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Combinatorial anti-leukemic disruption of oxidative homeostasis and mitochondrial stability by the redox reactive thalidomide CPS49 and flavopiridol.

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Running Title: Selective leukemic cell killing by flavopiridol and CPS49.

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ABBREVIATIONS: ROS, reactive oxygen species; NF-κB, nuclear factor-κB; MMP, mitochondrial membrane permeability; Cdk, cyclin-dependent kinase inhibitor; MTT, 3-[4,5-dimethylthiazol-2-yl]-2 5-diphenyl tetrazolium bromide; PHA, phytohaemagglutinin; DCFDA, dichlorodihydrofluorescein diacetate; GSH, glutathione; PMA, phorbol 12-myristate 13-acetate; $DiIC_1$, 1, 1', 3, 3,3′, 3'-hexamethylindodicarbocyanine iodide; PCR, polymerase chain reaction; RT, reverse transcription; IKK, I-kappa B (I-κB) kinase; NAC, N-acetyl-cysteine; FACS, fluorescent activated cell sorting,

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Abstract

CPS49 is a member of a recently identified class of redox-reactive thalidomide analogs that show selective killing of leukemic cells by increasing intra-cellular reactive oxygen species (ROS) and targeting multiple transcriptional pathways. Flavopiridol is a semi-synthetic flavonoid that inhibits cyclin-dependent kinases and also shows selective lethality against leukemic cells. The purpose of this study is to explore the efficacy and mechanism of action of the combinatorial use of the redox-reactive thalidomide CPS49 and the cyclin dependent kinase inhibitor flavopiridol as a selective anti-leukemic therapeutic strategy. In combination, CPS49 and flavopiridol were found to induce selective cytotoxicity associated with mitochondrial dysfunction and elevations of ROS in leukemic cells ranging from additive to synergistic activity at low micro-molar concentrations. Highest synergy was observed at the level of ROS generation with a strong correlation between cell-specific cytoxicity and reciprocal coupling of drug-induced ROS elevation with glutathione depletion. Examination of the transcriptional targeting of CPS49 and flavopiridol combinations reveals that the drugs act in concert to initiate a cell specific transcriptional program that manipulates NF-κB, E2F-1 and p73 activity to promote enhanced mitochondrial instability by simultaneously elevating the expression of the pro-apoptotic factors *BAX*, *BAD*, *p73* and *PUMA*, while depressing expression of the anti-apoptotic genes *MCL1*, *XIAP*, *BCL-xL*, *SURVIVIN* and *MDM2.* The co-administration of CPS49 and flavopiridol acts through coordinate targeting of transcriptional pathways that enforce selective mitochondrial dysfunction and ROS elevation and is therefore a promising new therapeutic combination that warrants further pre-clinical exploration.

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Introduction

Cancer is a complex multi-genic disease that results from the accumulation of a broad mixture of perturbations in cellular function that contributes to the maintenance and propagation of the malignant phenotype. Accordingly, most strategies for effective anti-cancer therapy employ combinatorial drug regimens designed to target one or more components within biological pathways that are thought to be critical for sustained tumor growth and survival. The long-term goal of these strategies is to provide therapeutic platforms that improve selective tumor killing while reducing undesired and off-target effects.

A well recognized feature of many transformed cells that distinguishes them from normal cells is their tendency to function at higher levels of oxidative stress (Litz et al., 2003;Pelicano et al., 2004;Trachootham et al., 2006). Though the precise mechanism that accounts for the elevated levels of reactive oxygen species (ROS) in tumor cells remains to be clarified, recent observation attributes this cellular state, in part, to mutations in components of the mitochondrial oxidative-phosphorylation chain combined with uncontrolled oncogenic signal transduction upstream of the mitochondria that cause them to be more prone to ROS leakage (Pelicano et al., 2004;Hlavata et al., 2003). This observation has led to the development of therapeutic strategies to exploit this selective vulnerability of cancer cells by manipulating intracellular levels of ROS. The mitochondria therefore has become viewed as a high impact biological target in strategies to exploit the redox vulnerabilities of malignant cells (Gottlieb and Thompson, 2003). Increased mitochondrial membrane permeability (MMP) plays a central role in

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determining cell fate through its ability to induce cell death by apoptosis or necrosis (Zamzami et al., 2005;Fiers et al., 1999;Newcomb, 2004). Key factors that regulate the levels of MMP include cellular redox status, calcium influx, and the targeting and function of Bcl-2 family members (Zamzami et al., 2005;Gottlieb et al., 2000). Pharmacological manipulation of these factors has therefore become a central aim in numerous therapeutic strategies.

Flavopiridol, is a synthetically derived flavone, that is known to target mitochondria and induce selective killing of leukemic cells through pathways linked to mitochondrial mediated apoptosis and necrosis (Dai and Grant, 2003;Shapiro, 2006;Blagosklonny, 2004;Newcomb, 2004;Grant and Dent, 2004;Sedlacek, 2001). Several recent studies have demonstrated its synergy with a variety of chemotherapeutic compounds (Grant and Roberts, 2003). Although flavopiridol has been defined as a cyclin dependent kinase (Cdk) inhibitor, its effects have been shown to be widely pleiotropic against a variety of malignant cells (Newcomb, 2004;Blagosklonny, 2004;Dai and Grant, 2003;Grant and Dent, 2004;Shapiro, 2006). One major mechanism underlying its therapeutic effect involves its selective repression of transcriptional elongation (Chao and Price, 2001). Recent studies have shown that flavopiridol also has selective effects on gene expression by repressing nuclear factor-κB (NF-κB) transcriptional activation and preferentially influencing the levels of genes with short mRNA half-lives (Wittmann et al., 2003;Takada and Aggarwal, 2004). Since many of the BCL-2 family of proteins that promote mitochondrial stability have short half-lives and rely on NF-κB for induction, flavopiridol treatment can induce significant mitochondrial dysfunction

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resulting in increased MMP and both apoptotic and necrotic cell death (Wittmann et al., 2003;Lam et al., 2001).

Recently we described the identification and characterization of a novel functional class of thalidomide analogs referred to as redox-reactive thalidomides (Ge et al., 2006). These compounds inhibit NF-κB activity, increase intra-cellular calcium, and produce a rapid elevation of intracellular ROS that results in dissipation of the mitochondrial membrane potential and subsequent caspase-independent necrotic cell death (Ge et al., 2006). The shared targeting of both NF-κB activity and mitochondrial function by flavopiridol and the redox reactive thaliodmides suggested that the combinatorial use of these agents may produce more effective tumor cell killing. CPS49 is a redox reactive thalidomide analog that has recently been shown to have effective cytotoxicity against lymphocytic leukemia cells, multiple myeloma, lung cancer, prostate cancer and endothelial cells (Ge et al., 2006;Ng et al., 2003;Ng et al., 2004;Warfel et al., 2006;Kumar et al., 2005). Like flavopiridol, it has also been shown to have anti-angiogenic potential (Ng et al., 2003;Newcomb, 2004).

In this study we explore the potential therapeutic efficacy of the combined use of flavopiridol and CPS49 as an anti-leukemic strategy. We find that the compounds show varying degree of synergistic, additive and occasional antagonistic influences on leukemic cell killing based on their combined ability to repress NF-κB, and destabilize mitochondrial function. Notably we find that pretreatment of leukemic cells with low dose, sub-cytotoxic levels of flavopiridol synergize with CPS49 to cause selective

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leukemic cell death. A central mechanism underlying this combined synergy is the overlapping transcriptional targeting of tumor survival factors that regulate mitochondrial stability. Mitochondrial destabilizers including Bax, Bak and Bad show enhanced up-regulation by flavopiridol and CPS49 combinations while mitochondrial stabilizers including BCL2, BCL-xL, and MCL1 are down regulated. These findings suggest that the combined use of flavopiridol and redox-reactive thalidomides such as CPS49 should be evaluated as a feasible and practical anti-neoplastic regimen against leukemia and other malignancies.

Materials and Methods

Cell lines and cell culture

Jurkat (acute lymphoblastic leukemia), HeLa (human epithelial-like cervical carcinoma), K562 (human chronic myelogenous leukemia), OPM2 (myeloma), HH (cutaneous T-cell lymphoma), LNCaP (prostate carcinoma) and RPMI-8226 (myeloma) cell lines were maintained in their respective growth media, as suggested by the American Type Culture Collection **(**ATCC, Manassas, VA). Peripheral-blood mononuclear cells (PBMCs) were isolated by apheresis from healthy human blood donors. Cells were harvested following treatment with different concentrations of mitogens and/or drugs for various time points depending upon experimental design. The antioxidant N-acetyl-cysteine (15 mM) was used to reverse the cytotoxic action of CPS49 and/or flavopiridol in Jurkat cells.

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Cell proliferation and survival assay

The viability and proliferation of cells were determined by MTT assay (Roche Applied Sciences, Indianapolis, IN), according to the manufacturer's instructions. The assay measures the dehydrogenase enzyme activity in metabolically active tumor cells, as reflected by the conversion of MTT to formazan, which is soluble in cell culture medium and was detected by absorbance at 570 nm. The production of formazan is proportional to the number of living cells, with the intensity of the produced color serving as an indicator of the cell viability. In brief, the cells were plated at 1×10^5 cells/well in 96-well plates and cultured for 16 h. The MTT mixed with medium without serum was added to the cell cultures after removing the old medium. The plates were incubated at 37°C for 2 h, and the absorbance (A) at 570 nm was determined using a 96-well microplate reader (Molecular Devices, Sunnyvale, CA). The percentage of cell survival was calculated using the background-corrected absorbance: % cell viability = 100 × (1 − A of experimental well)/A of untreated control well. All assays were performed in triplicate in three independent experiments, and representative data are presented in Figures 1 and 5. In flavopiridol pretreatment studies, flavopiridol was added to cells at a final concentration of 0.2 μM for 8 hours.

Annexin assay

Jurkat cells were exposed to increasing doses (0-10 μM) of flavopiridol and CPS49 either alone or in combination for 3 hours as experimental designs. Jurkat cells were washed twice with cold PBS and then resuspended in binding buffer at a concentration

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of 1 x 10^6 cells/ml. 5 µg FITC-annexin V (Invitrogen Corporation, Carlsbad, CA) were administrated to the cells and incubated in the dark for 20 minutes. FITC-annexin V was excited by 488nm primary laser and detected by FL-1 detector using FACScan (BD Biosciences, San Jose, CA). 10, 000 events were collected and data was analyzed by flowjo (Tree Star Inc Ashland, OR).

ROS determinations

Reactive oxygen species (ROS) generation was monitored by the increase in DCFDA fluorescence after drug stimulation. Cells were washed, resuspended in 1% bovine serum albumin in Hanks buffered saline solution (BSA-HBSS) at 1 x 10^6 cells/mL, and maintained at 37°C for analysis. The oxidation-sensitive dye DCFDA (Invitrogen, Carlsbad, CA) was incubated with cells for 15 min at 2 µM final concentration. The incubation was ended by 3-fold dilution of the sample with ice-cold 1% BSA-HBSS. The cells were washed with ice-cold 1% BSA-HBSS before flow cytometric analysis. The stimulated increase in dye oxidation was calculated as the percentage increase in mean channel fluorescence (MCF) of drug-stimulated cells over that of unstimulated cells for each time point using the following equation: [(MCF (stimulated) – MCF (unstimulated)/MCF (unstimulated)] x 100. Results shown were an average of three independent experiments.

Glutathione (GSH) determinations

10^6 cells were lysed and incubated with 100 µM monochlorobimane (mBCl) at 37^{o}C for 30 min. The formation of the fluorescent adduct was monitored in a final volume of 100

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µl with a 1420 Victor2 Multilable Counter (Perkin-Elmer, Shelton, CT) with excitation at 385 nm and emission at 478 nm

Measurement of mitochondrial membrane potential (Ψ_m)

Changes in the mitochondrial membrane potential were measured by flow cytometry analysis of cells stained with $DiIC_1$ (Molecular Probes Invitrogen Detection Technology**,** Carlsbad, CA), as recommended by the manufacturer. Flow cytometric analyses were performed with a FASCalibur flow cytometer using Flowjo (Ashland, OR). Data were collected for 10,000 events. All measurements were performed in duplicate and were representative of at least two independent experiments.

Antibodies and immunoblot analysis

The antibodies against Iκ-Bα, phospho-IκBα (Ser32), RelA (p65), phospho Rb (ser807/811) and phospho-RelA (Ser536) were obtained from Cell Signaling Technology (Beverly, MA). Antibodies against phospho-pol II CTD (Ser2) were from Covance (Princeton, N.J.) and the antibodies against β–actin, total RB, and E2F-1 were purchased from Santa Cruz Biotechnology, Inc. (Santa Cruz, CA). Jurkat cells were preincubated for 15 min in the presence or absence of 10 µM CPS49 and/or flavopiridol prior to stimulation with PHA (1 µg/ml) and PMA (50 ng/ml) for 15 min. Whole cell lysates were prepared in a buffer containing 50 mM HEPES, 20 mM sodium pyrophosphate, 25 mM β-glycerophosphate, 50 mM sodium fluoride, 5 mM sodium molybdate, 5 mM EDTA, 150 mM orthophenanthroline, 1% NP-40, 0.5% deoxycholate,

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1% Triton X-100, mammalian protease inhibitor (MPI; Sigma Chemicals, St. Louis, MO), and 0.2 mM Na_2VO_4. After protein quantitation using Bio-RAD protein assay (Bio-Rad Laboratories, Hercules, CA), equal amounts (10-30 µg) of proteins were separated by SDS-PAGE and blotted onto nitrocellulose membranes. The membrane was blocked with 5% non-fat dry milk in PBST (PBS, pH 7.5, containing 0.1% Tween 20) and incubated with a 1:1000 dilution of a primary antibody, as mentioned above, overnight at 4°C. The membrane was then washed with PBST and incubated with a peroxidase-conjugated secondary antibody (1:1000) (GE Healthcare UK Ltd., Little Chalfont Buckinghamshire, UK) for 1 h at room temperature. Specific antibody binding was detected using a chemiluminescence detection system (Amersham Biosciences, Little Chalfont Buckinghamshire, UK), according to the manufacturer's recommendations. After development, the membrane was stripped and reprobed with antibody against β–actin (1:1000) (Santa Cruz Biotechnology, Inc.) to confirm equal sample loading.

Analysis of mRNA expression of genes by real-time reverse transcription-polymerase chain reaction (RT-PCR)

Total cellular RNA was isolated from Jurkat cells using Qiagen Rneasy Mini Kit (QIAGEN, Valencia, CA) and quantitated with a NanoDrop® ND-1000 Spectrophotometer (NanoDrop Technologies, Wilmington, DE**)**. RNA (1 µg) was reversely transcribed using Qiagen Omniscript RT Kit as recommended by the manufacturer. Primer sequences were synthesized by Operon Biotechnologies, Inc. (Huntsville, AL). The primer sequences of the genes used in this study are as follows: β–Actin (NM_001101.2) 5'- GCACAGAGCCTCGCCTT-3' and 5'-

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GTTGTCGACGACGAGCG-3'; *Bad* (NM_032989.1) 5'- GGTAGGAGCTGTGGCGACT-3' and 5'- CAGGCCTCCTGTGGGAC-3'; *Bax* (NM_004324.3) 5'-AGCTTCTTGGTGGACGCAT-3' and 5'- CAGAGGCGGGGTTTCATC-3'; *Bcl-2* (NM_000633.2) 5'- GAGAAATCAAACAGAGGCCG-3' and 5'-CTGAGTACCTGAACCGGCA-3'; *Bcl-X_L* (NM_001191.2) 5'-CTGCTGCATTGTTCCCATAG-3' and 5'- TTCAGTGACCTGACATCCCA-3'; *Survivin* (NM_001012271.1) 5'- CTTTCTCCGCAGTTTCCTCA-3' and 5'-TTGGTGAATTTTTGAAACTGGA-3'; *MDM2* (NM_002392.2) 5'-CCTGATCCAACCAATCACCT-3' and 5'- TGTTGTGAAAGAAGCAGTAGCA-3'; *PUMA* (NM_014417.2) 5'- GTAAGGGCAGGAGTCCCAT-3' and 5'-GACGACCTCAACGCACAGTA-3'; *XIAP* (NM_001167.2) 5'-TGATGTCTGCAGGTACACAAGTT-3' and 5'- GGACCCTCCCCTTGGAC-3'; *MCL-1* (NM_182763.1) 5'- CATTCCTGATGCCACCTTCT-3' and 5'-TCGTAAGGACAAAACGGGAC-3'; and *p73* (NM_005427.1) 5'-CCCCATCAGGGGAGGTG-3' and 5'-AGGGGACGCAGCGAAAC-3'.

Quantitative real-time PCR (qRT-PCR) was performed with an ABI Prism® 7000 Sequence Detection System (Applied BioSystems, Foster City, CA). The amplification of the genes was done in the following amplification conditions: each 25 µl reaction mixture contained 0.3 µM primers (both forward and reverse primers), 2 µl template cDNA from reverse transcription, and 12.5 µl of 2× SYBR® GreenER™ qPCR SuperMix ABI PRISM® (Invitrogen Corp., Carlsbad, CA). Each reaction mixture was incubated at 50°C for 2 min and 95°C for 10 min hold, and then 50 cycles were performed for amplification at 95°C for 15 s and 60°C for 1 min. A melting curve analysis which read

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every 0.3°C from 65^{o} to 95°C was followed to assess the homogeneity of a PCR amplified product. The results of qRT-PCR were analyzed using a software provided by the manufacturer. The relative quantity of a specific mRNA was calculated with the comparative delta Ct method on the basis of β-actin *versus* the gene of interest.

Statistical analysis of data

The significance of difference between experimental conditions was determined using the Student's *t*-test for unpaired observations. A value of $P < 0.05$ was considered statistically significant. To assess the interactions between agents, Median Dose Analysis was employed (CalcuSyn, Biosoft, Ferguson, MO) to calculate the combination index (CI) using experimental readout as the endpoint. Median Dose Analysis for CI was designed based on the multiple drug-effect equation derived from enzyme kinetic models as follows: $CI = (D)_1/(Dx)_1 + (D)_2/(Dx)_2 + (D)_1(D)_2/(Dx)_1(Dx)_2$, where $(D)_1$ and $(D)_2$ (in the numerators) indicate the doses of drug 1 and drug 2 in combination to obtain x% effects in the actual experiment, and $(Dx)_1$ and $(Dx)_2$ (in the denominators) indicate the doses of drug 1 and drug 2 alone to achieve x% effects (Chou and Talalay, 1984). CalcuSyn software was used to display the results of this analysis in the form of isobolograms which are two-dimensional graphs that illustrates the interaction between two agents in terms of their antagonistic, additive or synergistic effect on single biological measurement (e.g. cytotoxicity) (Loewe, 1953).

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Results

The combinatorial addition of CPS49 and flavopiridol shows selective anti-leukemic synergy that improves with low dose flavopiridol pretreatment. Jurkat, K562, HeLa, RPMI-8226, and donor peripheral blood mononuclear cells (PBMCs) were each treated for 16 h with increasing concentrations (0-10 μM) CPS49 and flavopiridol as single drug treatments or in 1:1 combination (Fig.1A). As shown by the viability curves in Fig. 1A, both flavopiridol and CPS49 show selective cytotoxicity against Jurkat cells. However their cytotoxicity profiles are not identical since flavopiridol shows greater cytotoxicity against the multiple myeloma cell line 8226 than CPS49, as has been previously shown (Kumar et al., 2005), and requires greater than 20 fold higher levels to achieve an effect comparable to flavopiridol.

Though effective as single agents against Jurkat, the co-administration of both CPS49 and flavopiridol show only mild additive to synergistic effects with slight antagonism at high concentrations which can be objectively assessed by plotting the combination index (CI) against the fraction affected (see material and methods). This analysis yields an isobologram where CI< 1.0 indicates synergy, CI>1.0 indicates antagonism and CI=1.0 indicates additive influence of the drug combination (Fig. 1B and Table 1). These findings suggest that there may be a significant overlap between the pathways targeted by CP49 and flavopiridol. However the appearance of greater synergy at lower concentrations suggests that sequential pretreatment or “induction” of the cells with lower sub-cytotoxic concentrations of one of the drugs might improve their cytotoxicity against leukemic cells. Similar sequential strategies with low dose flavopiridol have

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been shown to be effective in combination with the BCL-2 inhibitor HA14-1 (Pei et al., 2004). We therefore assessed the possible use of low-dose flavopiridol as an inducing agent prior to sequential combined addition of flavopiridol and CPS49 (Fig. 1C). As shown in Fig. 1C and Table 1, 8 hour pretreatment with 0.2 μM flavopiridol causes much more effective leukemic cell killing at higher drug concentrations and produces a more synergistic trend in the isobolograms (Fig. 1B and C, right). Although this strategy produces more effective cell killing after prolonged incubation, it should be noted that more acute influences of cooperative targeting by combined treatment with CPS49 and flavopiridol treatment are readily detectable by annexin staining as early as 3 h after incubation in the absence of pretreatment (Fig. 1D).

CPS49 and Flavopiridol combinations produce selective and synergistic depletion of GSH with concomitant elevation of intracellular ROS. Both CPS49 and flavopiridol have shown to alter the redox status of leukemic cells (Ge et al., 2006;Decker et al., 2001). To assess the selective combined influence of CPS49 and flavopiridol on the redox properties of primary and transformed cells the intracellular levels of ROS and glutathione (GSH) were assessed in cells treated with different combinations of flavopiridol and CPS49 after 1 h and 16 h incubation respectively (Fig. 2). When added as single agents both flavopiridol and CPS49 produced significant elevation of ROS coupled with depletion of GSH in Jurkat cells (Fig. 2A). These effects were strikingly different from other cell types including PBMCs, K562, HeLa, and 8226 cells which show very little depletion of GSH and much smaller elevation in intracellular

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ROS (Fig. 2B). Quantitative analysis of the combined effects of flavopiridol and CPS49 on Jurkat show significant synergy for GSH depletion and ROS elevation (Table 1).

Synergistic targeting of NF-κB activation and the mitochondrial membrane potential by combinatorial administration of flavopiridol and CPS49. The mitochondria play a central role in regulating cellular redox status (Gottlieb and Thompson, 2003;Galluzzi et al., 2006). Both flavopiridol and redox-reactive thalidomides have been shown to reduce the mitochondrial membrane potential. To test their combined activity the mitochondrial membrane potential in Jurkat cells was measured 1 and 3 h after single or combined treatment with increasing concentrations of flavopiridol and CPS49. When added as single agents both compounds produced reduction in mitochondrial membrane potential however their action together showed antagonism at higher concentrations with moderate synergy at lower drug concentrations and with shorter incubation intervals (Fige 3A, and Table 1).

NF-κB activation is a central component of a major transcriptional program that controls mitochondrial stability in mammalian cells (Lin and Karin, 2003;Luo et al., 2005) This is particularly the case for lymphoid cells. Numerous transcriptional targets of NF-κB are genes that control cellular survival either at the level of maintaining mitochondrial stability (e.g. the BCL2 family of proteins) or by repressing cell-death inducing caspase activation (e.g. the inhibitor of apoptosis, (IAP) family of proteins). To test the combined influence of flavopiridol and CPS49 on and NF-κB activation Jurkat cells were stimulated 15 min with the mitogens phytohaemagglutinin (PHA) and phorbol myristate

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(PMA) after brief pre-incubation with CPS49, flavopiridol or the two combined. Whole cell lysates were prepared and analyzed by immunoblot analysis for NF-κB activation (Fig 3B and C). As shown in Fig. 3B, PHA/PMA induces a robust phosphorylation of the inhibitor of kappa B alpha (Iκ-B-α). This phosphorylation is significantly reduced after treatment with either CPS49 or flavopiridol and their combination nearly completely obliterates I-κB-α phosphorylation (Fig. 3B). Similarly, PHA/PMA produces an equally robust increase in phosphorylation of the RelA (p65) NF-κB subunit, that is synergistically squelched by flavopiridol and CPS49 (Fig. 3C).

Prior studies have shown that flavopiridol induces stabilization of E2F-1 (Jiang et al., 2003). The up regulated transcriptional targets of E2F-1 include *p73* which leads to increased expression of the mitochondrial destabilizers *BAX*, *BAD*, and *PUMA* (Irwin et al., 2000;Hitchens and Robbins, 2003). The down-regulated targets of E2F-1 included *MCL1*, a *BCL2 f*amily member that stabilizes mitochondria in lymphoid cells (Rosato et al., 2007;Craig, 2002). Interestingly although treatment of Jurkat cells with flavopiridol stabilizes E2F-1 protein levels, CPS49 does not (Fig 3D). In fact, the combination of flavopiridol and CPS49 appears to slightly antagonize E2F1 levels in both resting and stimulated Jurkat cells.

A common mode of flavopiridol action is through induction of caspase activation (reviewed in (Newcomb, 2004)). This activity is notably distinct from redox-reactive thalidomides which act through caspase independent pathways (Ge et al., 2006). To see if there is any influence of CPS49 on flavopiridol induced caspase activation Jurkat

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cells were treated with each agent alone or in combination and then analyzed for the activation of caspase 3 cleavage by western blot. As shown in Fig. 3E, flavopiridol clearly activates caspase 3 cleavage while CPS49 does not. Combined addition of CPS49 with flavopiridol also fails to increase the caspase cleavage beyond that elicited by flavopiridol treatment alone.

Combinatorial treatment with CPS49 and Flavopiridol coordinates a transcriptional program that triggers destabilization of mitochondrial function.

The coordinated targeting of NF-κB and E2F-1 pathways by the co-administration of flavopiridol and CPS49 implies that this regimen should have demonstrable effects on genes that control cell death and survival. To investigate this question we examined the influence of combinations of flavopiridol and CPS49 on pro-apoptotic and anti-apoptotic gene sets (Fig. 4). The set of pro-apoptotic genes includes *BAX*, *BAD*, *p73* and *PUMA* (Fig. 4A). Flavopiridol shows up-regulation of all four genes while CPS49 showed up-regulation of all but *PUMA* in both resting and PHA/PMA stimulated cells (Fig. 4A). Interestingly, the co-addition of CPS49 and flavopiridol showed no additional increase in expression of the pro-apoptotic genes and, in fact, showed mild antagonism for p73 expression.

Both flavopiridol and CPS49 show significant repression of the six anti-apoptotic genes we tested including *MCL1*, *XIAP*, *BCL-xL*, *BCL2*, *survivin*, and *MDM2* (Fig. 4B). For each of these genes, CPS49 produced more significant repression than flavopiridol in both resting and PHA/PMA stimulated cells. Again, the combination of CPS49 and

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flavopiridol did not synergize to induce repression and, in some instances, the pairing was antagonistic.

Cytotoxicity and transcriptional targeting of p73 and PUMA by CPS49 and flavopiridol is partially inhibited by free radical scavengers. Since both flavopiridol and CPS49 produce elevations in ROS we analyzed the influence of the free radical scavenger, N-acetyl-cysteine (NAC), on the cytotoxicity profile of CPS49, flavopiridol and the two combined. As shown in Fig. 4C, NAC partially rescued cellular viability when added under all three conditions. Cytotoxocity of flavopiridol, added as a single agent seemed to be the most sensitive to NAC (Fig. 4C). To see if the ROS generated by these compounds plays any role in the mechanism of transcriptional activation of downstream pro-apoptotic targets, we tested whether or not NAC could repress the ability of CPS49 and/or flavopiridol to elevate p73 and PUMA transcription (Fig. 4D). As shown in Fig. 4D, although NAC was partially effective at reducing the cytotoxicity of both flavopiridol and/or CPS49 combinations in Jurkat, influences on the transcriptional targets appeared to be more potent.

Combinatorial synergy and transcriptional targeting by CPS49 and Flavopiridol following low dose Flavopiridol pretreatment is highly cell type specific. Our data have shown thus far that combination therapy with CPS49 and flavopiridol shows significant synergy that can be enhanced by low dose flavopiridol pretreatment. To test the cell type specificity of this treatment regimen, five additional cell lines including HeLa (cervical carcinoma), LNCaP (prostate carcinoma), HH (cutaneous T-cell lymphoma),

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OPM2 (myeloma), and 8226 (myeloma) were exposed to increasing doses of flavopiridol, CPS49, and CPS49/flavopiridol combined each after 8 hour pretreatment with 0.2 μM flavopiridol (Fig. 5A). As shown in Fig. 5A , CPS49/flavopiridol treatment showed significant cytotoxicity against HH, OPM2 and 8226 cell lines, but showed minimal effect on either HeLa or LNCaP cells. Moreover, quantitative assessment of the synergy between CPS49 and flavopiridol showed significant synergy against both myeloma cell lines OPM2 and 8226 with additive to antagonistic influence on HH cells (Fig. 5B and Table 2). It is interesting to note that in terms of cytotoxicity, pretreatment with flavopiridol dramatically increased the potency of CPS49 against both myeloma cell lines (Fig 5A). This is also reflected in the higher levels of synergy between CPS49 and flavopiridol, following low dose pretreatment when compared to Jurkat even though this combination is still significantly more cytotoxic against Jurkat (compare Fig. 1B to Fig. 5A; and Table 1 to Table 2).

The addition of combinations of CPS49 and flavopiridol added in the absence of pretreatment as in Fig. 4 showed overlapping but distinct transcriptional targeting of the myeloma cell line 8226. CPS49, flavopiridol and the two combined did not produce significant up-regulation of pro-apoptotic genes. Instead most of these genes were repressed by flavopiridol, CPS49 alone had little effect, and the combination had little influence over flavopiridol added alone (Fig. 6A). Similar to Jurkat, flavopiridol produced significant inhibition of pro-survival genes that stabilize mitochondrial integrity (Fig. 6B). However, consistent with prior studies indicating that higher levels of CPS49 were necessary to influence 8226 growth and viability (Ge et al., 2006;Kumar et al., 2005),

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CPS49 was not effective at influencing pro-survival gene expression at the maximum concentrations used in this study (10 μM). Finally, pretreatment of Jurkat cells with low levels (0.2 μM) of flavopiridol show selective repression of CDK9 activity as demonstrated by the preferential decrease in pol II serine 2 phosphorylation as opposed to substrates targeted during cell cycle progression such as serine 807/811 on Rb (Fig. 6C).

Discussion

Despite its successful performance in numerous pre-clinical studies, the advance of flavopiridol to clinical trials has been disappointing. When used as a single agent flavopiridol produced the stabilization of disease expected due to its cytostatic activity as a general Cdk inhibitor. However few studies showed any additional response (Senderowicz et al., 1998;Tan et al., 2002;Blagosklonny, 2004;Shapiro, 2004). The mechanism through which flavopiridol is able to induce apoptosis through inappropriate stabilization E2F-1 activity in S-phase formed the rationale for its combined use with compounds that forced S-phase accumulation such as traditional DNA damaging agent and mitotic poisons. Yet, several clinical trials employing such combination with flavopiridol have yet to yield convincing results. Challenges that have emerged from these studies involve defining the optimum sequence, dose and timing of drug administration and identifying practical biomarkers for therapeutic end points.

This is the first study of the efficacy of the combinatorial use of a cyclin-dependent kinase inhibitor and a thalidomide-derived compound. Our rationale for the combined

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use of the redox-reactive thalidomides with flavopiridol is distinct and independent of its effect on cell cycle. Instead our hypothesis is formulated based on the ability of flavopiridol and CPS49 to target mitochondrial stability at multiple nodes in multiple pathways that lead to cell death. Since the reciprocal targeting of both pro-apoptotic and pro-survival pathways is reinforced by the combined action of CPS49 and flavopiridol we feel that this combination merits further pre-clinical development (Fig 6D).

Our approach of combining sequential low dose flavopiridol pretreatment with higher dose flavopiridol and CPS49 is counter to many approaches that have been advocated thus far for combination therapy using flavopiridol (Blagosklonny, 2004;Shapiro, 2004). Again this is based on the more selective transcriptional targeting of short lived transcripts for pro-survival genes at (0.2 μM) flavopiridol, which has been reported as the achievable plasma concentration of low dose flavopiridol treatment in clinical trials (Senderowicz et al., 1998). We feel that during this "induction phase" the resulting decrease in *BCL2*, *BCL-xL* , and *MCL1* increases the vulnerability of the mitochondria of malignant cells to further insult by the acute administration of higher doses of flavopiridol combined with CPS49. Surprisingly, this approach also showed a dramatic increase in cytotoxicity of CPS49 against myeloma cells. This is apparent when comparing Fig. 1A and Fig. 5B where 8 hour pre-incubation with 0.2 μM flavopiridol increase the cytotoxicity of CPS49 nearly twenty fold and was further effective with subsequent co-administration with micromolar concentrations of flavopiridol in combination with CPS49. Though the level of cell killing in myeloma is much lower than

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Jurkat, this finding indicates that further investigation of the potential of flavopiridol to increase the efficacy of fluoride-substituted thalidomide compounds against myeloma is justified. Future studies will be needed to sort out the precise mechanisms that differentiate the CPS49 sensitivity of myeloma cells and Jurkat cells, though the increased impairment of mitochondrial stability and possibly antioxidant reserve by flavopiridol pretreatment are likely to play a significant role. In this regard it will be critical to determine the most effective pretreatment doses.

Because of the pleiotropic effects of both CPS49 and flavopiridol there are some actions that are antagonistic. Since flavopiridol induces both G1 and G2 arrest, and cells are more sensitive to redox-reactive thalidomides in S-phase it not surprising that the cytotoxicity profile of the combination shows some antagonism. This antagonism is relieved by low dosed flavopiridol pretreatment most likely because of the increased synergy for targeting mitochondrial function. This is also consistent with observations that flavopiridol can induce mitochondrial dysfunction as an early primary event independent of caspase activation (Litz et al., 2003). It is not clear why CPS49 appears to antagonize the ability of flavopiridol to stabilize E2F-1 activity, but the stress response induced by CPS49 mediated elevation of ROS could provide a signal that increases the phosphorylation of E2F-1 independent of Cdks. Alternatively, the drop in intracellular ATP levels associated with mitochondrial mediated necrotic cell death may also contribute to the antagonism against caspase induced cell death since apoptosomes require ATP for function (Hu et al., 1999;Scholz et al., 2005). Finally the lack of synergy of the transcriptional targeting of both pro-apoptotic and anti-apoptotic

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pathways in Jurkat suggests that the associated transcriptional pathways may be saturated by the compounds or there may be other undefined mechanisms where flavopiridol and CPS49 may act at different nodes within the transcription programs. The higher resistance of myeloma cells to CPS49 may also explain the similar lack of synergy in 8226.

As illustrated in Fig 6D, CPS49 and flavopiridol can act in concert to enforce a transcriptional program that leads to cell specific reciprocal up-regulation of pro-apoptotic and down-regulation of anti-apoptotic effectors. The ability of CPS49 to up-regulate *BAX*, *BAD* and *p73* was unexpected and the mechanism underlying this form of transcriptional target will require further investigation, however, as known p53 targets, the induction of *BAX*, *BAD* is most likely to be the result of p73 activation (Jurkat cells are p53 negative). Similarly the down-regulation of *MDM2* by CPS49 occurs through a yet to be defined mechanism in both Jurkat and myeloma, however this could contribute to increased p53 and p73 transcriptional activity since MDM2 inhibits p73 function in the absence of degradation (Wang et al., 2001;Hu et al., 1999;Scholz et al., 2005). Though this influence of CPS49 was not seen in myeloma, it is tantalizing to speculate that further studies that examine pretreatment with differing levels of flavopiridol may reveal a similar profile of transcriptional targeting by CPS49 in myeloma. How p73 is upregulated transcriptionally by CPS49 remains unclear since unlike flavopiridol, CPS49 does not increase E2F-1 levels. Interestingly both CPS49 and flavopiridol are potent repressors of NF-κB activation and their action together cooperatively repress p65 and I-κB phosphoryation in both resting and mitogen-activated cells. The I-κB kinase

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complex (IKK) is responsible for these phosphorylation events and is therefore the likely direct target of both flavopiridol and CPS49. However, the robust effects of their combination suggest that their mechanism of IKK targeting may not be the same. NF-κB repression is probably the major mechanism for the repression of the anti-apoptotic genes in Fig. 6B since all of these genes are known NF-κB targets. It will be interesting to assess whether or not the efficacy of targeting of these pathways by CPS49 in myeloma may be influenced by differential low dose pretreatment with flavopiridol.

The addition of an ROS scavenger like NAC produces slight rescue of leukemic cell viability and slightly represses the activation of PUMA and p73 by flavopiridol. This observation suggests a contribution of ROS to pro-apoptotic activation of these genes however; the precise mechanism underlying this ROS influence will require further investigation.

In summary we have profiled the efficacy of the combined use of flavopiridol and the redox-reactive thalidomide CPS49 and find that their concerted actions show selective cell-type specific cytotoxicity against leukemic cells. The potency of their reciprocal targeting of general pro-apoptotic and anti-apoptotic cellular pathways suggests that strategies involving differential adjustment of the dose and sequential addition of flavopiridol and redox-reactive thalidomides may lead to therapeutic benefit against a variety of human blood borne cancers.

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Footnotes

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Legends for Figures

Fig. 1. Combinatorial treatment with CPS49 and flavopiridol shows selective cytotoxic synergy against transformed leukemic cells. (A) PBMCs, Jurkat, K562, HeLa, and 8226 cells were incubated with increasing concentrations of CPS49 alone (left panel) or flavopiridol alone (right panel). Cell viability was measured by MTT assay at 16 h following the drug treatments. * Asterisk indicates that 20 times higher concentrations of CPS49 were used in 8226 cells (left panel). (B) Jurkat cells (left panel) were incubated with increasing concentrations (0-5 μM) of CPS49 alone, flavopiridol (flavopiridol) alone, or CPS49 plus flavopiridol with a fixed ratio of 1:1. Cell viability was determined after 16 h incubation time with the drugs. CI values (right panel) for each fractional effect were calculated using a commercially available software (Calcusyn; Biosoft). (C) Following 8 h pretreatment with 0.2 μM flavopiridol (flavopiridol), Jurkat cells (left panel) were incubated with increasing concentrations (0-5 μM) of CPS49 alone, flavopiridol alone, or CPS49 plus flavopiridol (a fixed ratio of 1:1) for an additional 16 h, and cell viability was assessed at the termination of incubation. The viability of the Jurkat cells after 16 h exposure to flavopiridol at 0.2 μM was around 90%. The data presented are the means of three independent determinations after normalization to those of the untreated cells. CI values (right panel) for each fractional effect were calculated using the software, and a CI value < 1.0 indicates synergism, CI = 1.0 indicates an additive effect, and CI > 1.0 indicates antagonism. (D) FACS measurement of acute increase in annexin positive staining of Jurkat cells 3 hours following addition of increasing doses (0-10 μM) of flavopiridol and CPS49 either alone or in combination as indicated.

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Fig. 2. CPS49 and flavopiridol demonstrate selective disruption of homeostasis of intracellular glutathione (GSH) and reactive oxygen species (ROS) in transformed leukemia cells. (A) The profile of ROS generation in Jurkat cells after 1 h drug treatment and the profile of cellular GSH depletion in Jurkat cells after 16 h exposure to CPS49 alone (top panel), flavopiridol alone (flavopiridol; middle panel), or CPS49 plus flavopiridol (bottom panel) at the indicated concentrations. (B) The profile of ROS generation in PBMCs, K562, HeLa, and 8226 cells after 1 h drug treatment and the profile of intracellular GSH depletion in these cells after 16 h drug exposure to CPS49 alone (top panels), flavopiridol alone (flavopiridol; middle panels), or CPS49 plus flavopiridol (bottom panels) at the concentrations indicated. GSH and ROS were measured as described in the Materials and Methods. The data shown are the means of three independent experiments after normalized to those of the untreated cells.

Fig. 3. CPS49 and flavopiridol combinations synergistically reduce the mitochondrial membrane potential and NF-κB activation but differentially influence E2F-1 and caspase activation in transformed leukemic cells. (A) Flow cytometric measurement of CPS49- and/or flavopiridol-mediated loss of mitochondrial membrane potential in Jurkat cells following exposure to CPS49, flavopiridol, and CPS49 plus flavopiridol, respectively, for 1 h (left panel) or 3 h (right panel), as outlined above. (B) Jurkat cells were preincubated for 15 min in the presence or absence of 10 μM CPS49 and/or flavopiridol prior to stimulation with PHA (1 μg/ml) and PMA (50 ng/ml) for an additional 15 min. Whole cellular lysates were then prepared for immunoblot analysis of phospho-IκB-α (Ser32)

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and IκB-α (total) levels in the whole cell lysates from the Jurkat cells as described in the Materials and Methods. (C) Immunoblot analysis of phospho-relA (Ser536) and relA (p65) levels in the whole cell lysates from the Jurkat cells treated with the drugs as outlined above. (D) immunoblot analysis of E2F-1 and β–actin (ActB) protein levels. (E) Immunoblot analysis of caspase 3 in whole cell lysates from Jurkat cells pretreated 8 hr with 0.2 μM flavopiridol followed by the addition of 10 μM CPS49 and flavopiridol alone or in combination for an additional 8 hours.

Fig. 4. CPS49 and flavopiridol preferentially up-regulate the expression of pro-apoptotic genes, while simultaneously down-regulate the expression of anti-apoptotic genes. (A) Jurkat cells were stimulated with 1 μg/ml PHA and 50 ng/ml PMA in the presence or absence of 10 μM CPS49 and/or flavopiridol for 3 h. Total cellular RNA was then isolated from the cell lysates and cDNA was synthesized. mRNA levels of *BAX*, *BAD*, *p73*, and *PUMA* gene expression were analyzed by qRT-PCR, as described in the Materials and Methods. (B) mRNA levels of *MCL1*, *XIAP*, *BCL-2*, *BCL-XL*, *Survivin*, and *MDM2* gene expression were assessed by qRT-PCR analysis in the Jurkat cells treated with the drugs, as outlined above. The data presented are the means of three separate determinations after normalized to those of the house-keeping gene β-actin. * $P < 0.05$ and ** $P < 0.01$ vs. the untreated controls. (C) The reversal of CPS49- and/or flavopiridol (flavopiridol)-induced cell killing by 10 mM of the antioxidant N-acetyl-cysteine (NAC) in Jurkat cells, as determined by MTT assay. The data shown are the means of three separate experiments after normalized to those of the untreated cells. (D) Jurkat cells were stimulated for 3 h with PHA (1 μg/ml) and PMA (50 ng/ml) in the

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presence or absence of 10 μM CPS49 and/or flavopiridol, as well as 15 mM of the antioxidant N-acetyl-cysteine (NAC). Total cellular RNA was then isolated from the cell lysates and cDNA was synthesized. The reversal of CPS49- and flavopiridol-mediated mRNA expression of p73 (left panel) and PUMA (right panel) genes by NAC was assessed by qRT-PCR analysis, as described in the Materials and Methods. * $P < 0.05$ and ** $P < 0.01$ for the cells with NAC treatment vs. the cells without NAC treatment.

Fig. 5. The combinatorial synergy by CPS49 and flavopiridol following low dose flavopiridol pretreatment is highly cell type specific . (A) HeLa, LNCaP, OPM2, 8226, and HH cell lines were incubated with increasing concentrations (0-10μM) of CPS49 alone, flavopiridol (flavopiridol) alone, or CPS49 plus flavopiridol at a fixed ratio of 1:1. Cell viability was determined after 16 h incubation time with the drugs. (B) CI values were determined for HH, OPM2 and 8226 and plotted against fractional effect to construct isobolograms. CI value < 1.0 indicates synergism, CI = 1.0 indicates an additive effect, and CI > 1.0 indicates antagonism. No isobologram for HeLa or LNCaP could be derived.

Fig 6. Flavopiridol down-regulates genes important for mitochondrial stability and survival but CPS49 shows lower efficacy in 8226 myeloma cells. (A) 8226 myeloma cells were stimulated with 1 μg/ml PHA and 50 ng/ml PMA in the presence or absence of 10 μM CPS49 and/or flavopiridol for 3 h. Total cellular RNA was then isolated from the cell lysates and cDNA was synthesized. mRNA levels of *BAX*, *BAD*, *p73*, and *PUMA* gene expression were analyzed by qRT-PCR. (B) mRNA levels of *MCL1*, *XIAP*, *BCL-2*,

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BCL-XL, *Survivin*, and *MDM2* gene expression were assessed by qRT-PCR analysis in the 8226 cells treated with the drugs, as outlined above. The data presented are the means of three separate determinations after normalized to those of the house-keeping gene β-actin. * $P < 0.05$ and ** $P < 0.01$ vs. the untreated controls. (C) Jurkat cells (10^7) were treated with and without 8 h pretreatment with 0.2 μM flavopiridol. Whole cell lysates were prepared and analyzed by immunoblot for total and serine 2 C-terminal domain phosphorylated pol II and for total and serine 807/811 phosphorylated Rb. Shown at the right is a densitometer scan showing relative amount of serine 2 phosphorylated pol II compared to serine 808/811 phosphorylated RB normalized to the total levels of each respectively. (D) This schematic diagram shows that CPS49 and flavopiridol increase p73 directly or indirectly through sustaining the transcription factor E2F-1 and down-regulating MDM2. p73 mediates mitochondrial dysfunction via either the transcription of the pro-apoptotic genes PUMA, BAD, and BAX or mitochondrial localization of these proteins. On the other hand, CPS49 and flavopiridol induce cell death by inhibiting NF-κB and down-regulating NF-κB targeting anti-apoptotic genes, such as Survivin, XIAP, Bcl-2, Bcl-XL, and MCL1. Since both CPS49 and flavopiridol cause mitochondrial damage through closely related but distinct mechanisms, they may act collaboratively or synergistically to promote apoptotic death of leukemia cells through p73 and NF-κB and their downstream molecular events. Such a mechanism may serve to integrate the roles of p73 and NF-κB in culmination in mitochondrial damage and cell death, which may underlie the mechanism of CPS49 and flavopiridol mediated mitochondrial dysfunction and cell killing in transformed leukemic cells.

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Table 1 Differential Syngergism between CPS49 and Flavopiridol: Cytotoxicity, Mitochondrial Membrane Potential, and ROS

Cytotoxicity (MTT)								Mitochondrial ψ_m*				ROS			
no pretreatment				*w/ Pretreatment*				*w/ Pretreatment*				*w/ Pretreatment*			
CPS49 (μM)	**Flavo (μM)**	**Fa**	**CI**	**CPS49 (μM)**	**Flavo (μM)**	**Fa**	**CI**	**CPS49 (μM)**	**Flavo (μM)**	**Fa**	**CI**	**CPS49 (μM)**	**Flavo (μM)**	**Fa**	**CI**
0.078125	0.078125	0.176	0.817	0.078125	0.078125	0.118	1.707	1	1	0.264	0.5	1	1	0.136	0.876
0.15625	0.15625	0.245	0.924	0.15625	0.15625	0.295	0.75	5	5	0.401	0.926	2	2	0.221	1.044
0.3125	0.3125	0.358	0.874	0.3125	0.3125	0.447	0.635	10	10	0.480	1.12	5	5	0.377	1.333
0.625	0.625	0.500	0.787	0.625	0.625	0.581	0.64					10	10	1.000	1.81E-08
1.25	1.25	0.653	0.661	1.25	1.25	0.673	0.775								
2.5	2.5	0.714	0.9	2.5	2.5	0.814	0.612								
5	5	0.767	1.232	5	5	0.897	0.531								

Fa: fraction affected by the dose
CI: combination index which defines additive (CI=1.0), synergistic (CI<1.0) or antagonistic (CI>1.0) effects. * Measured at 3 h. All meaurements were conducted with Jurkat leukemic T-cells.

Table 2 Differential cell specificity of CPS49 and Flavopiridol Synergism following Flavopiridol pretreatment

Cytotoxicity (MTT)											
8226				HH				OPM2			
CPS49 (μM)	**Flavo (μM)**	**Fa**	**CI**	CPS49 (μM)	**Flavo (μM)**	**Fa**	**CI**	CPS49 (μM)	**Flavo (μM)**	**Fa**	**CI**
0.15625	0.15625	0.0181	2.322	0.15625	0.15625	0.047	1.12	0.15625	0.15625	0.050	1.942
0.3125	0.3125	0.0864	0.65	0.3125	0.3125	0.085	1.33	0.3125	0.3125	0.220	0.488
0.625	0.625	0.1394	0.682	0.625	0.625	0.143	1.63	0.625	0.625	0.277	0.671
1.25	1.25	0.2697	0.508	1.25	1.25	0.237	1.95	1.25	1.25	0.325	1.012
2.5	2.5	0.3695	0.585	2.5	2.5	0.331	2.67	2.5	2.5	0.469	0.951
5	5	0.5695	0.443	5	5	0.455	3.47	5	5	0.704	0.559
10	10	0.7762	0.281	10	10	0.731	2.66	10	10	0.882	0.272

Fa: fraction affected by the dose. CI: combination index which defines additive effect or synergism or antagonism

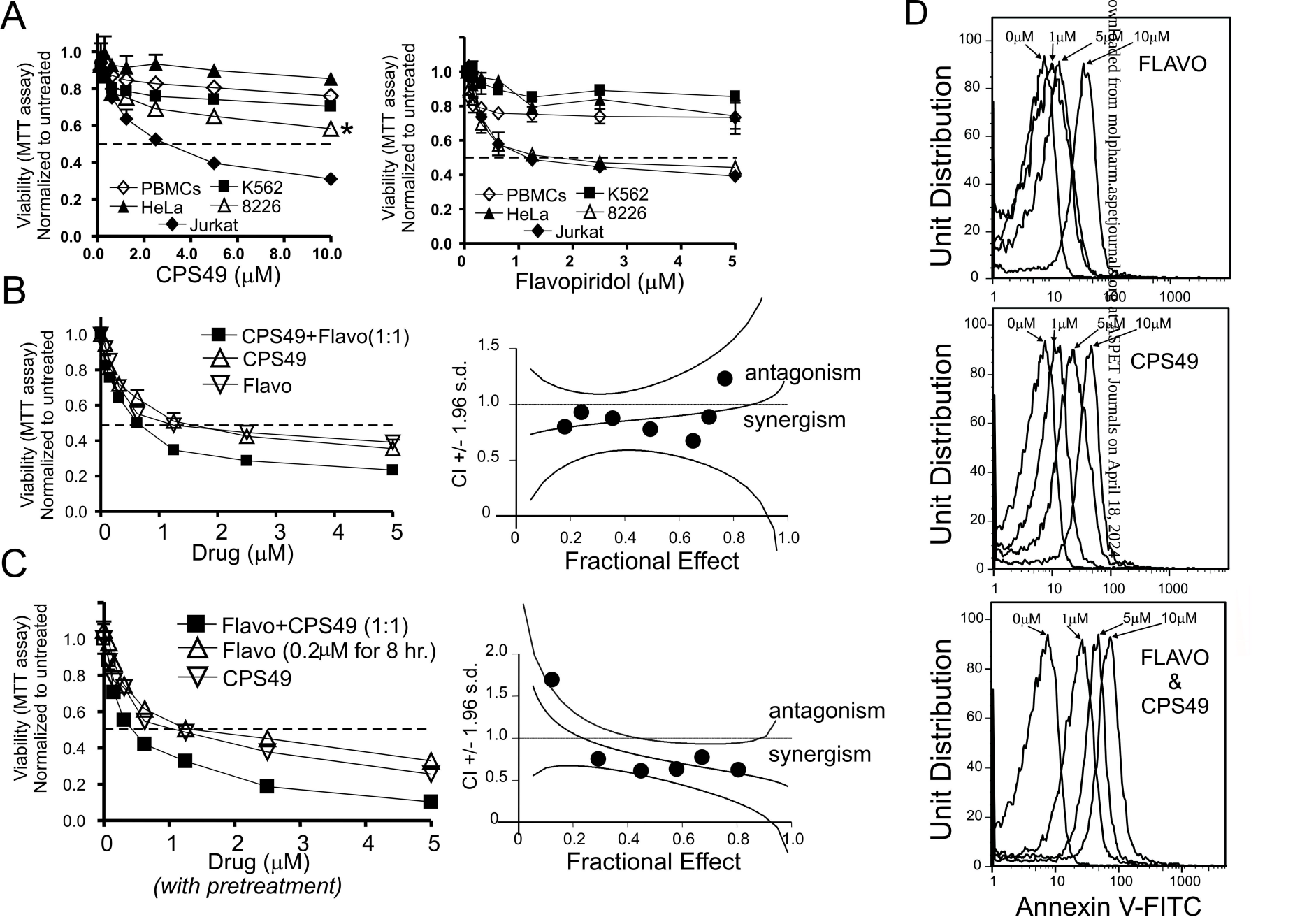

Figure 1

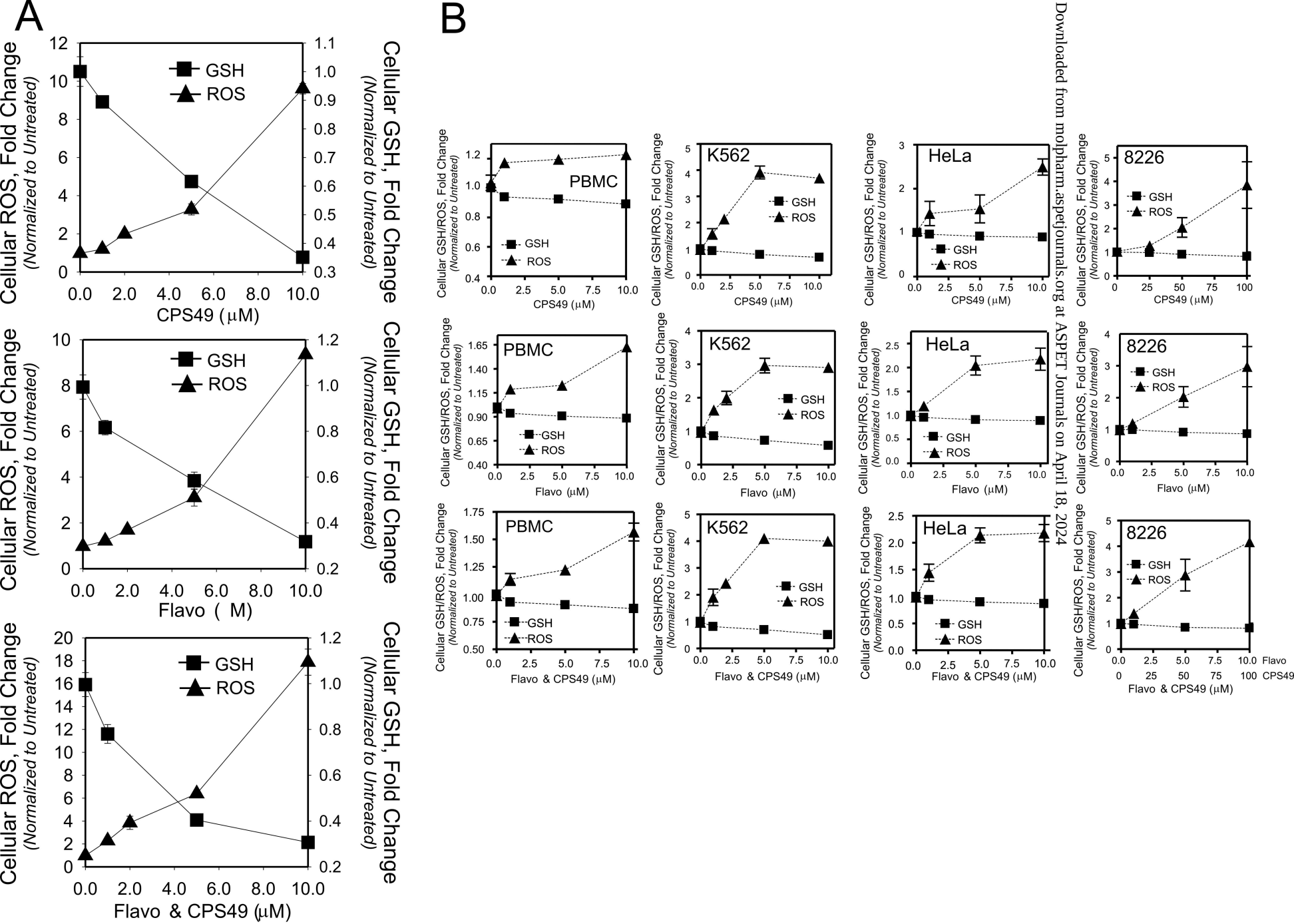

Figure 2

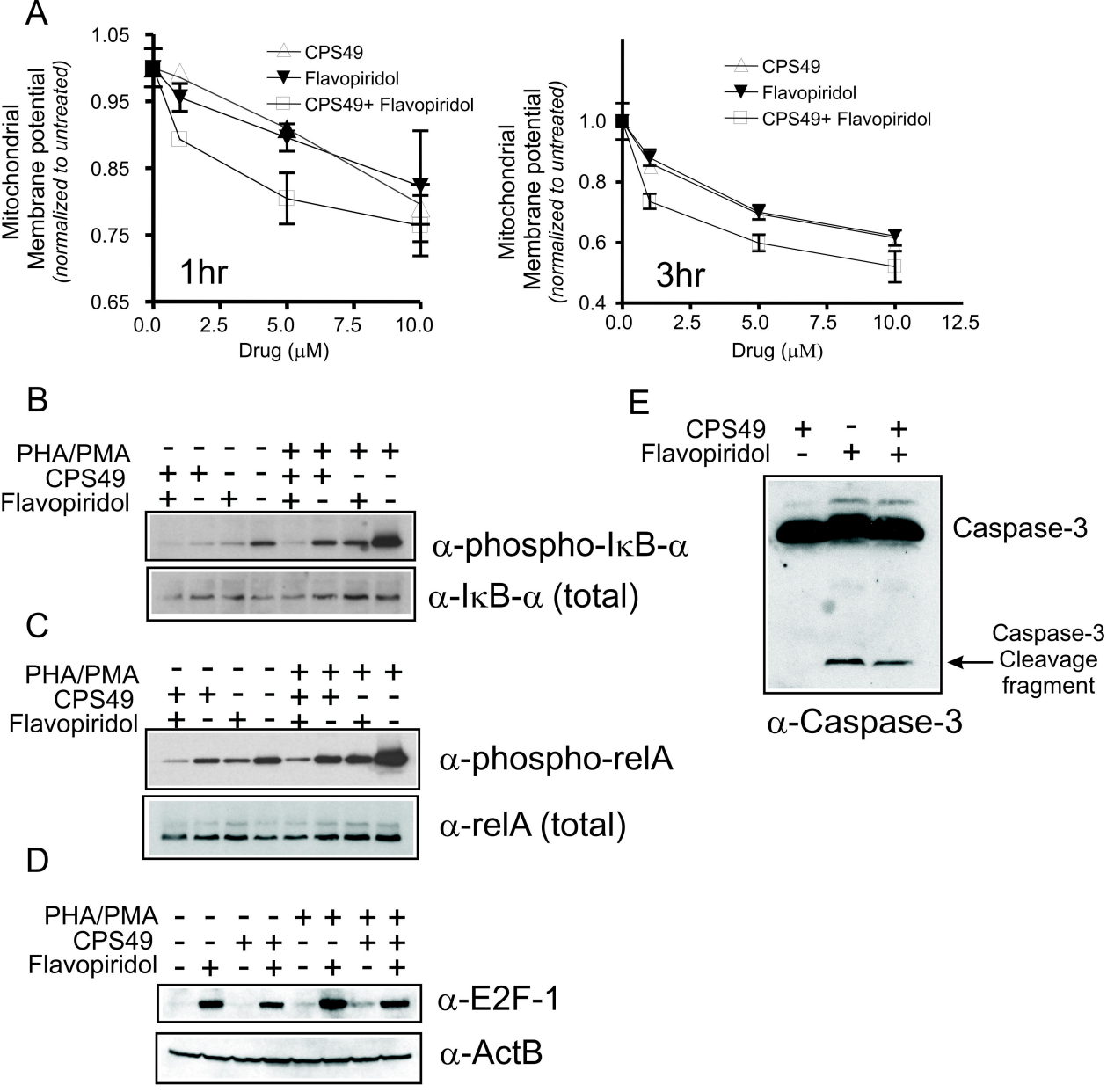
A
Mitochondrial Membrane potential (normalized to untreated)
1.05
0.95
0.85
0.75
0.65
CPS49
Flavopiridol
CPS49+ Flavopiridol
1hr
0.0
2.5
5.0
7.5
10.0
Drug (μM)
Mitochondrial Membrane potential (normalized to untreated)
1.0
0.8
0.6
0.4
CPS49
Flavopiridol
CPS49+ Flavopiridol
3hr
0.0
2.5
5.0
7.5
10.0
12.5
Drug (μM)
B
PHA/PMA
CPS49
Flavopiridol
α-phospho-IκB-α
α-IκB-α (total)
C
PHA/PMA
CPS49
Flavopiridol
α-phospho-relA
α-relA (total)
D
PHA/PMA
CPS49
Flavopiridol
α-E2F-1
α-ActB
E
CPS49
Flavopiridol
Caspase-3
Caspase-3 Cleavage fragment
α-Caspase-3

Figure 3

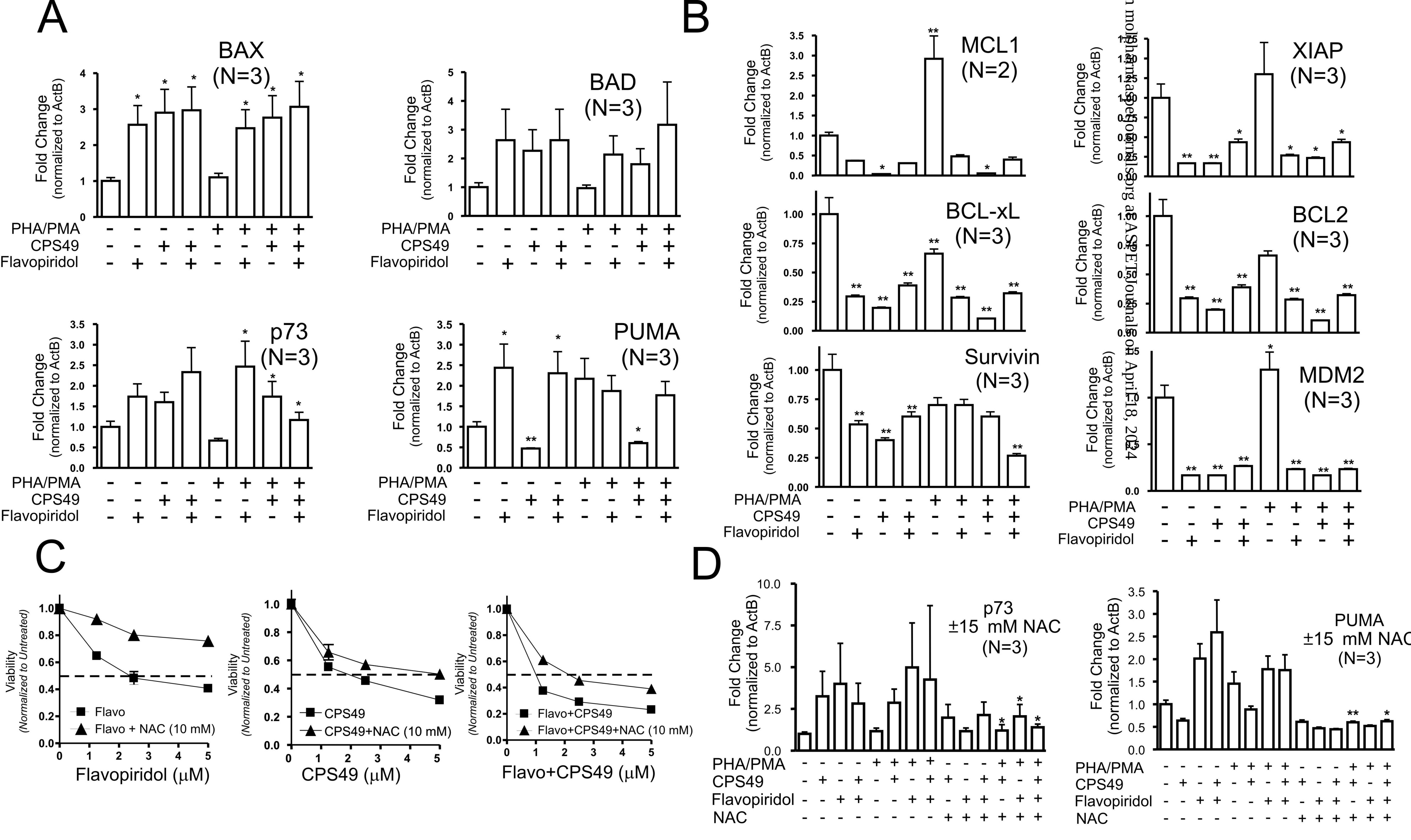

Figure 4

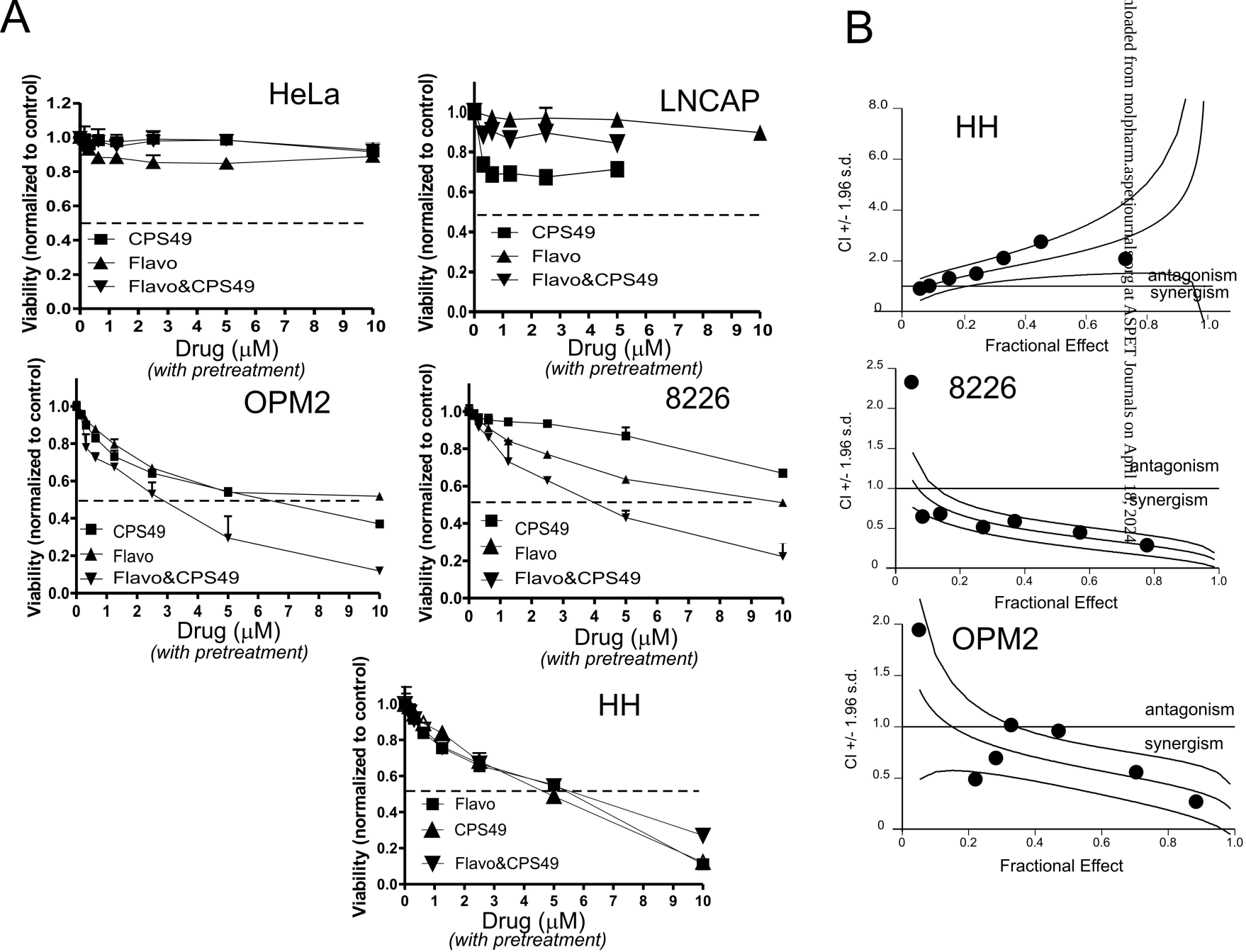

Figure 5

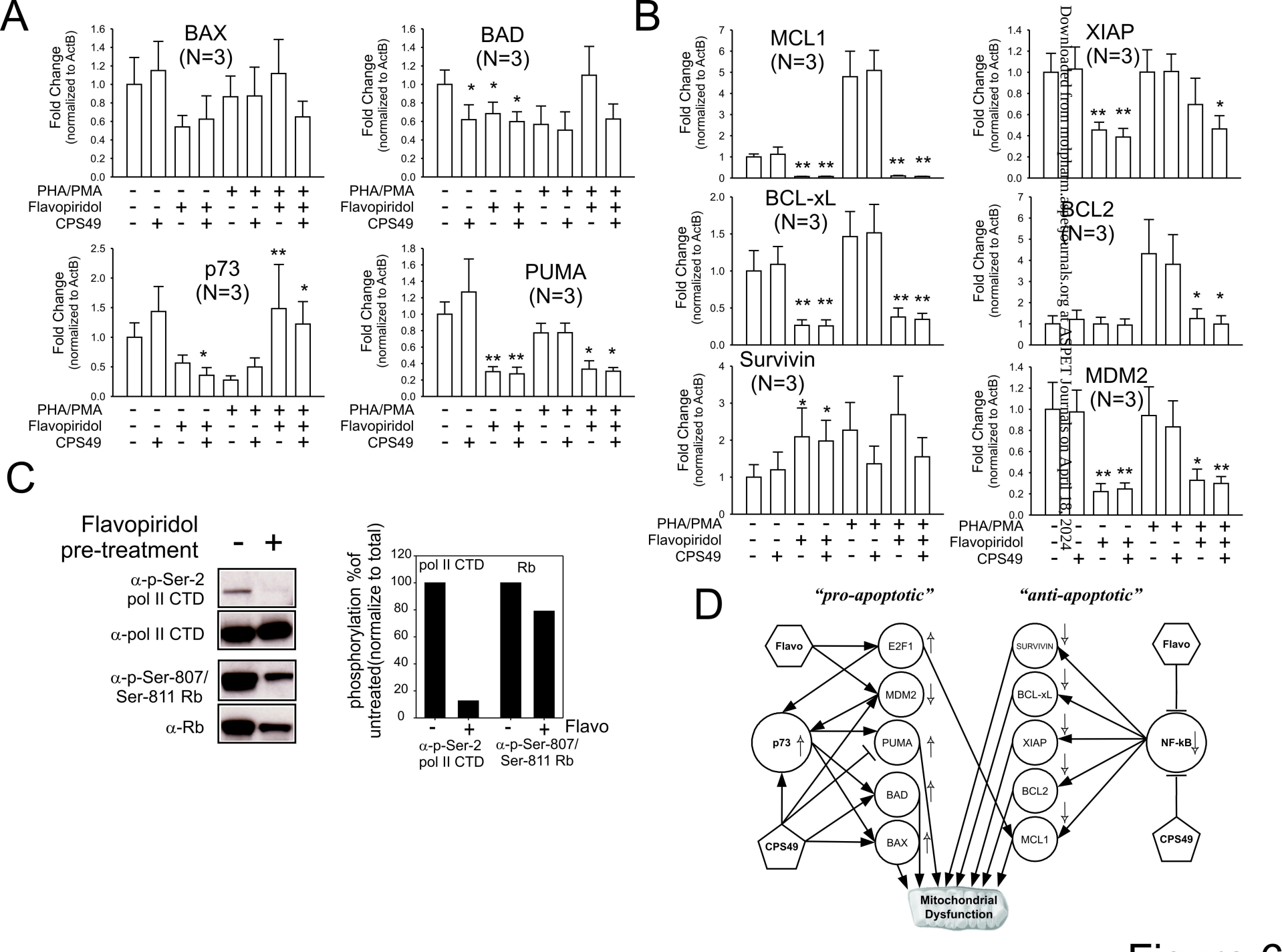

Figure 6