

MT1-MMP expression level status dictates the *in vitro* action of lupeol on inflammatory biomarkers MMP-9 and COX-2 in medulloblastoma cells

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Abstract Local inflammation-induced extracellular matrix structural changes are a prerequisite to neoplastic invasion by pediatric intracranial tumors. Accordingly, increased expression of matrix metalloproteinases MMP-2 and MMP-9, two inflammation-induced matrix metalloproteinases (MMPs), may further aid the transformed cells either to infiltrate adjacent tissues or to enter the peripheral circulation. In the context of neuroinflammation, MMP-9 has been linked to processes such as blood–brain barrier opening and invasion of neural tissue by blood-derived immune cells. Given its reported anti-inflammatory and anticancer properties, we investigated the *in vitro* pharmacological effects of lupeol, a diet-derived triterpenoid, on MMP-9 and cyclooxygenase (COX)-2 expressions in a pediatric medulloblastoma DAOY cell line model. Lupeol was unable to inhibit the increased MMP-9 and COX-2 expression in phorbol 12-myristate 13-acetate (PMA)-treated cells, but was rather found to synergize with PMA to induce both biomarkers' expression. A contribution of the membrane type-1 (MT1)-MMP was also revealed, since lupeol/PMA treatments triggered proMMP-2 activation, and that MT1-MMP gene silencing reversed

the combined effects of lupeol/PMA on both MMP-9 and COX-2. The mRNA stabilizing factor HuR was also found increased in the combined lupeol/PMA treatment, suggesting stabilization processes of the MMP-9 and COX-2 transcripts. We postulate that lupeol's anti-inflammatory properties may exert better pharmacological action within low MT1-MMP expressing tumors. Furthermore, these evidences add up to the new pleiotropic molecular mechanisms of action of MT1-MMP, and prompt for evaluating the future *in vitro* pharmacological properties of lupeol under pro-inflammatory experimental set-up.

Keywords Medulloblastoma · MMP-9 · MT1-MMP · NF- κ B · COX-2 · Lupeol

Abbreviations

COX	Cyclooxygenase
IL	Interleukin
MMP	Matrix metalloproteinase
MT1-MMP	Membrane type-1 MMP
NF- κ B	Nuclear factor kappa B
PMA	Phorbol 12-myristate 13-acetate
PGE	Prostaglandin E

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Introduction

The strong association assumed between inflammation and tumor progression has raised interest in the anti-inflammatory and chemopreventive properties of dietary phytochemicals (Béliveau and Gingras 2007; Wang et al. 2011). Accordingly, lupeol, a phytosterol and triterpene widely found in edible fruits and vegetables has been ascribed pleiotropic pharmacological activities that include anti-inflammatory, antimicrobial, antiprotozoal, antiproliferative, anti-invasive,

and antiangiogenic capacity (Moreau et al. 2002; Saleem 2009). Evidence has also been provided that lupeol modulates the expression or activity of several contributors to inflammation such as cytokines IL2, IL4, IL5, IL β , proteases, α -glucosidase, cFLIP, Bcl-2 and NF- κ B (Siddique and Saleem 2011). Given the complexity of carcinogenic processes and the fact that microenvironment dictates the acquisition of a tumor invasive and inflammatory phenotype, the wide spectrum of molecular mechanisms of action that characterize the pharmacological activity of lupeol may possibly be envisioned in the optimization and development of therapeutic modalities. The specific combined anti-inflammatory and chemopreventive activities of lupeol within pro-inflammatory *in vitro* conditions have however been poorly investigated.

Medulloblastoma is the most common and one of the most deadly malignant brain tumors of infancy (Packer 2007; Kanu et al. 2009). In addition to high tumor resistance to ionizing radiation and to chemotherapy, proximity of medulloblastomas to cerebrospinal fluid greatly enhances metastasis rate in the central nervous system (Bao et al. 2006; Mazloom et al. 2010). As part of our continuous effort to understand the molecular links between inflammation and tumorigenesis, we recently demonstrated that tumor microenvironment dictated the acquisition of an invasive phenotype in medulloblastoma cancer stem cells (Annabi et al. 2008). Such phenotype was in part linked to increased expression of MMP-9 and MT1-MMP, two MMPs involved in inflammation, angiogenesis, as well as cancer cell migration and metastasis (Chambers and Matrisian 1997; Amalinei et al. 2010). More importantly, a fundamental new role of MT1-MMP, besides its classical role in proMMP-2 activation, was later demonstrated in bioactive lysophospholipid signaling (Annabi et al. 2009), NF- κ B-mediated cyclooxygenase (COX)-2 regulation (Han et al. 2001; Annabi et al. 2009b; Sina et al. 2010), and as a cell death sensor/effector (Belkaid et al. 2007; Currie et al. 2007; Proulx-Bonneau et al. 2011). Furthermore, while involvement of COX-2/PGE₂ pathway in the upregulation of MMP-9 was demonstrated in pancreatic cancer (Bu et al. 2011), specific pharmacological targeting of NF- κ B was found to efficiently downregulate carcinogen-induced MMP-9 and COX-2 expression in brain endothelial cell as well as in medulloblastoma cell models (Annabi et al. 2010; Tahanian et al. 2011a).

Using a pediatric medulloblastoma-derived DAOY cell line model, we now assessed lupeol's multi-targeted capacity to temper pro-inflammatory stimulation, as induced upon phorbol 12-myristate 13-acetate-activated (PMA) treatment, on MMP-9 secretion and on COX-2 expression. MT1-MMP contribution was also evaluated in the transduction pathways modulated by the concerted action of lupeol/PMA.

Materials and methods

Materials

Sodium dodecylsulfate (SDS) and bovine serum albumin (BSA) were purchased from Sigma (Oakville, ON). Electrophoresis reagents were purchased from Bio-Rad (Mississauga, ON). The enhanced chemiluminescence (ECL) reagents were from Perkin Elmer (Waltham, MA). Micro bicinchoninic acid protein assay reagents were from Pierce (Rockford, IL). Lupeol was from Extrasynthese (Lyon, France) and reconstituted in ethanol as per the manufacturer's recommendation. The polyclonal antibody against MT1-MMP (AB815) was from Chemicon (Temecula, CA). The polyclonal antibody against I κ B α C-terminus was purchased from Cell Signaling (Danvers, MA). The polyclonal antibody against HuR was from Santa Cruz Biotechnology (Santa Cruz, CA). The polyclonal antibody against COX-2 and monoclonal antibody against GAPDH were from Advanced Immunochemical Inc. (Long Beach, CA). Horseradish peroxidase-conjugated donkey anti-rabbit and anti-mouse IgG secondary antibodies were from Jackson ImmunoResearch Laboratories (West Grove, PA). All other reagents were from Sigma-Aldrich, Canada.

Cell culture

The human DAOY medulloblastoma cell line was purchased from American Type Culture Collection and was maintained in Eagle's Minimum Essential Medium containing 10 % (v/v) calf serum (HyClone Laboratories, Logan, UT), 2 mM glutamine, 100 U/ml penicillin and 100 mg/ml streptomycin. Cells were incubated at 37 °C, with 95 % air and 5 % CO₂. Treatment was done in X-Vivo 15 from Lonza (Walkersville, MD) containing 20 ng/mL of basic fibroblast growth factor, 20 ng/mL of epidermal growth factor from Wisent (St-Bruno, QC), 20 ng/mL of leukemia-inhibitory factor from Sigma-Aldrich Canada and neural survival factor-1 also from Lonza.

cDNA synthesis and real-time quantitative RT-PCR

Total RNA was extracted from DAOY-derived cell monolayers using TriZol reagent (Life Technologies, Gaithersburg, MD). For cDNA synthesis, 2 μ g of total RNA was reverse transcribed using a high capacity cDNA reverse transcription kit (Applied Biosystems, Foster City, CA). cDNA was stored at -80 °C prior to PCR. Gene expression was quantified by real-time quantitative PCR using iQ SYBR Green Supermix (Bio-Rad, Hercules, CA). DNA amplification was carried out using an Icyler iQ5 (Bio-Rad), and product detection was performed by measuring binding of the fluorescent dye SYBR Green I to

double-stranded DNA. GAPDH primer sets were synthesized by Biocorp (Dollard-des-Ormeaux, QC) with the following sequences: forward CCATCA-CCATCTTC-CAGGAG and reverse CCTGCTTCACCACCTTCTTG. The following QuantiTect primer sets were provided by Qiagen (Valencia, CA): MMP-9 (QT00040040), COX-2 (QT00040586), MT1-MMP (QT00001533), HuR (QT00001533), and β -actin (QT01136772). The relative quantities of target gene mRNA compared against two internal controls, GAPDH and β -actin mRNA, were measured by following a ΔC_T method employing an amplification plot (fluorescence signal vs. cycle number). The difference (ΔC_T) between the mean values in the triplicate samples of target gene and those of GAPDH and β -actin mRNAs was calculated by iQ5 Optical System Software (v 2.0; Bio-Rad), and the relative quantified value was expressed as $2^{-\Delta C_T}$.

Transfection method and RNA interference

Cells were transiently transfected with 20 nM siRNA (Qiagen) against MT1-MMP (Hs_MMP14_6 FlexiTube siRNA, SI03648841) or scrambled sequences (AllStar Negative Control siRNA, 1027281) using Lipofectamine 2000 (Invitrogen, ON). Specific gene knockdown was evaluated by qRT-PCR as described above. Small interfering RNA and mismatch siRNA were synthesized by Qiagen (Valencia, CA) and annealed to form duplexes.

Gelatin zymography

Gelatin zymography was used to assess the extent of proMMP-9 activity as previously described (Belkaid et al. 2007). Briefly, an aliquot (20 μ l) of the culture medium was subjected to SDS-PAGE in a gel containing 0.1 mg/ml gelatin. The gels were then incubated in 2.5 % Triton X-100 and rinsed in nanopure distilled H₂O. Gels were further incubated at 37 °C for 20 h in 20 mM NaCl, 5 mM CaCl₂, 0.02 % Brij-35, 50 mM Tris-HCl buffer, pH 7.6, then stained with 0.1 % Coomassie Brilliant blue R-250 and destained in 10 % acetic acid, 30 % methanol in H₂O. Gelatinolytic activity was detected as unstained bands on a blue background.

Immunoblotting procedures

Proteins from control and treated cells were separated by SDS-polyacrylamide gel electrophoresis (PAGE). After electrophoresis, proteins were electrotransferred to polyvinylidene difluoride membranes which were then blocked for 1 h at room temperature with 5 % non-fat dry milk in Tris-buffered saline (150 mM NaCl, 20 mM Tris-HCl, pH

7.5) containing 0.3 % Tween-20 (TBST). Membranes were further washed in TBST and incubated with the primary antibodies (1/1,000 dilution) in TBST containing 3 % bovine serum albumin, followed by a 1 h incubation with horseradish peroxidase-conjugated anti-rabbit or anti-mouse IgG (1/2,500 dilution) in TBST containing 5 % non-fat dry milk. Immunoreactive material was visualized by enhanced chemiluminescence (Amersham Biosciences, Baie d'Urfé, QC).

Statistical data analysis

Data are representative of three independent experiments. Statistical significance was assessed using Student's unpaired *t* test. Probability values of less than 0.05 were considered significant and an asterisk identifies such significance in the figures.

Results

COX-2 expression is increased upon lupeol/PMA synergistic actions through an NF- κ B signaling pathway

We first wished to assess lupeol's actions within a pro-inflammatory *in vitro* environment (Annabi et al. 2010; Tahanian et al. 2011b). This was generated by the use of 1 μ M PMA stimulation of serum-starved medulloblastoma-derived DAOY cells in the presence of various concentrations of lupeol for 18 h. As expected, we found that COX-2 expression was significantly increased upon PMA treatment (Fig. 1a, upper panel), and this required NF- κ B signaling since I κ B levels decreased (Fig. 1a, middle panel). Unexpectedly, when increasing concentrations of lupeol were concomitantly added COX-2 levels further synergistically increased inversely correlating with a parallel decrease in I κ B expression (Fig. 1b). These results suggest new unreported effects of lupeol within pro-inflammatory culture conditions.

Concomitant increases in proMMP-9 secretion and proMMP-2 activation upon synergistic actions of lupeol/PMA

PMA is also well documented to induce MMPs secretion and/or activation processes (Ou et al. 2011; Tahanian et al. 2011b). We therefore harvested the conditioned media from above described conditions and used zymography to monitor both MMP-9 and MMP-2 gelatinolytic activities (Fig. 2a). We found that PMA alone significantly induced proMMP-9 secretion (Fig. 2b) and partially triggered latent

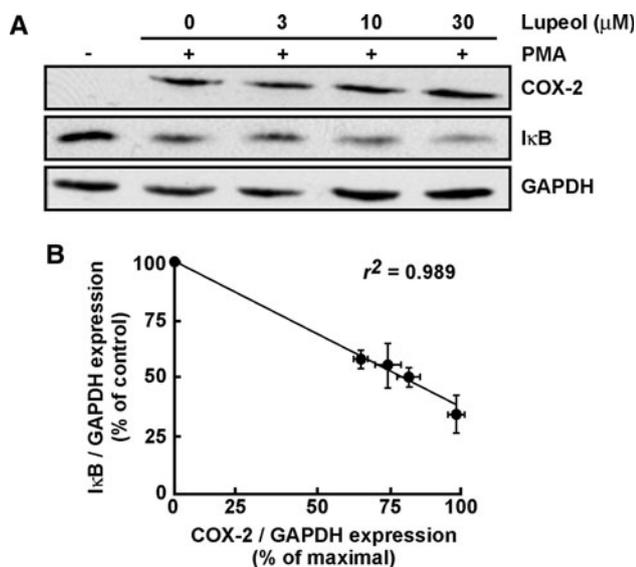


Fig. 1 COX-2 and MMP-9 expressions are increased upon synergistic actions of lupeol and PMA. DAOY cells were serum starved in the presence of various concentrations of lupeol in combination with vehicle (1 % ethanol) or 1 μ M PMA for 18 h. **a** Lysates were isolated, electrophoresed via SDS-PAGE and immunodetection of COX-2, I κ B and GAPDH proteins performed as described in the “Methods” section. **b** Quantification was performed by scanning densitometry of the respective autoradiograms from three independently performed experiments, data normalized on GAPDH, and correlation between I κ B and COX-2 expression represented

proMMP-2 processing into active MMP-2 (Fig. 2c). Again, addition of increasing concentrations of lupeol in the presence of PMA not only potentiated proMMP-9 secretion, but further triggered proMMP-2 activation. Collectively, this data add up to the pleiotropic targets of joint lupeol/PMA treatments, and further highlight potential new mechanisms possibly involving MT1-MMP in proMMP-2 activation and some mechanisms supporting proMMP-9 expression.

The synergistic lupeol/PMA effects require MT1-MMP

MT1-MMP signaling axis involvement in inflammation has been reported both directly (Sakamoto and Seiki 2009; Sina et al. 2010) and indirectly (Annabi et al. 2009b; Paquette et al. 2011). Here, in order to assess the joint contribution of lupeol/PMA treatment on COX-2 expression and on MMP-9 secretion, we used gene silencing strategies and transiently transfected DAOY cells with either scrambled (siScrambled) or MT1-MMP (siMT1-MMP) specific siRNA. Subsequent treatments were performed with lupeol, PMA, or lupeol/PMA as described above. MT1-MMP knockdown was confirmed at the protein level (Fig. 3a, upper panel). Consequently, the observed increases in COX-2 (Fig. 3b) and in

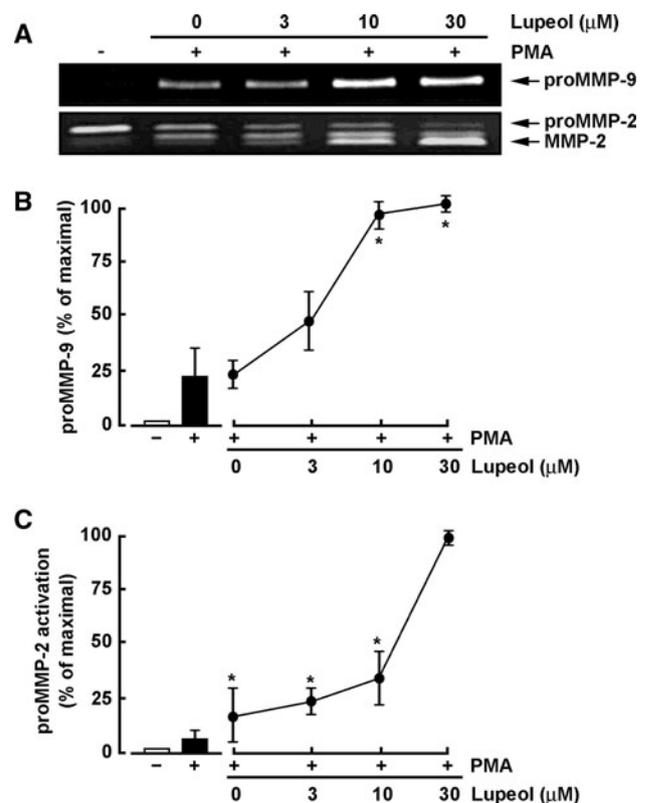


Fig. 2 Concomitant proMMP-9 secretion and proMMP-2 activation are increased upon synergistic actions of lupeol and PMA. DAOY cells were serum starved in the presence of various concentrations of lupeol in combination with vehicle or 1 μ M PMA for 18 h. **a** Gelatin zymography was performed with the respective conditioned media to assess the extent of proMMP-9, proMMP-2, and MMP-2 activities. Scanning densitometry of the zymogram was performed to quantify the extent of proMMP-9 secretion (**b** probability values of less than 0.05 were considered significant and an *asterisk* identifies such significance with reference to PMA-treated cells), or the extent of proMMP-2 activation (**c** MMP-2/proMMP-2; probability values of less than 0.05 were considered significant and an *asterisk* identifies such significance with reference to PMA/30 μ M lupeol-treated cells). Data are from four independently performed experiments

MMP-9 (Fig. 3d) levels upon PMA or lupeol/PMA were all reduced without affecting GAPDH expression. Interestingly, significant reversal in the I κ B expression was observed (Fig. 3c) and supports the MT1-MMP/NF- κ B signaling axis as previously reported (Annabi et al. 2009b). In addition to the MT1-MMP contribution in the synergistic action of lupeol/PMA on COX-2 and MMP-9, we also found increased expression of HuR which was revealed upon lupeol/PMA treatment (Fig. 3e) supporting a potential contribution to the 3'-UTR stabilization of MMP-9 mRNA (Annabi et al. 2008, 2009c). Consequently, whether any transcriptional regulation of COX-2, MMP-9 and of HuR occurs upon lupeol/PMA was next investigated.

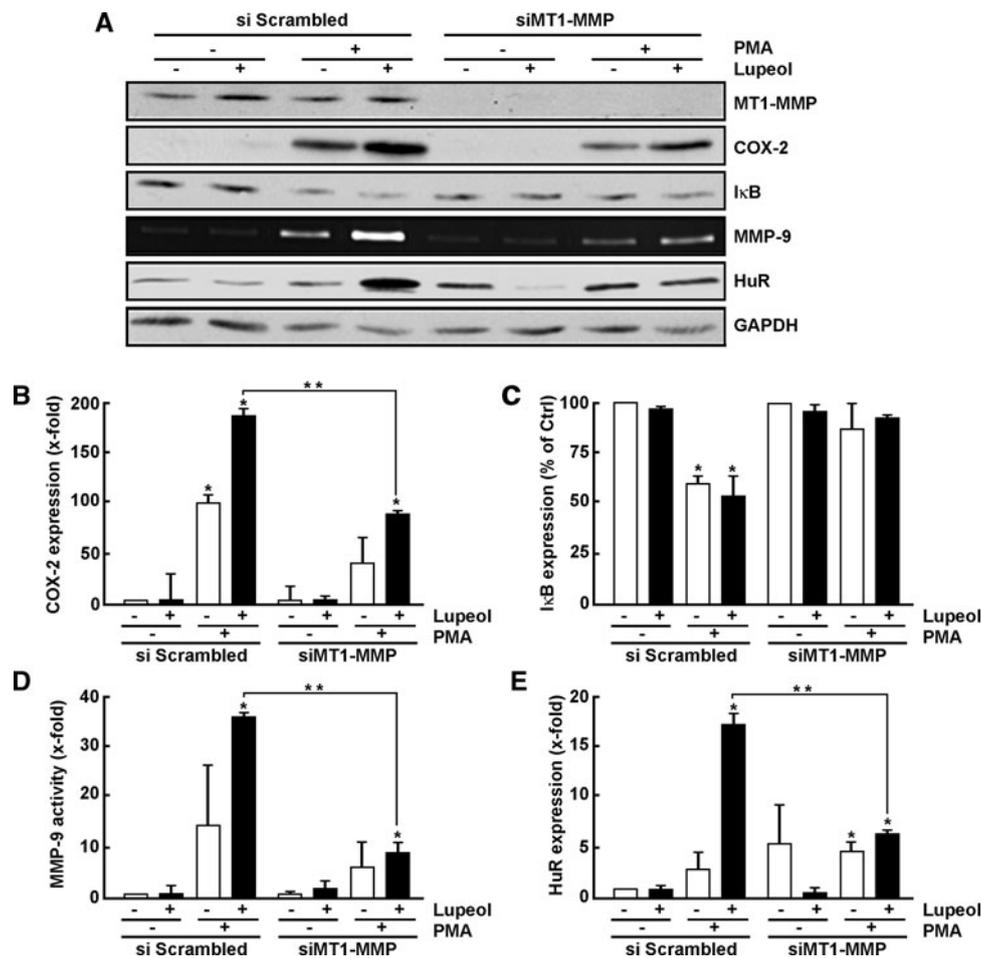


Fig. 3 The synergistic lupeol/PMA effects require MT1-MMP. DAOY cells were transfected with scrambled (siScrambled) siRNA sequences or with siMT1-MMP as described in the “Methods” section. The cells were then serum starved in the presence of 1 μM PMA and/or 30 μM lupeol for 18 h. **a** Lysates were isolated, electrophoresed via SDS-PAGE and immunodetection performed as described in the “Methods” section. Gelatin zymography also was used to assess the extent of proMMP-9 secretion in the conditioned

media. Scanning densitometry was used to quantify the autoradiograms for **b** COX-2, **c** IκB, **d** proMMP-9, and **e** HuR respective expression. Densitometric values are mean of two independent experiments. Probability values of less than 0.05 were considered significant and an *asterisk* identifies such significance with reference to untreated cells. A *double asterisk* also indicates such significant probability between siScrambled and siMT1-MMP cells treated with combined PMA/lupeol

MT1-MMP is required for the transcriptional regulation of COX-2 and MMP-9 upon synergistic actions of lupeol and PMA

Total RNA was extracted from the above siScrambled- or siMT1-MMP-transfected and treated DAOY cells. RT-PCR followed by qPCR enabled to assess transcriptional regulation of COX-2, MMP-9, and of HuR as described in the “Methods” section. Efficient MT1-MMP gene silencing was confirmed and small induction by PMA or lupeol/PMA observed (Fig. 4a) confirming the proMMP-2 activation previously observed by zymography. COX-2 gene expression was also induced by PMA and potentiated upon lupeol/PMA treatment (Fig. 4b). MT1-MMP gene silencing, however, did not significantly downregulate PMA or lupeol/PMA-induced COX-2 gene expression. In contrast,

MMP-9 gene expression was also induced by PMA or lupeol/PMA, but MT1-MMP gene silencing resulted in decreased MMP-9 gene expression (Fig. 4c). When HuR gene expression levels were assessed, they remained relatively unchanged independent of the treatment (Fig. 4d). Collectively, we provide evidence for post-transcriptional events that regulate MT1-MMP-mediated regulation of HuR that would, in turn, regulate MMP-9 transcript stabilization leading to increased MMP-9 expression in lupeol/PMA-treated cells.

Discussion

Pharmacological effects of lupeol have been reported within inflammation-associated signaling conditions involved

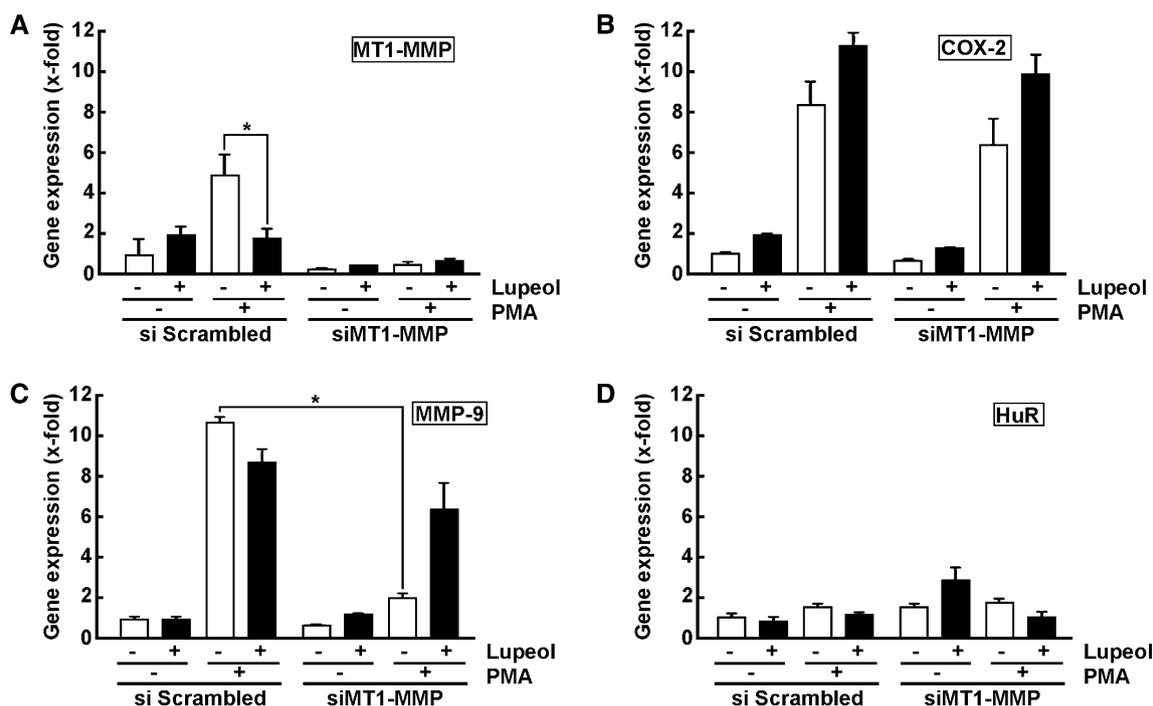


Fig. 4 MT1-MMP is required for the transcriptional regulation of COX-2 and MMP-9 upon synergistic actions of lupeol and PMA. DAOY cells were transfected with scrambled (siScrambled) siRNA sequences or with siMT1-MMP as described in the “Methods” section. The cells were then serum starved in the presence of 1 μ M PMA and/or 30 μ M lupeol for 18 h. Total RNA was extracted and

transcribed into cDNA as described in the “Methods” section. qPCR was then performed in order to assess gene expression levels of MT1-MMP (a), COX-2 (b), MMP-9 (c), and HuR (d). Values are mean of two independent experiments assessed in triplicate. Probability values of less than 0.05 were considered significant and an *asterisk* identifies such significance

in wound healing, diabetes, cardiovascular disease, kidney disease, and arthritis (Geetha and Varalakshmi 1999; Sudhakar et al. 2006, 2007; Papi Reddy et al. 2009). Some of lupeol’s anti-inflammatory properties arise, in fact, from its capacity to abrogate synthesis of pro-inflammatory mediators (Fernandez et al. 2001), and to interfere with several signaling pathways such as NF- κ B, MAPK, Ras, Wnt and PI3 K/Akt (Saleem et al. 2004, 2005; Tarapore et al. 2010). Given that deregulation of these signaling pathways is often associated with carcinogenesis, various *in vitro* and *in vivo* models have further inferred lupeol to exhibit anti-cancer properties (Saleem 2009). While the sum of the multi-targeted effects of such a pharmacological agent is expected to impact on a variety of intracellular biomarkers expression, its intrinsic mechanism of action however remains poorly assessed within *in vitro* pro-inflammatory stimulation conditions.

In this study, we highlight an unexpected mechanism of action of lupeol in synergy with PMA-mediated inflammatory signaling such as one would expect to occur within a given tumor microenvironment. Synergistic induction of MMP-9 and of COX-2, two preeminent mediators of inflammation in pathological conditions, upon combined lupeol/PMA treatment is shown to require a crucial balance in MT1-MMP expression levels. MT1-MMP contribution

to such signaling events was first inferred through its extracellular functions involved in proMMP-2 activation into MMP-2 (Fig. 2). Accordingly, lowering of MT1-MMP-mediated intracellular signaling through gene silencing strategies abrogated MMP-9 and COX-2 increases. We hypothesize that lupeol may exacerbate MT1-MMP-mediated NF- κ B signaling under pro-inflammatory stimulation and within highly MT1-MMP expressing tumor cells, while anti-inflammatory actions within normal-to-low MT1-MMP expressing tumor cells may classically elicit lupeol’s pharmacological effects in lowering inflammation biomarkers (Fig. 5).

Accordingly, we also highlight specific, yet not fully elucidated, transcriptional regulation properties of lupeol against MT1-MMP since lupeol did not affect neither of PMA-induced COX-2 nor MMP-9 gene expression. Interestingly, while attenuation of MT1-MMP expression was reported to decrease TGF- β 1-mediated MMP-9 expression, we further report that similar transcriptional regulation may possibly also occur in PMA-treated MT1-MMP-invalidated cells. Altogether, this evidence confirms the requirement of some MT1-MMP signaling axis in MMP-9 expression regulation. Evidence that MT1-MMP activates a number of intracellular signal pathways including the extracellular signal-related kinase (ERK) pathway, the focal adhesion

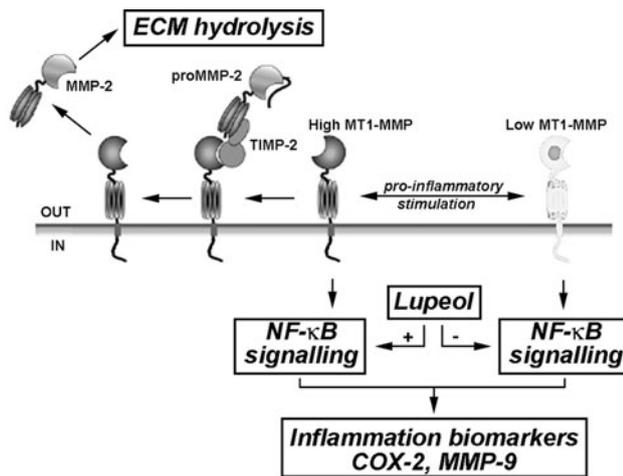


Fig. 5 MT1-MMP expression levels regulate lupeol's pharmacological actions. Pro-inflammatory stimulation (such as with PMA) triggers NF- κ B signaling within high or normal-to-low MT1-MMP expressing cells. While pro-inflammatory stimulation also elicits MT1-MMP-mediated proMMP-2 activation that leads to extracellular matrix (ECM) hydrolysis and cell invasion, lupeol may exert a dual role as it is found to exacerbate (*plus symbol*) MT1-MMP signaling that leads to increased expression of inflammation biomarkers. In contrast, lupeol may inhibit (*minus symbol*) NF- κ B signaling in low MT1-MMP expressing cells

kinase (FAK), Src, RhoA/ROK, Rac and NF- κ B pathways has been reported (Takino et al. 2004; Annabi et al. 2005; Sato et al. 2005; Sounni and Noel 2005; Annabi et al. 2009). Although not statistically significant, MMP-9 gene expression was also slightly abrogated by lupeol in those PMA-treated MT1-MMP-invalidated cells. Thereof, such unusual signaling contribution of MT1-MMP included a role in PGE₂-induced angiogenesis (Alfranca et al. 2008), platelet-mediated calcium mobilization (Fortier et al. 2008), regulation of cell death/survival bioswitch (Belkaid et al. 2007; Fortier et al. 2008), and radioresistance in both glioma cells (Wild-Bode et al. 2001; Wick et al. 2002) and endothelial cells (Annabi et al. 2003). In addition to signal transduction, some cellular contribution was also ascribed to MT1-MMP through the recent demonstration that it also played a role in medulloblastoma CD133(+) neurosphere-like formation and increased invasiveness (Annabi et al. 2009). Paradoxical molecular and cellular impact of MT1-MMP reinforces the concept of assessing the pharmacological properties of a given agent on alternative pathways. Recent COX inhibitors, for instance, have been shown to rather directly alter gene and protein expression of specific targets involved in tumorigenesis and inflammation (Wang et al. 2011).

Pharmacological targeting of NF- κ B-mediated MMP-9 expression was recently reported by us in DAOY medulloblastoma-derived cells and in human brain microvascular

endothelial cells (Annabi et al. 2008b, 2009c, 2010). In the current study, we now demonstrate that MT1-MMP-mediated signaling, in part, contributes to the transcriptional regulation of MMP-9 expression upon lupeol/PMA stimulation, and that this possibly involved stabilization of the 3'UTR site of the MMP-9 transcript by the ELAV-like protein HuR. Insufficient HuR-mediated transcript stabilization may ultimately result in the rapid degradation of the MMP-9 transcript (Fan and Steitz 1998). Moreover, it should be acquainted that HuR synthesis is, in part, regulated by NF- κ B signaling (Kang et al. 2008), further supporting that HuR downregulated expression upon silencing of the MT1-MMP-mediated signaling axis may significantly impact on its contribution to MMP-9 expression. As basal HuR protein levels remained unaffected by lupeol treatment in our MT1-MMP knockout conditions, this experimental evidence confirms that lupeol may bear dual pharmacological actions which can only be revealed under specific in vitro culture conditions that mimic inflammation.

In conclusion, this study is among the first in vitro investigation to report lupeol's mechanism of action under pro-inflammatory stimulation. Aside from its apparent protection against PMA-induced superoxide generation in human neutrophils (Yamashita et al. 2002), we provide new evidence that multiple signaling pathways may be involved in the lupeol regulation of inflammatory biomarkers gene expression such as MMP-2, MMP-9 and COX-2. Intracellular signaling cascades mediated by MT1-MMP, possibly through its intracellular cytoplasmic domain, will remain to be further investigated but seem to play a key role in lupeol's effects under such conditions. Whether similar mechanisms are also involved in the actions of other dietary phytochemicals is currently unknown. Based upon our results, unsuspected and dual pharmacological functions of anti-inflammatory agents may, under specific experimental conditions, possibly exacerbate neoplastic adaptative mechanisms and limit therapeutic efficacy. Given that adult and pediatric intracranial tumors are characterized by increased extravasation and infiltration of lymphocytes into regions of chronic local inflammation, design of alternate and more optimal therapeutic strategies based on targeting microenvironment-mediated chronic inflammation and angiogenesis will be required.

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