Antitumor effect of the histone deacetylase inhibitor LAQ824 in combination with 13-cis-retinoic acid in human malignant melanoma

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Abstract

Resistance to chemotherapy is a major hurdle in the treatment of malignant melanoma. Histone deacetylase (HDAC) inhibitors have been shown to have antitumor activity in different tumor types, including melanoma, and to reverse epigenetic repression of tumor suppressor genes, such as retinoic acid receptor β (RARb). In this study, we tested the antitumor effect of the HDAC inhibitor LAQ824 in combination with 13-cis-retinoic acid (CRA) on two human melanoma cell lines both in vitro and in vivo. Treatment of LAQ824 showed a dose-dependent inhibitory effect on A2058 and HMV-I cell lines in a clonogenic assay. These cell lines were relatively resistant to CRA. On treatment with combination of LAQ824 and CRA, a greater inhibitory effect (up to 98%) was achieved compared with single agents. Lack of RARb32 gene expression was associated with histone acetylation and gene methylation at the promoter level. Treatment with LAQ824 restored retinoid sensitivity by reverting RARb32 epigenetic silencing. The biological effect of LAQ824 was associated with p21 induction in both cell lines but G2 cell cycle arrest in A2058 and apoptosis in HMV-I cell line. The induction of apoptosis by LAQ824 was associated with increased reactive oxygen species and induction of SM22 gene expression in HMV-I but not in A2058 cell line. Administration of the free radical scavenger l-N-acetylcysteine blocked LAQ824 + CRA–-mediated apoptosis in HMV-I cells, suggesting a primary role for reactive oxygen species generation in LAQ824 + CRA–associated lethality. Combination treatment showed 61% and 82% growth inhibition in A2058 and HMV-I tumors, respectively. Greater induction of in vivo apoptosis was observed in the HMV-I but not in the A2058 tumors treated with combination therapy compared with single agents. These results suggest that the HDAC inhibitor LAQ824 has a greater antitumor activity in combination with CRA in melanoma tumors but the degree of induced apoptosis may vary. Combination of HDAC inhibitors and retinoids represents a novel therapeutic approach for malignant melanoma that warrants clinical testing. [Mol Cancer Ther 2007;6(1):70–81]

Introduction

Malignant melanoma is becoming increasingly prevalent worldwide and its incidence is growing more rapidly than other type of cancer (1). Its resistance to standard chemotherapeutic agents limits effective systemic therapy for metastatic disease. The alkylating agent dacarbazine, the only Food and Drug Administration–approved drug for the treatment of malignant melanoma as a single agent, has been reported to induce response rates of 7% to 13% in recent phase III clinical trials with 15% to 28% of patients having stable disease (2, 3). High-dose interleukin-2 has showed antitumor activity in melanoma with a response rate of 16%. Of particular interest is the fact that 6% of patients achieved a complete response and over half of those remained disease-free at >2 years (4). However, toxicity with high-dose interleukin-2 is considerable and has limited the use of this approach to highly selected patients (5). Combination chemotherapy with interleukin-2 and/or IFN-α has also failed to provide significant clinical benefit in large phase III randomized trials (6). Thus, novel therapeutic approaches are needed.

Retinoids, a group of natural and synthetic vitamin A analogues, are essential for growth and cell differentiation of epithelial tissue and may affect cancer development (7, 8). Retinoids exert their effects mainly via nuclear receptors, the retinoic acid (RA) receptors (RAR) and the retinoid X receptors, both of which are members of the nuclear receptor superfamily (9, 10). The human RARβ gene is expressed as three isoforms: β1, β2, and β4 (11). The biologically active RARβ2 isofrom is under the regulation of the F2 promoter containing a high-affinity RA-responsive element, which is associated with the transcriptional activation of RARβ2 by RA in a variety of cells (12).

The clinical activity of retinoids has been limited in patients with advanced cancer, including melanoma (13).
Several melanoma cell lines are resistant to retinoids (14). Retinoid resistance in epithelial tumors has been associated with epigenetic loss of RARβ2 expression due to DNA methylation affecting the RARβ2 P2 promoter of one or more RARβ alleles (15, 16). Our group and others have shown that chromatin remodeling agents, such as histone deacetylase (HDAC) inhibitors, reverse epigenetic repression of RARβ2 in epithelial tumors, including prostate, renal, and breast (17–19).

Histone proteins organize DNA into nucleosomes, which are regular repeating structures of chromatin. The acetylation status of histones alters chromatin structure, which in turn is involved in gene expression. Two classes of enzyme can affect the acetylation of histones, histone acetyltransferases and HDAC. Several inhibitors have been characterized that inhibit tumor growth in vivo and in vitro and are currently under clinical testing (20, 21). LAQ824 is a HDAC inhibitor in early clinical development. It is a structurally novel hydroxamic acid derivative that inhibits HDAC at concentrations below 0.15 μmol/L. LAQ824 has also been shown to have in vivo antitumor activity against human leukemia (22), lung, colon (23), prostate (24), and multiple myeloma xenografts (25).

In this study, we analyzed the expression of RARβ2 in two human melanoma cell lines and tested the hypothesis that the HDAC inhibitor LAQ824 may restore retinoid sensitivity by reverting RARβ2 epigenetic silencing and have a greater antitumor effect in combination with retinoids.

**Materials and Methods**

Cell Lines and Reagents

The human melanoma cell line, A2058, was purchased from American Type Culture Collection (Manassas, VA), and HMV-I was kindly provided by the Department of Aging and Cancer, Tohoku University of Sendai (Sendai, Japan). A2058 and HMV-I cells were cultured in DMEM and DMEM/F12 medium (Life Technologies, Carlsbad, CA) with 10% fetal bovine serum (FBS; Sigma, St. Louis, MO) and 1% penicillin/streptomycin (Life Technologies), respectively, and kept in an incubator at 37°C and atmosphere containing 5% CO2. For the in vitro experiments, tumor cells were treated with 13-cis-RA (CRA; Sigma), all-trans-retinoic acid (ATRA; Sigma), LAQ824 (Novartis Pharmaceuticals, East Hanover, NJ), or vehicle (DMSO). For in vivo experiments, CRA was suspended in propylene glycol (Sigma) and given by gavage, whereas LAQ824 was suspended in 6% IN lactic acid, 90% dextrose, and 4% 1N NaOH and given by i.p. injection. N-acetylcyesteine (NAC) and H2O2 were purchased from Sigma. 5-Chloromethyl-2,7'-dichlorodihydrofluorescein diacetate and 4',6-diamidino-2-phenylindole were purchased from Molecular Probes (Eugene, OR). Ki67 antibody was from Novocastra Laboratory (Newcastle upon Tyne, United Kingdom).

Colonies Formation Assay

The colony formation assay was done as described previously (26). In brief, cancer cells were seeded at 500 per well in a six-well format and allowed to attach overnight in medium supplemented with 10% FBS. The cells were starved for 24 h in serum-free medium at 37°C at 5% CO2. The medium was then replaced with increasing concentrations of LAQ824 (0, 50, 100, and 200 nmol/L) and CRA (0, 0.5, 1.0, and 2.5 μmol/L), n = 3. The cells were treated with the single agents or combination. After 72 h, the medium was replaced with medium supplemented with 10% FBS for 7 days. Cells were then washed once with PBS and stained with crystal violet (0.2% c.v. + 10% ethanol in water). Excess crystal violet solution was decanted, and the cells were destained with distilled water. Images of colony formation were captured using Kodak Image Station 440CF (Kodak, Rochester, NY), and colony counts were determined by Quantity One quantitation software (version 4.3; Bio-Rad, Hercules, CA). Percentage of growth inhibition was normalized to untreated control using the following formula: % growth inhibition (GI) = 1 – (Cexp / Cctl), where Cexp equals total colony number of experimental group and Cctl equals total colony number of untreated control. Results were reproducible in repeated experiments. Results are expressed as mean colonies number ± SE. The experiments were repeated twice with similar results.

**RNA Isolation and Reverse Transcription–PCR**

Tumor cell lines were treated for 24 h with 1.0 μmol/L CRA, 50 and 100 nmol/L LAQ824, or vehicle (DMSO) in DMEM/F12 medium for HMV and DMEM for A2058 supplemented with 10% FBS. Total RNA was extracted from tumor cells by Trizol (Life Technologies), and the first strand was synthesized with oligo(dT) as primer using 1μg total RNA according to the manufacturer’s instructions. PCR was done with primers for RARβ2 and glyceraldehyde-3-phosphate dehydrogenase (GAPDH; control) using cDNA synthesized from reverse transcription–PCR (RT-PCR). Primer sequences for RARβ2 covered exons 3 and 4, 5-GACTGTATGAGTGTTCGGTAC-3' (forward) and 5'-ATTGTCTGCGCAACGAAAGC-3' (reverse). Primers for GAPDH are 5'-CCACCACTGGAAATTCCATGGCA-3' (forward) and 5'-TCTAGAGCGCGTACGCTAC-3' (reverse). PCR products measured 256 and 574 bp, respectively. Results were reproducible in repeated experiments. Samples were processed in a Perkin-Elmer (Wellesley, MA) 9600 GeneAmp thermocycling system under the following conditions: 2 min denaturation step at 94°C, followed by 35 amplification cycles (30 s at 94°C for denaturation, 30 s at 60°C for primer annealing, and 45 s at 72°C for primer extension), and final extension at 72°C for 10 min.

**Chromatin Immunoprecipitation Assay**

The histone acetylation status of RARβ2 promoter was examined using the chromatin immunoprecipitation assay as described previously (19). An antibody specific for acetylated histone 3 (H3) was used to immunoprecipitate formaldehyde cross-linked, sonicated chromatin from cells treated with LAQ824 or the combination. Semiquantitative PCR analysis of DNA bound to immunocomplexes was done to detect a 192-bp fragment of the RARβ core promoter region (−165 to +27), which includes RA-responsive elements and TATA sequences (18).
Quantitative Real-time PCR Analysis

Quantitative real-time PCR for specific genes was done to confirm the differences in RARβ gene expression identified by RT-PCR (19). Single-strand cDNA was synthesized from melanoma cell total RNA (1 µg) by reverse transcription using oligo(dT) as the primer. According to the manufacturer’s protocol, quantitative real-time PCR was done using an ABI Prism 7700 Sequence Detector System (PE-Applied Biosystems, Foster City, CA) with a 2× SYBR Green PCR Master Mix (PE-Applied Biosystems), reverse transcribed cDNA, and gene-specific primers. To quantify the amount of target mRNA in the samples, a standard curve of RARβ2 was prepared for each run using the plasmid containing the target gene, as well as a standard curve for GAPDH, as internal control. This enabled standardization of the initial mRNA content of cells relative to the amount of GAPDH. The sequences of the specific primers were as follows: RARβ2 primers are the same as in RT-PCR (256 bp), and the sense sequence was 5’TGAACCGGAAGCTCAGCTGG-3’ and the antisense sequence was 5’TCCACGACCTCTGTGCTGTA-3’ for GAPDH and the sense sequence was 5’TGGGATGTTGA-TGTCGAGAACGC-3’ (downstream) and the unmethylated sequence was 5’CTGCCAAGTCGCCAAGG-3’ for Sm22. The relative expression of target gene was determined by the difference of the threshold cycle (Ct) between target gene and GAPDH (relative expression = 2^ΔCt, where ΔCt = Ct GAPDH – Ct target gene).

DNA Extraction and Methylation-Specific PCR

Genomic DNA was isolated from cell lines following the instruction of the DNeasy Tissue kit (Qiagen, Valencia, CA). Approximately 1 µg DNA was modified by bisulfite treatment and subjected to methylation-specific PCR. The first methylation-specific PCR primers were designed from +80 to +284 bp (upstream 5’TATGYGAGTTGGTGGAGGA-TTGGGAA-3’ and downstream 5’-AATAATCTATTACCA-TTTITCCAAACTTA-3’). The next methylation-specific PCR primer sequences that specifically recognized methylated GAGCGATTC-3’ and downstream 5’TGTTGA-TAATAATCATTTACCA-3’ (upstream) and 5’-CGACCAATCCAACC-GAAACGA-3’ (downstream) and the unmethylated RARβ2 sequences (+100 to +261) were 5’TGGGATGTTGA-GAATGTGAGTGATTT-3’ (upstream) and 5’-CCTACT-CACACCGATTCAACCCCAAACCAA-3’ (downstream).

Flow Cytometric Analysis of Cell Cycle and Apoptosis

Cell cycle analysis was done using the Cellular DNA Flow Cytometric Analysis kit (Roche Diagnostics, Indianapolis, IN). Cells treated with agents (1 µmol/L LAQ824, 10 µmol/L CRA, and 1 µmol/L ATRA) from 24 to 72 h were harvested by trypsin, washed, and fixed in 70% ethanol on ice followed by incubation with RNase. The cells were then stained with propidium iodide (PI) and subjected to a flow cytometry analysis of cell cycle. Aliquots of 10^6 cells were washed thrice in PBS and resuspended in buffer. A total of 5 mL Annexin V-FITC and/or 5 mL PI was added followed by incubation at room temperature in the dark for 15 min using Annexin V-FITC Apoptosis Detection kit I (BD Biosciences). Cells were immediately analyzed by FACSCalibur (Beckton Dickinson Immunocytometry Systems, San Jose, CA) and CellQuest software (Beckton Dickinson). PI+ and Annexin V+ cells were considered apoptotic, and PI+ and Annexin V+ cells were considered dead cells. The experiments were repeated twice with similar results.

Tumor Growth In vivo

The animal protocol was approved by the Institutional Care and Use Committee at the Johns Hopkins Medical Institutions and was in accordance with the NIH Guide for the Care and Use of Laboratory Animals. Male 4- to 6-week-old athymic nude mice (National Cancer Institute) were kept in a temperature-controlled room on a 12/12 h light/dark schedule with food and water ad libitum. Animals were injected s.c. in the flank region with 1 x 10^6 tumor cells (A2058 and HMV-I) resuspended in Hank’s solution and mixed with Matrigel (1:1; Collaborative Biomedical Products, Bedford, MA) in a final volume of 0.2 mL. As the tumor volume reached a measurable size (50-100 mm^3), 20 animals for each tumor were randomly placed in four groups (five animals per group): control, CRA, LAQ824, and combination. Animals in the control group were treated with a daily administration (5 days/wk) of vehicle (polyethyleneglycol) by gavage. LAQ824 (10 mg/kg/d) and CRA (20 mg/kg/d) were given by either i.p. injection or by gavage, respectively. Tumor volume was measured with a caliper twice weekly and reported as mean mm^3 ± SE. The animals were treated for ~2 weeks and then euthanized by carbon dioxide inhalation. The experiments were repeated twice with similar results.

Western Blot Analysis

To evaluate the effect of LAQ824 and CRA in vivo, HMV-I xenografts from mice treated with LAQ824 and CRA were homogenized in M-PER mammalian protein extraction reagent (Pierce, Rockford, IL) with protease inhibitor cocktail (Roche Diagnostics). Proteins (10 µg/lane) from the homogenized tissues were applied to 4% to 15% Tris-Glycine gels (Bio-Rad) and blotted with primary antibodies for acetyl H3 or α-tubulin. The antibodies were purchased from Upstate (Lake Placid, NY) for acetyl H3 and from Sigma for α-tubulin.

In vivo Measurement of Apoptosis

Formalin-fixed, paraffin-embedded tissues were deparaffinized and washed with PBS, incubated in 0.85% NaCl for 5 min at room temperature, and treated with a 4% formaldehyde solution in PBS for 10 min. Slides were washed, incubated in 20 µg/mL protease K solution for 10 min, and washed again. DNA fragmentation was visualized by staining tissue sections with a commercial kit [DeadEnd fluorometric terminal deoxynucleotidyl transferase–mediated dUTP nick end labeling (TUNEL) system, Promega, Madison, WI]. Tissues were incubated in equilibration buffer for 10 min before the addition of the reaction cocktail containing terminal dNTP transferase and FITC-conjugated nucleotides. Slides were incubated for 1 h at 37°C, and reactions
Figure 1.  Effect of combination of LAQ824 and CRA on A2058 and HMV-I melanoma cell growth in vitro.  A, A2058 and HMV-I melanoma cells were treated with increasing dose of LAQ824 (0.05–1 μmol/L), fixed concentration of CRA (10 μmol/L), or combination, and colony numbers were assessed. Columns, mean percentage of controls; bars, SE. *, P < 0.05 versus untreated controls; **, P < 0.05 versus single agents.  B, colony formation assay was done in HMV-I tumor cells treated for 72 h with increasing doses of LAQ824 (50, 100, and 200 nmol/L) in combination with increasing doses of CRA (0.5, 1.0, and 2.5 μmol/L).  Left, results are expressed as means of percentage of inhibition; right, representative colony formation (left, shaded area): Untreated control (top left), 0.5 μmol/L CRA (top right), 50 nmol/L LAQ824 (bottom left), and combination (bottom right).
Statistical Analysis
Differences between means of unpaired samples were evaluated by Student’s t test using the Sigmastat program; \( P < 0.05 \) was considered of statistical significance.

Results
LAQ824 Restores Retinoid Sensitivity in RAR\(\beta\)2-Negative Melanoma Cell Lines In vitro

To determine the antiproliferative effect of CRA and LAQ824, we used a clonogenic assay. A2058 and HMV-I cells were exposed to increasing doses of LAQ824 (0.1-1.0 \( \mu \)mol/L) and CRA (0.5-10 \( \mu \)mol/L) for 72 h (Fig. 1A and B). CRA treatment did not induce a significant inhibition of cell proliferation in ether cell lines. Treatment with LAQ824 induced a dose-dependent inhibition as single agent; however, the combination of LAQ824 with CRA had a greater inhibitory effect (up to 99% growth inhibition).

Combination of LAQ824 and CRA Induces RAR\(\beta\)2 Reexpression in RAR\(\beta\)2-Negative Melanoma Cell Lines

Based on previous evidence of RAR\(\beta\)2 induction by HDAC inhibitors in other tumor cell lines, we hypothesized that the greater inhibitory effect of the combination of LAQ824 and CRA was due to RAR\(\beta\)2 induction and consequent restoration of retinoid sensitivity. To assess the status of RAR\(\beta\)2 expression and associated retinoid resistance in the human melanoma cell lines, RT-PCR assay was done. A2058 and HMV-I cell lines were treated with increasing doses of LAQ824 in the presence or absence of CRA (1 \( \mu \)mol/L) for 24 h. RT-PCR analysis revealed reinduction of RAR\(\beta\)2 by LAQ824 in the presence of retinoid (Fig. 2A). There was no induction of RAR\(\beta\)2 in CRA-only–treated cells. Quantitative PCR analysis of RAR\(\beta\)2 gene expression was done and revealed a synergistic induction of RAR\(\beta\)2 by combination treatment with LAQ824 and CRA in both A2058 and HMV-I cell lines (Fig. 2B). The next step was to determine whether reexpression of RAR\(\beta\)2 was due to the direct effect of LAQ824 on histone acetylation by chromatin immunoprecipitation assay analysis. The results showed a high constitutive H3 deacetylation at the RAR\(\beta\)2 promoter in both melanoma cell lines, and treatment with CRA alone did not increase histone acetylation status. However, LAQ824 induced a significant increase of histone acetylation associated with the RAR\(\beta\)2 promoter after 24 h of treatment (Fig. 2C). To determine whether lack of RAR\(\beta\)2

![Figure 2](https://example.com/figure2.png)

**Figure 2.** Effect of LAQ824 and CRA on RAR\(\beta\)2 gene expression in melanoma cell lines. *A,* reexpression of RAR\(\beta\)2 in HMV-I and A2058 cell lines treated for 24 h with indicated concentrations of CRA and LAQ824 as single agents or in combination. RT-PCR was used to assess gene expression of RAR\(\beta\)2 and GAPDH (internal control) as described in Materials and Methods. *B,* RAR\(\beta\)2 relative expression by quantitative real-time PCR in A2058 and HMV-I cells treated with increased concentrations of LAQ824 and CRA (10 \( \mu \)mol/L). *C,* RAR\(\beta\)2 promoter acetylation was assessed by chromatin immunoprecipitation assay. RAR\(\beta\)2-negative cell lines were treated with LAQ824 (1 \( \mu \)mol/L), CRA (10 \( \mu \)mol/L), or combination (Comb). Chromatin acetylation associated with RAR\(\beta\)2 promoter in A2058 and HMV-I cell lines at baseline and following treatments was determined by using anti–acetyl H3 antibody. *Bottom,* DNA input as internal control. *D,* methylation-specific PCR analysis of RAR\(\beta\)2 in A2058 and HMV-I cell lines was done. DNA from MDA-MB-231 (RAR\(\beta\)2 methylation) and RCC 1.11 (RAR\(\beta\)2 unmethylation) cell lines were used as controls. *U,* unmethylated; *M,* methylated.
expression was due to aberrant methylation at the promoter level, the RAR/β2 promoter was analyzed by methylation-specific PCR. The results showed that A2058 cell line presented both unmethylated and methylated bands, whereas HMV-I cell line showed only a methylated band (Fig. 2D).

**p21 Status and Modulation by LAQ824 and CRA in A2058 and HMV-I Human Melanoma Cell Lines**

p21 represents a critical checkpoint in cell cycle regulation and its gene expression modulation is considered a hallmark of HDAC inhibition. Thus, we analyzed the status of p21 in the human melanoma cell lines following treatment with LAQ824 and CRA. p21 gene and protein expression was induced by LAQ824 and LAQ824 + CRA in both cell lines as assessed by RT-PCR (Fig. 3A) and Western blot analysis (Fig. 3B), respectively. p14 gene expression was present in HMV-I but not in A2058, whereas p16 and p27 gene expression was present in both cell lines by RT-PCR (data not shown). No modulation of these genes by LAQ824 was observed (data not shown).

**LAQ824 Induces G2 Arrest in A2058 and Apoptosis in HMV-I Cell Line**

The melanoma cell lines were cultured with 0.1 to 1.0 μmol/L LAQ824 and/or 10 μmol/L CRA and assayed for cell cycle analysis at different time points by the PI staining method. Combination treatment with 1.0 μmol/L LAQ824 and CRA for 24 h induced A2058 cell line in G2-M phase (32% in CRA + LAQ824 versus 24.2% in medium only; Fig. 4A). The induction of G2-M phase was also dose dependent following 72 h of treatment (Fig. 4B). HMV-I cells were induced in sub-G0 phase (33.5% in 1 μmol/L CRA + LAQ824 versus 3.5% in medium only; Fig. 4A). The induction of sub-G0 phase was also dose dependent following 72 h of treatment (Fig. 4B). Administration of 0.1 to 1.0 μmol/L LAQ824 and/or 10 μmol/L CRA for 24 h induced apoptosis in both melanoma cell lines by Annexin V and PI staining (Fig. 4C). Treatment with 0.5 μmol/L CRA + LAQ824 induced greater apoptosis in HMV-I cells compared with A2058 cells (51.2% and 9.5%, respectively; Fig. 4C). Dead cell fraction (Annexin V+ and PI+ cells) increased in a dose-dependent manner following 72 h of treatment (Fig. 4D). These results were consistent with the cell cycle analysis data.

**LAQ824 Restores Retinoid Sensitivity in RAR/β2-Negative Cell Lines In vivo**

To determine the effect of LAQ824 and CRA on in vivo tumor growth, melanoma cells were injected s.c. in nude mice. Once the tumors were established, animals received either control vehicle, CRA (20 mg/kg/d), LAQ824 (10 mg/kg/d), or combination. Tumor weight analysis showed that treatment with LAQ824 had a significant inhibitory effect on both A2058 and HMV-I tumor growth (Fig. 5A). CRA had no significant inhibitory effect. Combination of LAQ824 and CRA had a greater inhibitory effect than LAQ824 alone. Then, we assessed the pharmacodynamic effect of this combination. Protein extracts from HMV-I tumor samples were analyzed for histone acetylation. Animals treated with either LAQ824 or combination presented increased tumor histone acetylation (Fig. 5A). We also did TUNEL immunofluorescence in tumor sections counterstained with 4,6-diamidino-2-phenylindole to quantify the percentages of in vivo apoptosis. The results confirmed that LAQ824 and the combination of LAQ824 and CRA stimulated significant increases in apoptosis in HMV-I but not in A2058 xenografts (Fig. 6A). Staining for the proliferation marker Ki-67 in the same sections showed that combination treatment produced a decrease in proliferation signal in HMV-I but not in A2058 tumors.

**Exposure to LAQ824 and CRA Induces Reactive Oxygen Species Production in HMV-I but not in A2058 Cells**

HDAC inhibitors have been reported to induce reactive oxygen species (ROS) production in transformed cells (27). HMV-I cells cultured with 1.0 μmol/L LAQ824 and 10 μmol/L CRA for 24 h revealed a greater accumulation of ROS than cells cultured with single agents (Fig. 7A). Treatment with NAC markedly diminished ROS production (Fig. 7A). Consistent with these findings, NAC significantly blocked CRA/LAQ–mediated apoptosis in HMV-I cells (Fig. 7B). A2058 cells cultured with 1.0 μmol/L LAQ824 and 10 μmol/L CRA for 24 h had no detectable increased accumulation of ROS compared with cells cultured in absence of any agents (Fig. 7A).

**LAQ824 Induces SM22 Expression in HMV-I but not A2058 Cell Line**

Based on previous evidence of the role of actin dynamics in regulating ROS generation (28), we tested the hypothesis whether the different proapoptotic effect of combination of LAQ824 and CRA in the two melanoma cell lines was attributable to modulation of specific genes linked to cytoskeleton organization. The SM22/transgelin gene has homology with the actin-bundling protein Sc1p linked to the aging process in yeasts (29). Thus, we assessed SM22 gene expression modulation in the human melanoma cell lines by RT-PCR analysis. A2058 and HMV-I cell lines were treated with 1.0 μmol/L LAQ824 in the presence or absence of 10 μmol/L CRA for 24 h. RT-PCR analysis revealed induction of SM22 by LAQ824 and/or CRA in HMV-I (Fig. 8A and B). No significant modulation was observed in A2058 cells treated with LAQ824 and CRA.
Figure 4. Effect of LAQ824 and CRA on cell cycle in melanoma cell lines. A2058 and HMV-I cells treated with 1.0 μmol/L LAQ824 and/or 10 μmol/L CRA for 24 h. Cell cycle analysis (A) and apoptosis assessment (C) by flow cytometry were done. Cell cycle analysis (B) and apoptosis assessment (D) by flow cytometry were repeated following 72 h of treatment with increasing LAQ824 doses. Points, mean percentages; bars, SE.
In this study, we reported that the loss of RARβ2 gene expression in two human melanoma cell lines was associated with histone hypoacetylation and methylation at the promoter level and retinoid resistance. Treatment with the hydroxamic acid derivative HDAC inhibitor LAQ824 increased histone 3 acetylation at the RARβ2 promoter level and induced reexpression of RARβ2 in the presence of CRA. Restoration of RARβ2 expression in these melanoma cell lines was associated with a greater inhibitory effect of the combination of LAQ824 with CRA on tumor growth both in vitro and in vivo compared with single agents.

**Discussion**

In this study, we reported that the loss of RARβ2 gene expression in two human melanoma cell lines was associated with histone hypoacetylation and methylation at the promoter level and retinoid resistance. Treatment with the hydroxamic acid derivative HDAC inhibitor LAQ824 increased histone 3 acetylation at the RARβ2 promoter level and induced reexpression of RARβ2 in the presence of CRA. Restoration of RARβ2 expression in these melanoma cell lines was associated with a greater inhibitory effect of the combination of LAQ824 with CRA on tumor growth both in vitro and in vivo compared with single agents.
Retinoids have been found to be ineffective against melanoma in clinical trials, and several human melanoma cell lines have shown resistance (30, 31). As reported in other tumor types, we hypothesized that the epigenetic silencing of RARβ2 gene expression may be in part responsible for retinoid resistance in melanoma. Recent studies have documented the presence of a hypermethylated RARβ2 promoter in tumor and blood samples from melanoma patients (32, 33). In a recent report, the combination of the HDAC inhibitor sodium butyrate and RA synergistically activated transcription of a RA-dependent reporter gene in a RA-sensitive murine melanoma cell line but not in a human RA-resistant cell line (34). The authors concluded that HDAC inhibitors may enhance the activity of RA in RA-responsive melanoma cells. Our results suggest for the first time that a specific HDAC inhibitor may restore sensitivity in human RA-resistant melanoma cell lines both in vitro and in vivo. The restored sensitivity to

**Figure 7.** Effect of combination of LAQ824 and CRA on ROS generation. A, A2058 and HMV-I cells were incubated with 1.0 μmol/L LAQ824 and/or 10 μmol/L CRA for 24 h ± the free radical scavenger NAC (24 mmol/L). Following the incubation, cells were labeled with an oxidative-sensitive dye (dichlorodihydrofluorescein diacetate) and detected on the Fluorescence channel of a Beckman Coulter Multimode Detector. As controls, cells were treated with 10 μmol/L H2O2 for 50 min and analyzed in parallel. *, P < 0.05 versus control; **, P < 0.05 versus single agents. B, the effect of increasing concentrations of LAQ824 in the presence of CRA on sub-G0 fraction in the presence of the scavenger NAC was assessed. HMV-I cells were treated for 24 h with 0.01 to 1.0 μmol/L LAQ and CRA (10 μmol/L) in the absence or presence of 24 mmol/L NAC. *, P < 0.05 versus NAC.

**Figure 8.** Effect of LAQ824 on SM22 gene expression in melanoma cell lines. SM22 and GAPDH (internal control) gene expression in A2058 and HMV-I melanoma cells treated with LAQ824 (1 μmol/L), CRA (10 μmol/L), or combination was analyzed by RT-PCR (A) and quantitative real-time PCR (B) as described in Materials and Methods.
independent induction of induced G2 checkpoint remain unclear (39). The molecular events responsible for HDAC inhibitor–

HDAC inhibitors have been reported to have antitumor activity in melanoma preclinical models (35–38). Most of the cultured melanoma cells undergo apoptosis following treatment with the HDAC inhibitors, such as trichostatin A, FK-228, and valproic acid via a mitochondrial and caspase- dependent pathway. These agents have been shown to induce growth arrest in several tumor cell types by affecting different phases of the cell cycle (39). Most of the HDAC inhibitors cause growth arrest in G1. Treatment of untransformed human fibroblasts with HDAC inhibitors have been reported to induce G2 checkpoint, which caused cell cycle arrest with little or no cytotoxicity (40). The growth arrest has been reported to be mediated by p53-independent induction of p21WAF1/CIP1, loss of activity of cycle-dependent kinases, and transcriptional inactivation of CTP synthesis in S phase (41–43). G2 arrest has been detected in some tumor cell lines and, in general, requires higher dose of HDAC inhibitors than G1 arrest (41, 43). Cells with an intact G2 checkpoint are growth arrested by HDAC inhibitors, whereas cells with a defective G2 checkpoint undergo apoptosis within hours from the mitotic exit (44). Recent studies have shown that Gadd45 expression induced by the HDAC inhibitor trichostatin A caused cell cycle arrest at the G2-M transition phase (45). The molecular events responsible for HDAC inhibitor–induced G2 checkpoint remain unclear (39).

Tumor cell death has been reported to be induced by HDAC inhibitors via generation of ROS (46). ROS production leads to activation of caspase cascade and degradation of critical proteins, such as p21CIP1/WAF1, p27Kip1, Bcl-2, and pRb. LAQ824 at low concentrations has been shown to trigger cell cycle arrest in G1 phase, relatively delayed generation of ROS, and cellular matura- tion in leukemia cells, whereas at higher concentrations induced apoptosis associated with early ROS generation, G2-M arrest, and generation of ceramide (47). In an acute T-cell leukemic cell line, suberoylanilide hydroxamic acid has also been shown to induce cell death pathway acting via cleavage of Bid and production of ROS (48). HDAC inhibitors have been reported to activate both the death-receptor and the intrinsic apoptosis pathway (46). Specific either genetic or epigenetic defects affecting regulation of the cell cycle and apoptosis may be involved. In our study, equivalent doses of LAQ824 and CRA induced A2058 cells to undergo primarily G2-M arrest, whereas HMV-I cells underwent apoptosis via generation of ROS. We observed a minimal induction of apoptosis in A2058 cell line with combination of LAQ824 and CRA (up to 19%). No differences in caspase-3 activity on treatments were observed between A2058 and HMV-I cell lines (data not shown). The combination treatment induced also p21 gene and protein expression in both cell lines. The mechanism responsible for the difference in sensitivity to combination-induced lethality between the two cell lines remains to be

elucidated. Preclinical results suggest that generation of ROS is necessary but not sufficient for HDAC inhibitor–

induced lethality in transformed cells (46, 47). The increased induction of ROS induced by LAQ824 and CRA in HMV-I cells compared with A2058 translated into higher degree of apoptosis both in vitro and in vivo and in some extent greater antitumor activity in vivo. Identification of the molecular mechanisms responsible for this susceptibility to ROS induction and consequent lethality will be critical for the optimal clinical development of HDAC inhibitors.

Induction of the cell cycle inhibitors p16 and p21 and high levels of ROS have been linked to programmed cell death pathways and replicative senescence (49, 50). Replicative senescence plays an important role in maintaining tissue integrity and is impaired during tumorigen-esis (51). Recent reports have suggested that changes in the dynamics of the actin cytoskeleton are associated with senescence, ROS release from mitochondria, and subse- quent cell death (52). Increased actin turnover, which can be induced by gene mutation or by deleting the gene for the actin-bundling protein Scp1, leads to decreased production of ROS and to increased cell viability (53). Homology between Scp1 and mammalian SM22/transgelin, which itself has been isolated in senescence screens and once deleted can increase life span, suggests a conserved mechanism linking aging to actin stability (54, 55). HDAC inhibitors have been shown recently to induce premature senescence in normal human fibroblast (55). Reduced HDAC1 expression level in senescent cells has been reported to mediate the transition to senescent phenotype. Interestingly, overexpression of HDACs has been reported to decrease, whereas trichostatin A treatment stimulates SM22 promoter activity in smooth muscle cells (56). Chromatin immunoprecipitation assay showed that trichostatin A treatment induces chromatin hyperacetylation in the SM22 gene. Our results showed that SM22 gene expression was induced by LAQ824 + CRA treatment in HMV-I cell line, which underwent apoptosis via ROS production but was not modulated in the A2058 cell line, which did not present increased ROS generation. The free radical scavenger NAC blocked LAQ824 + CRA–mediated ROS generation and apoptosis, suggesting a primary role for oxidative injury in LAQ824 + CRA lethality. Our data also suggest that SM22 induction by LAQ824 + CRA may be associated with the difference in biological effects between HMV-I and A2058 cell lines. Additional experiments are needed to determine the possible role of SM22 gene and protein expression and actin dynamics in HDAC inhibitor–induced lethality.

Several HDAC inhibitors are currently in clinical trials both in solid and hematologic malignancies (57). Some studies have already provided important information on the pharmacodynamics of these novel agents (58, 59). Preliminary reports have also shown promising clinical activity in different tumor types, including melanoma (60). Based on preclinical studies, several rational strategies are being developed with combinations of HDAC inhibitors and either molecular targeted or standard therapies.
In summary, this study reports for the first time that retinoid sensitivity can be restored in retinoid-resistant melanoma by a targeted therapy with RARβ2 agonists and chromatin remodeling drugs. This therapeutic approach induced promoter epigenetic changes at expression RARβ2 promoter. Inducible RARβ2 expression may represent a rational predictor for tumor response in patients undergoing ‘differentiation’ therapy with the combination of a HDAC inhibitor and a retinoid. The clinical success of HDAC inhibitors will require rational combination strategies with other compounds that may enhance the cell cycle blocking and proapoptotic activity of this novel class of agents. A Cancer Therapy Evaluation Program-National Cancer Institute-sponsored phase I clinical study of the HDAC inhibitor MS-275 in combination with CRA in metastatic progressive cancer is currently accruing patients at our institution.

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