>1</sub> phase target of p21<sup>WAF1</sup>, the cyclin D1-CDK4 complex, are early targets of quinidine in MCF-7 cells. This profile of activity is consistent with the observed cell cycle arrest of quinidine-treated MCF-7 cells in mid-G<sub>1</sub> phase (12).

In MCF-7 cell extracts probed using anti-pRb antibodies, two separate but closely migrating bands were distinguishable. The upper band contained more highly phosphorylated pRb, and the lower band contained unphosphorylated or hypophosphorylated pRb. Control cells showed a faint pRb signal at 12 h, typical of cells in early G<sub>1</sub> phase, and increased expression of both phosphorylated and unphosphorylated pRb at 24 and 48 h. Quinidine-treated MCF-7 cells had no detectable hyperphosphorylated pRb at any time point examined, and total levels of pRb protein failed to increase with progression through G<sub>1</sub> phase as seen in the control, proliferating cells (Fig. 3). The decrease in pRb phosphorylation level was predictable based on the increase in p21<sup>WAF1</sup> and decreased levels of both cyclin D1 and CDK4 (Fig. 4). In addition, Nakanishi *et al.* (24) showed that p21<sup>WAF1</sup> can bind pRb protein and block its phosphorylation. However, the actions of quinidine upon p21<sup>WAF1</sup> and cyclin D-CDK4 activity do not explain why the levels of total pRb protein were so low. Reductions in the cellular content of phosphorylated pRb protein in MCF-7 cells by quinidine is an important additional level of cell cycle control that effectively attenuates progression of cells out of G<sub>1</sub> phase and has been reported in other tumor cell lines in response to HDAC inhibition (22). In Fig. 5 we show data suggesting that the 26 S proteasome pathway regulates the total pRb content. MCF-7 cells incubated for 24 h in MG-132 or MG-132 plus quinidine had more total pRb than cells incubated with quinidine alone. Thus, quinidine promoted the loss of both HDAC1 and pRb, and inhibition of the 26 S proteasome pathway restored the levels of both of these proteins to that seen in the untreated cells. We have no direct evidence that quinidine promotes the proteasomal degradation of either protein. We hypothesize that



**FIG. 4. Cyclin D-CDK4 in MCF-7 cells.** Confluent MCF-7 cells were subcultured in control medium or medium containing 90  $\mu$ M quinidine. Whole cell lysates were prepared 0.5, 12, 24, and 48 h after subculture. Equal protein aliquots (50  $\mu$ g/lane) were electrophoresed in 12% SDS-polyacrylamide gels and assayed for cyclin D1 and CDK4 protein levels by immunoblotting. Results shown are representative of three independent experiments.



**FIG. 5. Proteasome inhibitor modulates retinoblastoma protein levels.** Confluent MCF-7 cells were subcultured in the presence of 90  $\mu$ M quinidine, 30  $\mu$ M MG-132, or quinidine + MG-132 for 24 h, then harvested, and whole cell extracts (100  $\mu$ g/lane) were analyzed for pRb. A Coomassie Blue-stained protein is shown as the loading control.

quinidine may direct degradation of HDAC1 by the proteasome or, alternatively, quinidine might stimulate the proteasomal degradation of other regulatory factor(s) that act to maintain HDAC1 and pRb protein levels.

MCF-7 cells express wild-type p53 protein. Normal p53 is a short lived protein that is maintained at low levels, but in response to cell stress or DNA damage, p53 is stabilized and accumulates in the nucleus where it functions as a transcription factor inducing p21<sup>WAF1</sup>, G<sub>1</sub> cell cycle arrest, and apoptosis (25). Wild-type p53 down-regulates pRb levels in MCF-7 cells (26). Although Saito *et al.* (22) showed that p53 is not required for pRb down-regulation by HDAC inhibitors in all cell lines, quinidine-treated MCF-7 cells have elevated p53 levels (5–7-fold) (Fig. 3). Thus, p53 could contribute to the maintenance of the G<sub>1</sub> cell cycle arrest in MCF-7 by sustaining p21<sup>WAF1</sup> protein levels and suppressing pRb protein levels.

**Growth Arrest and Cellular Differentiation in Human Breast Tumor Cell Lines**—In contrast to MCF-7 cells, human breast tumor cell lines T47D, MDA-MB-231, and MDA-MB-435 express p53 proteins with distinct point mutations (27). To test for a requirement of p53, this panel of human breast tumor cell lines was exposed to quinidine, and the effects of quinidine on cell growth were compared (Fig. 6). The data shown are viable cell numbers/well, bioreductive metabolism/well, or both. In all four cell lines growth was suppressed in a concentration-dependent fashion between 10 and 90  $\mu$ M quinidine, and maximal growth inhibition was observed at  $\sim$ 90  $\mu$ M quinidine (data not shown). These data showed that growth suppression by quinidine is a p53-independent response. It is interesting that quinidine was not overtly cytotoxic in HMEC, a line of normal human mammary cells (28).

Evidence that quinidine elicited cellular differentiation in MCF-7 human breast tumor cells in conjunction with the inhibition of cell growth was obtained using maximally effective concentrations of quinidine or retinoic acid (data not shown). Antibodies directed against cytokeratin 18 (29) were used to probe the organization of the cytoskeleton (Fig. 7). In these studies, all-*trans*-retinoic acid (10  $\mu$ M) was used to compare the differentiation response (30). Control MCF-7 cells showed expression of cytoplasmic cytokeratin 18 in a disorganized fash-

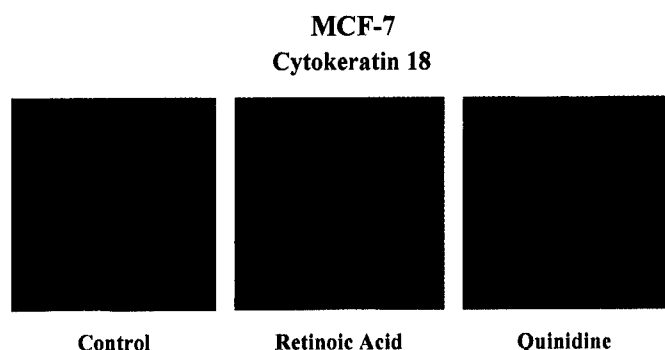


FIG. 7. **Cytokeratin 18 in MCF-7 cells.** Cells were replica-plated ( $2 \times 10^5$ ) on sterile coverslips in 35-mm<sup>2</sup> dishes in medium containing 0.01% ethanol (control), 10  $\mu$ M retinoic acid, or 90  $\mu$ M quinidine and grown for 96 h. Cytokeratin 18 detection using a Texas Red-tagged secondary antibody is shown using confocal microscopy. Data shown are typical fields representative of two independent experiments.

lines and increased by retinoic acid and quinidine. Lipid droplet accumulation was more marked in all four cell lines treated with quinidine than with retinoic acid. These data demonstrate that induction of a more differentiated phenotype is a general response of human mammary tumor cells to quinidine.

**Hyperacetylation of Histone H4 in Mammary Tumor Cell Lines by Quinidine**—To determine whether differentiation and histone acetylation were linked, we investigated the histone H4 acetylation status of quinidine-treated T47D, MDA-MB-231, and MCF-7<sub>ras</sub> cells. MCF-7, MCF-7<sub>ras</sub>, T47D, and MDA-MB-231 cells were incubated for 24 h in the presence or absence of quinidine, and then histones were extracted for immunoblotting. Fig. 9 shows that histone H4 was hyperacetylated in all cell lines treated with quinidine. Control cells contained no hyperacetylated histone H4.

#### DISCUSSION

Quinidine-induced histone H4 hyperacetylation in MCF-7 human breast carcinoma cells can be attributed to the rapid elimination of HDAC1 protein, a response that was blocked by MG-132 and lactacystin, two inhibitors of proteasome-mediated proteolysis. HDAC1 protein was undetectable within 30 min after the addition of quinidine to the medium of MCF-7 cells, and hyperacetylated histone H4 appeared between 1 and 2 h. Levels of HDAC1 protein were completely suppressed between 0.5 and 6 h, and during this time H4 acetylation levels increased. H4 acetylation was maintained at 12 and 24 h, despite the partial restoration of HDAC1 protein at these same time points. These data indicate that quinidine-induced reductions in HDAC1 protein levels are unlikely to explain fully the regulation of H4 acetylation state in MCF-7 cells by quinidine. Additional HDAC enzymes or effects upon histone acetylation rates could possibly play a role as well.

An earlier study showed that over this initial 48-h period, 80% of the MCF-7 cell population had shifted into G<sub>0</sub>, a quiescent state marked by the absence of Ki67 antigen immunoreactivity (12). Cellular differentiation manifested as the accumulation of lipid droplets, and a reorganization of the cytokeratin 18 cytoskeleton was evident after this initial 48-h period. Quinidine exhibited all the responses typical of known HDAC inhibitory drugs, with the exception that quinidine had no direct inhibitory effect upon HDAC1 enzymatic activity. We conclude from the current studies that quinidine is a novel differentiating agent that causes histone hyperacetylation, in part, by physical elimination of HDAC1 protein rather than the inhibition of HDAC enzymatic activity.

Histone H4 hyperacetylation and induction of cellular differentiation by quinidine were seen in a panel of human breast

tumor cell lines that were selected for study on the basis of their diversity of genetic backgrounds. The differentiation response to quinidine was independent of the estrogen receptor (ER) status. Cell lines representative of ER-positive and ER-negative human breast carcinoma cells were induced to differentiate in the presence of quinidine. The ER status of the estrogen receptor positive cell lines is MCF-7 (ER- $\alpha$  and ER- $\beta$ ), T47D (ER- $\alpha$  and ER- $\beta$ ), and MDA-MB-231 (ER- $\beta$ ). MDA-MB-435 cells expressed very low levels of ER- $\beta$  and no ER- $\alpha$  (37, 38). MCF-7 and T47D cells display an epithelial morphology and show similarities with mammary ductal and luminal epithelial cells, respectively (30, 39). MDA-MB-231 cells exhibit an elongated cellular morphology that is also typical of MDA-MB-435 cells. Our results demonstrate that quinidine is a differentiation agent in both types of mammary tumor cells.

HDAC inhibitors reverse the transformed phenotype of NIH3T3<sub>ras</sub> cells, and this property has been used successfully as a screening assay for the identification of new HDAC inhibitors (40, 41). Quinidine elicited a more differentiated phenotype in MCF-7<sub>ras</sub> cells, an MCF-7 cell derivative produced by stable transformation with v-Ha-*ras*, thus demonstrating that quinidine, like other HDAC inhibitors, can reverse an Ha-*ras*-induced phenotype.

Quinidine induced differentiation independently of wild-type p53. The ability of quinidine to cause differentiation of p53 mutant cell lines is consistent for a role of histone hyperacetylation in the response. HDAC inhibitors typically induce a p53-independent activation of p21<sup>WAF1</sup> gene expression (5, 22). Growing MCF-7 and T47D cells express p21<sup>WAF1</sup> protein in moderate to low levels (42), and quinidine raised p21<sup>WAF1</sup> protein levels in MCF-7 cells approximately 11-fold within 12 h. Although p21<sup>WAF1</sup> was reported to be low to undetectable in MDA-MB-231, p21<sup>WAF1</sup> was detected in Western analyses of both MDA-MB-231 and T47D cells in a p53-independent fashion in response to serum deprivation, adriamycin, etoposide (42, 43), and quinidine (data not shown). These data support the idea that the p21<sup>WAF1</sup> gene is present but inactive in growing MDA-MB-231 cells. Since histone hyperacetylation of the p21<sup>WAF1</sup> gene occurs in response to HDAC inhibitors, it might be involved in the pathway of p53-independent activation of p21<sup>WAF1</sup> gene expression (5).

The processes of cellular differentiation and cell cycle progression are interdependent. G<sub>1</sub> arrest is a necessary but insufficient condition for differentiation in numerous cell types including leukemic cells, keratinocytes, colonic epithelium, and muscle cells. In all of these cells, induction of p21<sup>WAF1</sup> protein and G<sub>1</sub> cell cycle arrest occurred prior to differentiation (44–50) and was generally independent of p53. We hypothesize that the differentiated state can be viewed as a cellular response to G<sub>1</sub> arrest, requiring a change in gene expression profile and suppression of cell death pathways. The response of MCF-7 breast tumor cells to quinidine is consistent with this model.

To begin to understand how quinidine might elicit G<sub>1</sub> arrest of MCF-7 cells, we have focused on the action of quinidine as a potassium channel blocking agent. Quinidine enters cells and inhibits cardiac potassium channels by binding to the intracellular face of the ion pore (51). Although the location of the quinidine-binding site on the ATP-sensitive potassium channel is unknown, quinidine is freely permeable across membranes and inhibits the ATP-sensitive potassium channels whether it is applied to the external or internal surface of a lipid membrane bilayer (52).

In the presence of quinidine, MCF-7 cells accumulate at a position 12 h into G<sub>1</sub> phase (12). This position, defined by cell cycle arrest and release experiments, precedes the lovastatin arrest point by 5–6 h and is clearly distinct from the restriction

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