Regulation of inflammation by histone deacetylases in rheumatoid arthritis: beyond epigenetics
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CHAPTER 6

HISTONE DEACETYLASE INHIBITORS SUPPRESS RHEUMATOID ARTHRITIS FIBROBLAST-LIKE SYNOVIOCYTE AND MACROPHAGE IL-6 PRODUCTION BY ACCELERATING mRNA DECAY

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ABSTRACT

Background: Histone deacetylase inhibitors (HDACi) display potent therapeutic efficacy in animal models of arthritis and suppress inflammatory cytokine production in rheumatoid arthritis (RA) synovial macrophages and tissue.

Objectives: To determine the molecular mechanisms contributing to the suppressive effects of HDACi on RA synovial cell activation, using IL-6 regulation as a model.

Methods: RA fibroblast-like synoviocytes (FLS) and healthy donor macrophages were treated with IL-1β, TNFα, LPS or poly(I:C) in the absence or presence of the HDACi trichostatin A (TSA) or ITF2357 (givinostat). IL-6 production and mRNA expression was measured by ELISA and quantitative PCR, respectively. Protein acetylation and the activation of intracellular signalling pathways were assessed by immunoblotting. The DNA-binding activity of NF-κB and AP-1 components was measured by ELISA-based assays.

Results: HDACi (0.25–1.0 μM) suppressed RA FLS IL-6 production induced by IL-1β, TNFα and TLR ligands. Phosphorylation of mitogen-activated protein kinases and IκBα following IL-1β stimulation were unaffected by HDACi, as were AP-1 composition and binding activity, and c-jun induction. TSA induced a significant reduction in nuclear retention of NF-κB in FLS 24 hours after IL-1β stimulation, but this did not reduce NF-κB transcriptional activity or correlate temporally with reductions in IL-6 mRNA accumulation. HDACi significantly reduced the stability of IL-6 mRNA in FLS and macrophages.

Conclusions: Our study identifies a novel, shared molecular mechanism by which HDACi can disrupt inflammatory cytokine production in RA synovial cells, namely the promotion of mRNA decay, and suggests that targeting HDAC activity may be clinically useful in suppressing inflammation in RA.
INTRODUCTION

Excessive production of inflammatory mediators pivotally contributes to pathology in many chronic immune-mediated diseases (IMIDs), including rheumatoid arthritis (RA).\(^1\) In RA, activated immune cells infiltrating the synovial tissue secrete large quantities of tumour necrosis factor-\(\alpha\) (TNF\(\alpha\)), IL-1, IL-8 and IL-6, amongst other cytokines and chemokines. These secreted products, as well as cell-cell contacts, activate stromal fibroblast-like synoviocytes (FLS), which are potent effector cells in RA, generating enzymes which degrade cartilage and bone, and serving as a primary source of inflammatory cytokines in the synovium.\(^2,3\)

Production of inflammatory cytokines is tightly regulated at multiple levels, including activation of signalling pathways, induced and epigenetic mechanisms regulating transcription factor access to gene promoters, post-transcriptional mRNA processing, and protein secretion. Each of these processes can be regulated by reversible protein acetylation. Inflammatory stimuli activate transcriptional coactivators possessing intrinsic histone acetyltrasferase (HAT) activity, leading to histone acetylation and increased accessibility of gene promoters for transcription.\(^4\)

Histone deacetylases (HDACs), including the ubiquitously expressed class I HDACs (HDACs 1-3 and 8), and tissue-restricted class II HDACs (HDACs 4-7, 9, 10), counteract the activity of HATs to terminate ongoing transcriptional processes.\(^5\)

While some studies have indicated that decreased expression of HDACs in synovial tissue may contribute to pathology in RA,\(^6,7\) analyses of murine and human monocytes revealed that HDAC inhibitors (HDACi) are potent anti-inflammatory agents, which suppress LPS- and TNF\(\alpha\)-induced cytokine production.\(^8-10\) Also, HDACi uniformly ameliorate inflammation and prevent joint destruction in both prophylactic and therapeutic protocols in animal arthritis models.\(^11-16\) These findings are relevant to RA as we have previously demonstrated that HDACi suppress IL-6 and TNF\(\alpha\) production by RA synovial macrophages and synovial tissue explants.\(^17\) Moreover, RA FLS proliferation and survival in vitro is suppressed by HDACi.\(^15,18,19\) The exact mechanisms by which HDACi alleviate inflammation in acute and chronic inflammatory diseases remain unclear, but could be related to regulation of histone acetylation. Alternatively, HDACi may target some 1700 structural and signal transduction proteins, many of which are relevant to RA, including components of the mitogen-activated protein kinase (MAPK) and STAT pathways, transcription factors such as p53, NF-\(\kappa\)B p65 and c-Jun, as well as regulators of mRNA stability, protein degradation and secretion.\(^20-22\)

Further understanding of the molecular mechanism(s) contributing to anti-inflammatory effects of HDACi may facilitate hypothesis-driven decisions as to the suitability of HDACi in the treatment of RA, especially now that one HDACi, ITF2357 (givinostat), has demonstrated initial clinical efficacy in the treatment of systemic onset juvenile idiopathic arthritis (SOJIA).\(^23,24\)

Expression of IL-6 in RA synovial tissue strongly correlates with disease activity and inflammation severity in RA,\(^25\) and targeting of IL-6 signalling using tocilizumab, an anti-IL-6 receptor monoclonal antibody, demonstrates clinical efficacy in RA.\(^26\) Here we examined the mechanism by which HDACi might suppress IL-6 expression in RA FLS and macrophages, assessing effects on intracellular signalling pathways leading to IL-6 transcription and post-transcriptional regulatory events. We identify inhibition of IL-6 mRNA stability as a novel common mechanism by which HDACi regulate inflammatory gene expression in RA.
CHAPTER 6

MATERIALS AND METHODS

Cell culture and stimulation. FLS were isolated from synovial biopsies of RA patients (n = 18) fulfilling the American College of Rheumatology (ACR) revised criteria for RA,\textsuperscript{27} cultured as previously described,\textsuperscript{28} and used for experiments between passages 4-9, following overnight culture in medium containing 1% FBS (Invitrogen, Breda, The Netherlands) (see supplemental table 1 for patient characteristics). Monocytes were isolated from buffy coats (Sanquin, Amsterdam, the Netherlands) of healthy donors (HD) and differentiated into macrophages as described previously.\textsuperscript{17} Cells were treated with medium alone or medium containing trichostatin A (TSA) (Sigma-Aldrich, St. Louis, MO) or ITF2357 (Italfarmaco, Cinisello Balsamo, Italy) at the indicated concentrations for 30 minutes, followed by stimulation with IL-1\textsubscript{β} (0.2-10ng/ml) (R&D Systems, Minneapolis, MN), TNFα (10ng/ml) (Biosource International), LPS (1μg/ml) or poly(I:C) (10μg/ml) (both from Sigma-Aldrich) for up to 24 hours.

Measurement of cell viability. RA FLS viability was assessed 24 hours post-treatment by incubating cells with 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) (Sigma-Aldrich) (1mg/ml) for 2 hours, followed by solubilization of cells in acidified isopropanol solution containing 0.1% Igepal CA-630 (Sigma-Aldrich) and optical density measurement at 590 nm.

Quantitative measurement of IL-6 protein and mRNA expression. IL-6 protein production was measured in cell-free supernatants 24 hours post-stimulation, using a PeliKine Compact ELISA kit (Sanquin Reagents, Amsterdam, The Netherlands). mRNA expression in FLS and macrophages was assessed by quantitative (q)PCR as described in detail in Supplementary Materials and Methods.

Protein extraction and immunoblotting. For determination of protein acetylation status and signaling pathway activation, FLS were left untreated or treated with TSA or ITF2357 for 30 minutes, prior to further incubation in medium alone or IL-1\textsubscript{β} for time periods indicated in figure legends. Protein extraction from whole cell lysates was as previously described, and nuclear fraction extraction, as well as their analysis by immunoblotting are described in detail in Supplementary Material and Methods.\textsuperscript{17}

Measurement of transcription factor DNA-binding and transcriptional activity. DNA binding activities of NF-κB components p65 and p50, and AP-1 components p-c-Jun, JunB and JunD in FLS nuclear fractions were determined using a TransAM transcription factor ELISA (Active Motif, Carlsbad, CA) according to the manufacturer’s instructions. NF-κB transcriptional activity in FLS was assessed using a recombinant adenoviral vector encoding a NF-κB-luciferase reporter. Construction of the vector, generation of viral particles, transduction of FLS, and measurement of luciferase activity are described in detail in Supplementary Materials and Methods.

Statistical analyses. Data are presented as means ± SEM unless otherwise indicated. For analyzing HDACi treatment dose responses, data sets were subjected to an overall Kruskal-Wallis test followed by post hoc Dunns’ multiple comparison test, using cells not exposed to HDACi as reference controls. In mRNA stability experiments, the rate of mRNA degradation over time was determined in each experimental condition and area under the curve (AUC) values were calculated and compared using the Mann-Whitney U test. The Mann-Whitney U test was used for all other comparisons. P values ≤ 0.05 were considered statistically significant.
RESULTS

**HDACi suppress RA FLS IL-6 production.** Multiple HDACi block IL-6 production by monocytes and macrophages derived from HD, as well as RA patient synovial macrophages and tissue. To determine if HDACi could also inhibit RA FLS IL-6 production, we treated RA FLS with increasing concentrations of TSA or ITF2357 prior to stimulation with agonists found in RA synovial tissue. Both HDACi dose-dependently suppressed IL-6 production induced by IL-1β. TSA achieved 50% inhibition of IL-6 production at 0.25 μM and more than 80% at 1 μM (p < 0.001). A trend towards reduced IL-6 production was observed at clinically relevant concentrations of ITF2357 (0.25 μM), reaching 80% inhibition at 1 μM (p < 0.01) (Fig. 1A). HDACi also suppressed IL-6 production in response to TNFα and the TLR ligands LPS and poly(I:C) by 50-80% (p < 0.05) (Fig. 1B). HDACi suppression of IL-6 production could not be attributed to changes in FLS viability following exposure to HDACi, as measured by

![Graph A](image1.png)  
**Figure 1.** HDACi suppress IL-6 production by RA FLS without affecting cell viability. (A) FLS were stimulated with 10 ng/ml of IL-1β alone or in the presence of increasing concentrations of TSA or ITF2357 for 24 h (n = 6-10). (B) Alternatively, cells were left untreated or pre-exposed to 1 μM TSA followed by 24 h stimulation with IL-1β (10 ng/ml), TNFα (10 ng/ml), LPS (1 μg/ml) or poly(I:C) (10 μg/ml) (n = 4). IL-6 levels in cell-free tissue culture supernatants were determined by ELISA. Results, presented as mean IL-6 concentration ± SEM, were either subjected to the Kruskal-Wallis test followed by Dunns’ multiple comparison analysis with cells not treated with HDACi used as reference controls (A), or to the Mann-Whitney U test (B). *p < 0.05; **p < 0.01; ***p < 0.001. (C) Viability of cells after 24 h stimulation with IL-1β (10 ng/ml) in the presence or absence of increasing doses of TSA or ITF2357 was assessed by measurement of MTT reduction (n = 5). Values representing changes in MTT processing are shown as mean optical density at 590 nm ± SEM.
MTT reduction (Fig. 1C). As previously observed in RA macrophages, TSA suppressed the induction of IL-6 mRNA in FLS. \(^1\) \(1 \mu M\) TSA reduced IL-1\(\beta\)-induced IL-6 mRNA accumulation by 70\% (\(p < 0.01\)) (Fig. 2A), while 0.25 \(\mu M\) ITF2357 reached 45\% inhibition (\(p < 0.01\)) (Fig. 2B). ITF2357 blocked IL-6 mRNA accumulation in a concentration-dependent manner regardless of the dose of IL-1\(\beta\) used (Fig. 2C).

Suppression of IL-6 production by HDACi does not require epigenetic induction of transcriptional repressors. To determine if inhibition of IL-6 transcription by HDACi might result from induced expression of transcriptional co-repressors or negative regulatory signalling components, we examined histone (H)3 and H4 acetylation following HDACi treatment. HDACi induced acetylation of H3 and H4, as well as a protein of 52 kDa (identified as tubulin, data not shown) (Fig. 3A and 3B). No global changes in FLS protein acetylation status could be detected in response to IL-1\(\beta\), TNF\(\alpha\) or LPS alone (Fig. 3B). Both TSA and ITF2357 induced H3, H4 and total cellular protein acetylation within 15 minutes of HDACi exposure (Fig. 3A), consistent with the possibility that histone hyperacetylation might lead to transcriptional induction of repressors of IL-6 transcription. However, both in the absence or presence of the protein translation inhibitor cycloheximide (CHX), TSA suppressed IL-1\(\beta\)-induced IL-6 mRNA accumulation in FLS (\(p < 0.05\)) (Fig. 3C). The failure of CHX to rescue IL-6 mRNA accumulation suggested that de novo synthesis of a repressor protein is not required for HDACi suppression of IL-6 in RA FLS.

HDACi fail to affect MAP kinase signalling and AP-1 activation in RA FLS. Activation of MAPK and NF-\(\kappa\)B signalling pathways, leading to transcriptional activation of NF-\(\kappa\)B and AP-1, are required for IL-1\(\beta\)-induced IL-6 production, and can be modulated by reversible acetylation.\(^2\)\(^0\),\(^2\)\(^9\) We analyzed the effects of TSA on the phosphorylation status of p38 and ERK

Figure 2. HDACi reduce IL-6 mRNA accumulation in RA FLS. FLS were left unstimulated, or were stimulated with IL-1\(\beta\) (10 ng/ml) with or without 1 \(\mu M\) TSA (A), or with IL-1\(\beta\) (1 ng/ml) in the presence or absence of 0.25 \(\mu M\) ITF2357 (B) for 4 h, total RNA was extracted, reverse transcribed and IL-6 mRNA accumulation analyzed by qPCR. Results are presented as mean IL-6 expression relative to 18S ± SEM of 5 independent experiments. **\(p < 0.01\), Mann-Whitney U test. (C) Alternatively, FLS (n = 3) were stimulated as above with increasing concentrations of IL-1\(\beta\) (0.2-10 ng/ml) in the absence (med) or presence of increasing concentrations of ITF2357 (0.1-1.0 \(\mu M\)) and IL-6 mRNA expression assessed as in A and B.
MAPK in RA FLS by immunoblotting. IL-1β induced rapid phosphorylation of both p38 and ERK, which peaked 30 min post-stimulation. TSA treatment affected neither phosphorylation levels, nor temporal regulation of p38 and ERK activation (Fig. 4A), indicating that HDACi blockade of RA FLS IL-6 production is not mediated by suppression of MAPK signalling.

Phosphorylation of JNK, activation of the c-Jun component of the AP-1 transcription factor and subsequent rapid induction of c-Jun expression are essential prerequisites for optimal IL-6 gene transcription, and are sensitive to acetylation.30,31 However, similarly to p38 and ERK, IL-1β-stimulated JNK phosphorylation in FLS was unaffected by TSA (Fig. 4B). Also, IL-1β induced a transient 5-fold increase of c-Jun mRNA levels which was unaffected by TSA (Fig. 4C). Stimulation with IL-1β caused a 2.5 fold increase in p-c-Jun DNA binding compared to unstimulated FLS (Fig. 4D). However, FLS exposure to TSA did not suppress the induction of c-Jun binding activity, (Fig. 4D), and had no influence on DNA binding of Jun family members JunB and JunD (data not shown). Collectively, these results suggest that HDACi-dependent IL-6 suppression in RA FLS is not mediated by direct regulation of MAPK and AP-1 signalling pathways.

**Figure 3. New protein synthesis is not required for FLS IL-6 suppression by HDACi.** (A) FLS were left untreated (med) or were treated with TSA (1 μM) or ITF (1 μM) for the indicated time (in minutes). Protein extracts were prepared and analyzed by immunoblotting for acetylated lysine (Ac-Lys), acetylated (Ac)-H3, H3, Ac-H4, H4 and tubulin content. (B) FLS were left unstimulated in medium (med) or were stimulated with IL-1β (10 ng/ml), TNFα (10 ng/ml) or LPS (1 μg/ml), lysed and examined by immunoblotting with antibodies recognizing Ac-Lys, Ac-H3, H3, Ac-H4, H4 and tubulin (Tub). FLS treated with 1 μM TSA for 4 h were used as a positive control. Results are representative of 3 independent experiments. (C) FLS were left untreated or were treated with IL-1β (10 ng/ml) with or without 1 μM TSA for 4 h. To block protein translation, cells were preincubated with 1 μg/ml cycloheximide (CHX) for 30 min prior to stimulation. IL-6 mRNA levels were assessed by qPCR and presented as relative IL-6 expression ± SEM (n = 4). *p < 0.05, Mann-Whitney U test.

**HDACi modulate NF-κB signalling in RA FLS.** NF-κB signalling makes pivotal contributions to the induction of IL-6 expression, and the activity as well as nuclear retention of NF-κB subunits is tightly regulated by reversible acetylation.32 In initial experiments, we found that TSA treatment had no effect on the magnitude or kinetics of IκBα phosphorylation or degradation in RA FLS (Fig. 5A). To examine the influence of HDACi on the temporal
regulation of NF-κB nuclear retention, FLS were cultured in the absence or presence of TSA, and then stimulated with medium alone or IL-1β, and nuclear accumulation of p50 and p65 NF-κB subunits assessed by immunoblotting. TSA had little effect on nuclear p50 and

![Figure 4](image)

*Figure 4. HDACi fail to affect MAP kinase signalling and AP-1 activation in RA FLS.* (A) FLS were left unstimulated (med) or were stimulated with 10 ng/ml of IL-1β for the indicated time (in minutes) in the presence or absence of 1 μM TSA, proteins were extracted and MAP kinase activation analyzed by immunoblotting with antibodies specific for phospho (p)-p38, p38, p-ERK, ERK and tubulin (Tub). Anti-acetylated lysine (Ac-Lys) antibody was used to confirm TSA HDACi activity in this experiment. (B) FLS were subjected to the same treatment as in (A) and JNK activation determined in cellular lysates by immunoblotting for p-JNK and Tub content. (C) HDACi do not modulate c-Jun induction by an inflammatory stimulus. FLS were stimulated with medium alone (med) or with IL-1β (10 ng/ml) with or without 1 μM TSA for 1 h or 4 h, total RNA was reverse transcribed, and changes in c-Jun mRNA levels were determined by qPCR. Results of 4 independent experiments are shown as relative expression ± SEM. (D) HDACi have no effect on c-Jun DNA binding activity. FLS were left unstimulated in medium (med) or were treated with IL-1β (10 ng/ml) for 4 h in the presence or absence of 1 μM TSA, nuclear fractions were extracted and levels of active p-c-Jun were determined using an ELISA-based DNA-binding assay. Data represent the mean optical density at 450 nm ± SEM for 5 independent experiments.
p65 in the absence of inflammatory stimulation, but slightly increased the amounts of both proteins 1 hour after IL-1β stimulation. However, nuclear retention of these subunits 24 hours post-stimulation was strongly reduced (Fig. 5B). In DNA-binding assays we observed a trend towards elevated p50 and p65 binding 1 hour after IL-1β stimulation in the presence of TSA, while a significant reduction of DNA binding was observed only after 24 hours (Fig. 5C). To determine if p65 retained transcriptional activity in the presence of TSA, we co-transduced RA FLS with adenoviral vectors encoding 4xNF-κB-MLP-luciferase reporter, and evaluated the effects of TSA on luciferase enzymatic activity. TSA did not inhibit, and clearly increased, the transcriptional activity of NF-κB early after stimulation with IL-1β (Fig. 5D). Together, these findings indicate that HDACi-induced suppression of IL-6 mRNA, detectable 4 hours after inflammatory stimulation, precedes inhibitory effects of HDACi on p50 and p65 DNA binding and nuclear retention.

Figure 5. HDACi increase NF-κB transcriptional activity early after stimulation, but inhibit NF-κB nuclear retention at later time points.  (A) FLS were left untreated (med) or were treated with IL-1β (10 ng/ml) for 5 - 120 minutes in the presence or absence of 1 μM TSA, and total cell lysates examined by immunoblotting for phospho (p)-IkBα and Tub content. Alternatively, FLS were cultured in the presence or absence of 1 μM TSA and then stimulated with medium alone or 10 ng/ml of IL-1β for 1 h, 4 h or 24 h. Nuclear extracts (n = 4) were either separated by electrophoresis and nuclear accumulation of NF-κB subunits analyzed by immunoblotting with antibodies recognizing p50, p65 and H3 (B), or were used for determination of p50 and p65 DNA-binding activities by an ELISA-based DNA binding assay (C). Values representing changes in p50 (left panel) and p65 (right panel) are shown as mean optical density at 450 nm ± SEM. *p < 0.05; **p < 0.01, Mann-Whitney U test.  (D) FLS were co-transduced with a 4xNF-κB-MLP-luciferase and a control CMV-β-gal adenoviral vectors. 48 h after transduction, cells were serum-starved for 24 h and then left untreated or stimulated with IL-1β (10 ng/ml) with or without 1 μM TSA for 2 h, 4 h or 8 h. Cellular lysates were prepared and the luciferase (Luc) and β-galactosidase (β-gal) enzymatic activities determined by luminometry and spectrophotometry, respectively. Data are presented as relative luciferase activity normalized to β-gal activity ± standard deviation and a representative of two independent experiments is shown.
HDACi modulate IL-6 mRNA stability in RA FLS and HD macrophages. To gain more insight into the kinetics of IL-6 suppression by HDACi in RA FLS, we treated the cells with IL-1β for 1–8 hours with or without TSA, and measured changes in IL-6 mRNA levels over time. IL-1β induced a 20-fold increase in IL-6 mRNA levels within 1 hour, which remained stable until 4 hours before further increasing. TSA failed to affect IL-6 mRNA accumulation 1 hour after stimulation, but a strong reduction was observed at 4 hours and became more pronounced at 8 hours (p < 0.05) (Fig. 6A). As we had previously ruled out a need for de novo repressor synthesis in HDACi-mediated IL-6 suppression, we examined if differences might be attributable to effects on mRNA stability. FLS were stimulated with IL-1β for 4 hours in the presence or absence of TSA, and after inhibiting transcription with actinomycin D (ActD), we analyzed time-dependent IL-6 mRNA decay. Accelerated degradation of IL-6 mRNA in TSA-

Figure 6. HDACi accelerate IL-6 mRNA degradation in RA FLS and HD macrophages. (A) FLS were left untreated (med) or were treated with IL-1β (10 ng/ml) with or without 1 μM TSA for the indicated time (in hours), total RNA was extracted, cDNA was synthesized, and temporal changes in IL-6 mRNA accumulation were monitored by qPCR. Data represent the mean ± SEM of 5 or 6 independent experiments. *p < 0.05, Mann-Whitney U test. (B) FLS were stimulated with IL-1β (10 ng/ml) in the presence or absence of 1 μM TSA (n = 5) or (C) with IL-1β (1 ng/ml) in the presence or absence of 250 nM ITF2357 (n = 3). Alternatively, (D) monocyte-derived HD macrophages (n = 4) were stimulated with LPS (1 μg/ml). After 4 h of stimulation cells were washed and fresh medium containing 10 μg/ml of actinomycin D (ActD) was added. RNA was extracted at the indicated time points (in hours) from the beginning of ActD treatment and the rates of IL-6 mRNA degradation in the presence or absence of HDACi were examined by qPCR. Values for 0 h time point were normalized to 100%, and remaining values were expressed as the mean percentage ± SEM of IL-6 mRNA levels compared with controls. For (B) and (D) the areas under the curves (AUC) obtained for cells treated with an inflammatory stimulus alone or in the presence of TSA were calculated and differences between AUC values were analyzed by the Mann-Whitney U test (insets, mean AUC ± SEM). *p < 0.05.
HDACi SUPPRESSION OF IL-6 PRODUCTION BY ACCELERATION OF mRNA DECAY

...treated FLS was detectable within 1 hour of ActD treatment, becoming more pronounced at later time points (p < 0.05 for AUC) (Fig. 6B). Similar effects were observed in the presence of 0.25 μM ITF2357 (Fig. 6C). The presence of TSA also significantly accelerated IL-6 mRNA decay in LPS-stimulated macrophages (Fig. 6D). Together, these results indicate that modulation of mRNA stability is a common mechanism by which IL-6 production is suppressed by HDACi in macrophages and RA FLS.

DISCUSSION

IL-6 acts pleiotropically to induce acute-phase protein synthesis, stimulate B cell antibody production, modulate Th17 and cytotoxic T cell differentiation, activate endothelial cells, and induce osteoclast differentiation. Under physiological conditions, both pro- and anti-inflammatory effects of IL-6 contribute to an effective but self-limiting acute immune response, but in RA and other IMIDs, excessive IL-6 production leads to deregulation of the immune system and pathology. Despite the dual role of IL-6 in regulating inflammation, targeting of the IL-6 receptor has shown strong clinical benefits in RA.

However, since a substantial fraction of RA patients remains non-responsive to currently available anti-cytokine therapies, there is growing interest in identifying novel therapeutic targets which could suppress inflammatory cytokine production, such as HDACi. Pharmacological inhibition of HDAC activity has shown anti-inflammatory effects in animal arthritis models, and RA patient synovial macrophages and tissue explants. Here, we show that HDACi reduce RA FLS IL-6 production induced by cytokines and TLR ligands, and identify modulation of IL-6 mRNA stability as a primary molecular mechanism contributing to this effect in both FLS and macrophages.

RA FLS treatment with HDACi, as previously observed with RA synovial macrophages, rapidly induced acetylation of both histone and non-histone proteins, raising the possibility that HDACi-induced expression of transcription co-repressors might explain the suppressive effects of HDACi on IL-6 production. However, treatment of cells with CHX, to prevent translation of putative repressors, failed to rescue IL-6 production in the presence of HDACi. Consistent with this, even though HDACi induce H4 hyperacetylation in the IL-6 promoter region in murine bone marrow-derived macrophages, IL-6 production is downregulated, arguing against involvement of changes in histone acetylation status in HDACi regulation of IL-6. Surprisingly, we also found little evidence supporting a role for HDACi in modulating acute signal transduction events downstream of IL-1β stimulation. Previous reports have indicated that HDACi might regulate inflammatory gene expression via blockade of MAP kinase signalling, suppression of c-Jun induction and activation, or reduction of NF-κB nuclear retention. In murine macrophages, HDACi treatment causes acetylation and activation of MAP kinase phosphatase-1 which prevents p38 phosphorylation, ultimately leading to inhibition of TLR signalling. However, we observed no effect of TSA on IL-1β-induced activation of p38, ERK, and JNK MAP kinases, c-Jun gene induction, or DNA binding activity of Jun family members. Our negative results highlight the difficulties of extrapolating effects of HDACi in various cell types to primary cells from RA synovial tissue in the absence of formal studies.

NF-κB signalling is complexly regulated by reversible acetylation, as p65 can be acetylated on at least 5 unique lysine residues, each having a distinct effect on p65 function. Acetylation at Lys221 promotes p65 dissociation from IκBα and nuclear import, while acetylation at 310...
enhances p65 transcriptional activity. Alternatively, p65 acetylation at Lys122 and Lys123 decreases DNA binding affinity, enhances IκBα association, and promotes nuclear export. We observe a similarly complex regulation in RA FLS, as p65 nuclear import, DNA binding activity, and transcriptional capacity are all enhanced by HDACi in the initial hours following IL-1β stimulation. However, HDACi promote dissociation from DNA and nuclear export at later time points, consistent with recent observations in an SV40 Tag-transformed RA FLS cell line. The changes we observe in NF-κB activity are consistent with temporal acetylation of NF-κB at distinct regulatory sites, but direct studies are needed to address this possibility. However, the kinetics of alterations in NF-κB activity can not explain the acute suppression of IL-1β-induced IL-6 production by HDACi, but may confer a protective effect in the face of chronic inflammatory stimulation.

While many of the HDACi effects on cellular activation have been attributed to epigenetic regulation or influences on signal transduction, studies in cancer biology have provided initial evidence that these compounds can modulate gene expression via regulation of mRNA stability. We observe a similar and shared mechanism of action in the suppression of IL-6 production in macrophages and RA FLS. mRNA stability is regulated by hundreds of gene products, some of which have been identified as functionally associated with HDACs. Selectivity is also observed in mRNAs targeted by these proteins as, for example, Zc3h12 RNAse specifically regulates IL-6 mRNA stability. Alternatively, as observed in cancer biology studies, HDACi might differentially modulate microRNA (miR) expression. IL-6-specific miRs have yet to be identified, but the expression of several miRs associated with inflammatory responses is altered in RA FLS and synovial tissue. Future studies will be needed to elucidate how HDACi enhance IL-6 mRNA degradation, and test how globally this mechanism regulates gene expression in RA synovial tissue. Preliminary experiments indicate that HDACi might also regulate FLS production of IL-8 and MMP-1 without affecting mRNA stability (our unpublished observation), indicating additional mechanisms by which HDACi modulate gene expression in RA FLS. Intriguingly, HDACi can accelerate decay of DNA methyltransferase -3B mRNA in human endometrial cells, raising the possibility that HDAC-dependent mRNA destabilization might regulate inflammatory gene expression through cross-talk with epigenetic DNA methylation pathways. Results presented here provide the first mechanistic evidence by which HDACi might suppress inflammatory cytokine production in RA, and, together with the initial proof of principle that has recently been obtained in SOJIA, support the notion that HDACi may represent a novel therapeutic approach for the treatment of RA.

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REFERENCES


Supplemental table 1. Clinical features of RA patients (N = 18) included in the study*

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<td>57.5 (48-80)</td>
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<tr>
<td>Male: Female</td>
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<tr>
<td>Disease duration [months]</td>
<td>84 (1-348)</td>
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<tr>
<td>ESR [mm/hour]</td>
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<tr>
<td>CRP [mg/l]</td>
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<td>DAS28</td>
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*ESR = erythrocyte sedimentation rate; CRP = C-reactive protein; DAS28 = disease activity score

SUPPLEMENTARY MATERIAL AND METHODS

Protein extraction and immunoblotting. FLS were lysed in 1x Laemmli’s buffer or FLS nuclear fractions were extracted using a Nuclear Extraction Kit (Active Motif, Carlsbad, CA) and protein content quantitated with a BCA Protein Assay Kit (Pierce, Rockford, IL). Equivalent amounts of lysate or nuclear extract were resolved by electrophoresis and analyzed by immunoblotting using primary antibodies recognizing acetylated lysine, acetylated histone 3 (H3), acetylated histone 4 (H4), H3, phospho (p)-IκBα, p-p38, p-ERK, p-JNK, p38, ERK (all from Cell Signaling Technology, Beverly, MA), H4 (Upstate, Temecula, CA), NF-κB p65 and p50 (both from Santa Cruz Biotechnology, Santa Cruz, CA), and tubulin (Sigma-Aldrich), followed by development with IRDye-680-labelled anti-rabbit or IRDye-800-labelled anti-mouse immunoglobulin secondary antibodies (LI-COR Biosciences, Bad Homburg, Germany) and visualization using an Odyssey infrared imaging system (LI-COR Biosciences).

Quantitative measurement of mRNA expression. FLS were left unstimulated or were stimulated for 1-8 h with IL-1β in the presence or absence of TSA. Alternatively, cells were treated with IL-1β for 4 h with or without TSA and cycloheximide (CHX) (Sigma-Aldrich). Total RNA was extracted using a GenElute RNA isolation kit (Sigma-Aldrich) and reverse transcribed using a First-Strand cDNA synthesis kit (Fermentas, Vilnius, Lithuania). Quantitative (q)PCR was performed on a StepOne Plus Real-Time PCR System (Applied Biosystems, Foster City, CA) using Power SybrGreen PCR Master Mix (Applied Biosystems) and the following primers: IL-6 forward, GACAGCCACTCACCTTTCA; IL-6 reverse, CCTCTTTGCTGTTCACAC; c-Jun forward, GGAAGCTGGAGAGAATCGCC; c-Jun reverse, TTCTGTTTAAGCTGTGCCACCTG; 18S forward, CCGCTACCACATCCCAAGGA; 18S reverse, GCTGGAATTACCGCGGCT (Invitrogen). For measurement of mRNA stability, FLS or macrophages were incubated in medium alone or IL-1β or LPS, respectively, for 4 h in the presence or absence of TSA. Culture medium was replaced with medium containing 10 μg/ml actinomycin D (ActD, Sigma-Aldrich), and RNA isolated at 0, 1, 2, 4 and 20 h following ActD exposure. qPCR reactions were performed in duplicate. Specific PCR product amplification was confirmed by dissociation curve analysis for each primer pair. Relative gene expression was calculated using StepOne Software v2.1 (Applied Biosystems) and expressed as the ratio between the gene of interest and 18S.
Measurement of NF-κB transcripational activity in RA FLS. Adenoviral 4xNF-κB-MLP-luciferase (Luc) reporter vector was generated using previously described methodologies. A 4xNF-κB enhancer was excised from a 4xNF-κB-TK-SEAP plasmid (Clontech/BD Biosciences) and cloned into pGL3-MLP-Luc in front of a major late adenoviral minimal promoter (MLP). Next, a cassette containing an artificial polyA track, 4xNF-κB enhancer, MLP promoter, Luc ORF and a polyA signal was re-cloned into pShuttle vector and recombined with an Easy-1 adenoviral backbone in BJ1583 bacteria. The linearized cosmid was transfected into HEK-293 cells and amplified as an adenovirus. Adenoviruses encoding 4xNF-κB-MLP-Luc and control CMV-β-galactosidase (β-Gal) were amplified and titrated in transcomplemental HEK-293 cells and purified by cesium chloride gradient ultracentrifugation. FLS were co-transduced with 4xNF-κB-MLP-Luc and CMV-β-Gal at a multiplicity of infection of 300 and 30, respectively. 48 hours after transduction, cells were serum starved for 24 hours and then left unstimulated or stimulated with IL-1β in the presence or absence of TSA for 2-8 hours. Cells were lysed in 1x Passive Lysis Buffer (Promega, Madison, WI). Luc activity was measured with a Luciferase Assay reagent (Promega) using a Victor3 Multilabel Reader (Perkin Elmer, Norwalk, CT). β-Gal activity, measured at OD_{405} in 100 mM Na_{2}HPO_{4}/NaH_{2}PO_{4}, 1 mM MgCl_{2}, 100 mM β-mercaptoethanol, and 0.67 mg/ml O-nitrophenyl-β-D-galactopyranoside, was used to correct for transduction efficiency.