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Arnica montana effects on gene expression in a human macrophage cell line. Evaluation by quantitative Real-Time PCR

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ABSTRACT

Background: Arnica montana is a popular traditional remedy widely used in complementary medicine, also for its wound healing properties. Despite its acknowledged action in clinical settings at various doses, the molecular aspects relating to how *A. montana* promotes wound healing remain to be elucidated. To fill this gap, we evaluated the whole plant extract, in a wide range of dilutions, in THP-1 human cells, differentiated into mature macrophages and into an alternative IL-4-activated phenotype involved in tissue remodelling and healing.
Methods: Real-time quantitative Reverse Transcription Polymerase Chain Reaction (PCR) analysis was used to study the changes in the expression of a customized panel of key genes, mainly cytokines, receptors and transcription factors.
Results: On macrophages differentiated towards the wound healing phenotype, *A. montana* affected the expression of several genes. In particular CXC chemokine ligand 1 (CXCL1), coding for an chief chemokine, exhibited the most consistent increase of expression, while also CXC chemokine ligand 2 (CXCL2), Interleukin8 (IL8) and bone morphogenetic protein (BMP2) were slightly up-regulated, suggesting a positive influence of *A. montana* on neutrophil recruitment and on angiogenesis. MMP1, coding for a metalloproteinase capable of cleaving extracellular matrix substrates, was down-regulated. Most results showed non-linearity of the dose-effect relationship.
Conclusions: This exploratory study provides new insights into the cellular and molecular mechanisms of action of *A. montana* as a promoter of healing, since some of the genes it modifies are key regulators of tissue remodelling, inflammation and chemotaxis.

INTRODUCTION

Arnica montana L. (*Arnica m.*) is a herbaceous perennial plant belonging to the *Asteraceae* family, native to the temperate region of Europe and widely distributed in mountainous areas. It is a popular traditional remedy widely used in complementary medicine to treat various pathological conditions such as contusion, swelling associated with trauma, pain, inflammation, wounds and post-operative clinical conditions.[1-3] However, the evidence of its clinical efficacy is subject to debate.[4-6] A recent systematic review of herbal remedies for treating osteoarthritis concluded that topical *Arnica m.* gel probably improves pain and function in this common condition.[7] There is some experimental evidence, in laboratory animals, of an anti-

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inflammatory action of *Arnica m.* administered as crude ethanolic extract[8] or at the 6th centesimal homeopathic dilution (6c).[9,10]

The chemical composition of *Arnica m.* depends on the part of the plant that is used, principally the flowers and roots, and in general the most pharmacologically active compounds are sesquiterpene lactones, thymol derivatives, flavonoids, acid polysaccharides and their glycoconjugates.[11,12] One of the major components of *Arnica m.* with acknowledged biological activity is the sesquiterpene lactone helenalin, known for its anti-inflammatory properties. In a lymphoid cellular model, helenalin was found to inhibit the transcription factor NF-kappaB--a central mediator of human immune response--by the alkylation of p65 subunit (RelA), thus preventing its binding to DNA.[13] However the cited studies did not evaluate the contribution of the whole plant extract, nor did they evaluate the pharmaceutical properties of different doses and formulations employed in medicine,[1,3,14] ranging from crude herbal extract or low dilutions, to high dilutions (homeopathic doses).

In fibroblast-like cells, whole ethanolic extract of *Arnica m.* showed antioxidant activity and a cytoprotective effect against oxidative damage.[15] Defence against oxidative stress was reported in studies where a 30th centesimal dilution (30c) of *Arnica m.,* administered orally to laboratory rats, decreased oxygen consumption of isolated liver mitochondria and protected from oxidative damage caused by lipid peroxidation.[16] Only one paper reported an inhibitory action of *Arnica m.* on nitric oxide and TNF-α production by murine macrophages.[17]

Although the action of *Arnica m.* on wound healing is regarded as a promising therapeutic property of this plant, the current knowledge of the effects of *Arnica m.* in laboratory models of wound healing is scant. A commercial homeopathic complex containing a low dilution (4th decimal, 4x) of *Arnica m.*, *Calendula* and *Hypericum* promoted fibroblast growth in a scratch model of cellular wound closure;[18] *Arnica m.* 3x as a topical gel improved the healing of surgically-induced wounds in Wister rats, but significant differences were noted only when the drug was delivered together with microcurrent application.[19]

Wound healing involves different cell types such as fibroblasts, leukocytes, and monocytes/macrophages, as well as endothelial and epidermal cells which cooperate to restore the damaged tissue through hemostasis, inflammation, angiogenesis and remodelling of the new tissue. The delicate balance between inflammation--with its potentially destructive phases--and tissue repair depends on a number of local and systemic factors and can be pharmacologically influenced. In the early inflammatory phase, a prominent role is played by cytokines derived by epithelial cells and macrophages such as IL-8, IL-1α, IL-1β, IL-6, TNF-α. A pivotal role in immune defence and repair is played by Interleukin-4 (IL-4), whose pleiotropic effects on leukocytes include TH2 differentiation[20] and class switch of naïve B cells to IgE,[21] immunological events that increase antibody defence. On macrophages, IL-4 is essential for 'alternative' polarization, by which these cells take on characteristic properties functional to immune regulation, wound healing and tissue remodelling.[22-24] In the subsequent phase, additional factors are important to healing, including CXC chemokine ligand 1 (CXCL1) and 2 (CXCL2), CC chemokine ligand 2 (CCL2, also known as monocyte chemotactic protein-1, MCP-1), colony-stimulating factors, CC chemokine ligand 3 (CCL3 also known as macrophage inflammatory protien-1 alpha, MIP-lα), vascular endothelial growth factor (VEGF), and others.[25,26] This cascade of events eventually leads to repair and reconstruction of the wounded area, but it needs to be optimally orchestrated, since prolonging the inflammation phase frequently leads to wound impairment.

We formulated the hypothesis that one of the cellular targets of *Arnica m.* action is the macrophage, a key cell in all phases of inflammation and wound healing, and accordingly decided to evaluate--through an *in vitro* model--the action of several dilutions of this plant extract on gene expression of key regulatory factors. We used the THP-1 human cell line, which is a cell line commonly employed to explore the function and regulation of monocytes and

macrophages.[27] These cells resemble primary monocytes, but when treated with low doses of phorbol esters (PMA) differentiate to cells with morphologic and functional features of tissue macrophages, including adhesion, phagocytosis, free-radical production, and release of a number of inflammatory cytokines. Using a cell line has the advantage of assuring a homogeneous genetic background and treatment, greatly reducing the inter-individual variability that is instead present in the cell phenotype of human donors. This uniformity is particularly important when studying the biological function of chemicals at high dilutions.[28-30]

Arnica m. dilutions were tested both on normal PMA-differentiated THP-1 cells (here defined as "Normal Mac") and on PMA-differentiated THP-1 cells that were further differentiated by IL-4 treatment for 24 hours (here defined as "IL-4 Mac"). As suitable molecular markers of drug activity at the cellular level, we analysed by RT-array PCR the gene expression of a series of cytokines, receptors, and transcription factors that are involved in the wound-healing cellular process. We evaluated a customized RT-array PCR panel made of 384 microwells that allowed simultaneous detection of 28 different RNA species plus the housekeeping gene RPLPO, which in preliminary experiments was found to be the most stable in these cells under different experimental conditions. Besides the responses of many chemokines, the expression of some genes involved in NF-kappaB-related signalling pathways was also included in the panel. It has been shown that gene expression of THP-1 cells mimics that of peripheral blood-derived macrophages and represents a good model system for studying NF-kappaB dependent gene expression.[31] Since *Arnica m.* is used at several doses in clinical settings,[3] we explored a wide range of dilutions, from the 2nd centesimal dilution of the mother tincture (2c, i.e. diluted 10^4 times) to the 15c (i.e. diluted 10^{30} times).

Materials and Methods

Materials

The human monocytic leukemia cell line THP-1 was purchased from DSMZ (Germany). Growth media (RPMI 1640) and Ultraglutamine 20 mM solution were purchased from Lonza (Belgium). Foetal bovine serum (FBS), phorbol 12-myristate 13-acetate (PMA), pure ethanol and ultra-pure water (W3500) were purchased from Sigma-Aldrich Co. (St. Louis, MO, USA). Human Interleukin 4 (IL-4) was purchased from Macs-Miltenyi Biotec (Germany). Cell proliferation reagent WST-1 was purchased from Roche Diagnostics GmbH (Germany) and the dye reagent for the Bradford protein assay was purchased from Bio-Rad Laboratories GmbH (Germany). RNeasy Mini kit, RT first strand kit and RT SYBR Green Rox Master Mix were from Qiagen, (CA, USA). The 384 RT-Array custom was made by Sabiosciences (Qiagen Company, CA, USA). *Arnica m.* was produced by Boiron Laboratoires (Lyon, France) according to the French Homeopathic pharmacopoeia and provided as a first centesimal dilution of the whole hydroalcoholic extract (Mother Tincture, MT) in 30% ethanol/distilled water. The MT was characterised by a content of sesquiterpene lactones of 0.036% (W/V).

Test solutions

Starting from the 1c dilution of *Arnica m.*, the 2c dilution was prepared by adding 50 µl of 1c to 4.95 ml of 30% ethanol/distilled water; this solution was filtered with a 0.22 µm Millipore filter and subjected to vigorous succussion with a Dyna-A mechanical shaker delivering 20 strokes/second for 7.5 seconds with an 11-mm travel distance. This process was done in sterile conditions using 10-ml sterile glass test tubes with screw cap. The subsequent serial 100x dilutions were prepared in the same 30% ethanol/distilled water solvent, in a final volume of 5 ml, up to the 14c dilution. After each dilution step, the solutions were subjected to succussion

as above described. Before the experiments, the working solutions were prepared in sterile conditions through a further 100x dilution of the 1c, 2c, 4c, 8c and 14c solutions in ultra-pure water, followed by vigorous mixing as above, thus obtaining the 2c, 3c, 5c, 9c and 15c dilutions. In this way, the ethanol concentration was decreased from 30% to 0.3% in test samples and was 0.03% in the final cell cultures. Preliminary experiments showed that this dose does not affect cell viability and function. The control test solution (pure vehicle) was prepared, before each experiment, using the same 30% ethanol/distilled water batch used for the *Arnica m.* preparations; it was diluted 100x in ultra-pure water and subjected to shaking with Dyna-A as described above.

Cell culture and treatments

The THP-1 cell line was cultured in RPMI 1640 medium, supplemented with FBS 10% and 2mM final concentration of Ultraglutamine, at 37°C in 5% CO_2 in a humidified incubator. Cells were sub-cultured twice a week and used between passage 3 and 10. In a typical experiment, on day one the cells were seeded at a density of 2.5×10^5 cells/mL in 24-well plates in 1 ml medium with 2mM Ultraglutamine and 2% FBS ("complete culture medium"). On day 2 all the cell cultures were supplemented with 20 ng/mL of PMA in order to develop the macrophage-like phenotype.[32,33] On day 3 the cells were divided in two groups: a) in the first group the culture was continued for a further 24 h in the complete culture medium containing 20 ng/mL of PMA ("Normal Mac"), b) in the second group, where indicated, IL-4 was added at a concentration of 50 ng/mL to develop the "wound healing" phenotype (here defined as "IL-4 Mac").[33] On day 4 the plates were washed twice with complete culture medium and group (b) was again supplemented with 50 ng/mL IL-4 while group (a) continued the culture in complete culture medium. Where indicated, both types of macrophages were exposed for 2 h or 24 h to *Arnica m.* or control solvent (1 ml cell culture + 110 μl test solutions). In each experiment, each experimental treatment was performed in triplicate wells.

Pictures of THP-1, Normal Mac and IL-4 Mac in the experimental plates were acquired by means of contrast phase microscopy using an Olympus IX50 microscope with 100x original magnification. Cell viability was checked by the WST-1 assay.[34] Briefly, after 24 h treatment with *Arnica m.* dilutions or with control, 1:10 (v/v) pre-warmed WST-1 solution was added to the cells cultivated in parallel plates in the same conditions, and the was plate incubated for 20 minutes. The absorbance (OD) of the samples was measured using a Victor3 multilabel reader (PerkinElmer, Shelton, CT, USA) at 450 nm, and cell metabolic activity was evaluated as the difference between OD of the drugs and control solution. Total proteins of cell extracts were quantified by Bradford assay according to the manufacturer's instructions.

RT-Array PCR

For the RNA extraction procedure, cell cultures from triplicate wells were collected in a single tube. RNA extraction was performed with the RNeasy Mini kit including two DNA elimination steps. The extracted RNA was precipitated for 3 h at -20°C with 0.1 volume of 3M Na-acetate solution and 2.5 volumes of ice-cold 100% ethanol. The pelleted RNA was washed with ice-cold 70% ethanol and dissolved in 15 μl of ultra-pure water in order to concentrate and clean the nucleic acid. RNA was then immediately stored at -80 °C until use. The RNA quality was assessed with Bioanalyzer (Agilent Technologies, USA) and the RNA quantity with Nanodrop (Thermo Fisher Scientific, USA). One μg of total RNA for each sample was reverse transcribed with random hexamer primers, and the resulting cDNA was amplified in a volume of 10 μl with RT SYBR Green Rox Master Mix in ViiA7 real time platform (Life Technologies, USA) following the thermal profile suggested by the manufacturer for the 384-well format plate. The customized RT-Array PCR contained the validated intron-spanning primers of the indicated transcripts (see list and abbreviations in Table 1), the internal reference gene Large

Ribosomal Protein PO (RPLPO) and as controls the Genomic DNA Contamination (GDC), the Reverse Transcription Control (RTC), and the Positive PCR Control (PPC). Preliminary experiments showed that RPLPO was the most stable reference gene among the 5 candidates (ACTB, B2M, GADPH, HPRT1 and RPLPO). All the genes included in the custom array were sufficiently expressed by THP-1 macrophages and gave only specific amplicons on inspection of melting curve. The quantification cycle (Cq) for each well was calculated applying the same conditions of baseline and threshold across all the PCR-Array runs, since all genes had same reaction efficiency; runs were analysed in the PCR Array data analysis web portal (http://www.SABiosciences.com/pcrarraydataanalysis.php) for the validation of the control wells.

Table 1. List of genes of THP-1 macrophages included in the panel.

Gene full names	Gene code	Gene symbol and abbreviation
Chemokine (C-C motif) ligand 1	NM_002981	CCL1
Chemokine (C-C motif) ligand 2; MCP-1	NM_002982	CCL2
Chemokine (C-C motif) ligand 3; MIP-1a	NM_002983	CCL3
Chemokine (C-C motif) ligand 4; MIP-1B	NM_002984	CCL4
Chemokine (C-C motif) ligand 5; RANTES	NM_002985	CCL5
Chemokine (C-C motif) ligand 7; MCP-3	NM_006273	CCL7
Chemokine (C-C motif) ligand 17; TARC	NM_002987	CCL17
Chemokine (C-C motif) ligand 22	NM_002990	CCL22
Chemokine (C-C motif) ligand 23	NM_005064	CCL23
Chemokine (C-X-C motif) ligand 1; GRO-a	NM_001511	CXCL1
Chemokine (C-X-C motif) ligand 2; GRO-b	NM_002089	CXCL2
Chemokine (C-X-C motif) ligand 13; BCA-1	NM_006419	CXCL13
Interleukin 1 – beta	NM_000576	IL1B
Interleukin 1, receptor antagonist	NM_000577	IL1RN
Interleukin 8	NM_000584	IL8
Interleukin 10	NM_000572	IL10
Tumor necrosis factor – alpha	NM_000594	TNFA
Vascular endothelial growth factor A	NM_003376	VEGFA
Bone morphogenetic protein 1	NM_001200	BMP2
Colony stimulating factor 1	NM_000757	CSF1
Chemokine (C-C motif) receptor 5	NM_000579	CCR5
Coagulation factor XIII, A1 polypeptide	NM_000129	F13A1
Mannose receptor, C type 1	NM_002438	MRC1
Matrix metallopeptidase 1 (collagenase)	NM_002421	MMP1
V-rel reticuloendotheliosis viral oncogene homolog A (p65)	NM_021975	RELA
Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p50)	NM_003998	NFKB1
Nuclear factor of k light polypeptide gene enhancer in B-cells inhibitor, alpha	NM_020529	NFKBIA
Inhibitor of kappa light polypeptide gene, kinase beta	NM_001556	IKBKB

Statistical analysis

The experimental model had a dose–response setup, comprising 5 dilutions of *Arnica m.* and the control solvent. Data from 11 independent experiments were considered for Normal Mac at 24 h of treatment; data from 6 independent experiments were considered for Normal

Mac at 2 h of treatment and for IL-4 Mac at 2 h and 24 h of treatment. We considered 28 different genes, and for each gene we had four different categories of analysis: Normal Mac (2 h), Normal Mac (24 h), IL-4 Mac (2 h), IL-4 Mac (24 h).

The main statistical working variable was the normalized Cq (ΔCq), calculated using the formula $\Delta Cq = Cq_{\text{Gene of Interest}} - Cq_{\text{RPLPO}}$. The effect of treatment (here defined as Differential Regulation, Diff. Reg.) was calculated by the Log$_2$(Fold Change) where Fold Change is $2^{(-\Delta\Delta Cq)}$ and $\Delta\Delta Cq = \Delta Cq_{\text{treated sample}} - \Delta Cq_{\text{control}}$. By this calculation a Diff. Reg. = 0 means no treatment effect, while a Diff. Reg. = 1 or = -1 means that the RNA content in the treated sample is respectively twice or half that of the control sample.

For each gene and each category, we considered 6 conditions: 5 different treatments (*Arnica m.* 2c, 3c, 5c, 9c and 15c) and one control consisting of the solvent. We thus obtained a total of 772 (28x4x6) samples of data, each corresponding to a single gene/treatment combination. The sample size was not constant, ranging from a minimum of n=5 to a maximum of n=11. We compared the ΔCq of each treatment (T) with that of the control (C). In this way, each treatment value was paired with the control value recorded at the same time, and we then checked whether the differences between them were significantly different from zero. We started by performing an evaluation of equality of variance by Levene's test; since data for each gene and category proved to have similar variance, a parametric ANOVA was done, simultaneously comparing the six conditions of treatment. We then singled out the gene/category combinations for which ANOVA proved significant. Next, we carried out all the T-test pairwise comparisons between treatment and control, calculating the Pearson skewness index to check for possible large deviations from normality. Comparisons with skewness index < -1.0 or > 1.0 were not considered to be reliable even if statistically significant. This occurred very rarely (see tables 2-3). The null hypothesis was then δ=0, where δ is the difference between treatment and control in the whole population. For each treatment, we thus checked four features: the statistical homogeneity, the global comparison by means of ANOVA, the level of skewness, and the result of the T-test comparisons between control sample and treatment.

The differences between expression profiles of the whole panel of genes in various treatment conditions was calculated by the Wilcoxon signed-rank test for paired data. For each *Arnica m.* dilution, the differences versus control were ranked and statistically compared using the specific Wilcoxon tables. The null hypothesis was that the median of differences is equal to zero. If the resulting sums were significantly different, the null hypothesis of the absence of treatment effect was rejected.

Results

Characterization of THP-1 macrophages and IL-4 differentiation

The macrophage populations used in the experiments are described in Figure 1. Original myelomonocytic cells of THP-1 line (panel A) have a rounded shape with homogeneous morphology. After differentiation with PMA (Normal Mac, panel B) the cells are characterized by slightly larger dimensions and many cells exhibit an evident adhesion attitude and flat shape. IL-4 Mac (panel C) show an elongated profile and some long cytoplasmic extensions.

Figure 1. Morphology of THP-1 cells at different stages of differentiation. The panels show images of THP-1 cells untreated (A), treated with 20 ng/ml PMA (B) and with 20 ng/ml PMA + 50 ng/ml IL-4 (C) as described in Methods. Scale bar = 50 μm.
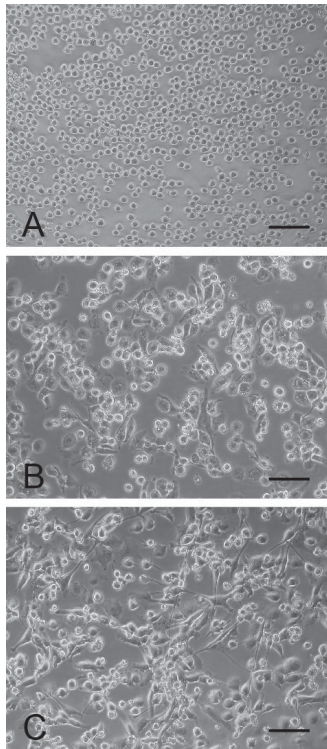
The polarization induced by IL-4 was analysed by monitoring the gene expression panel of several well-known marker genes, such as interleukins, chemokines, transcription factors involved in inflammation, coagulation and angiogenic factors (Table 1). Comparative analysis of the transcripts profile of Normal Mac and IL-4 Mac (Figure 2) demonstrated that IL-4 treatment caused a marked increase (Diff. Reg > 2.0) of the chemokines transcripts for CCL2, CCL4, CCL5, CCL17, CCL22 and a marked decrease (Diff. Reg < -2.0) of transcripts for CXCL1, CXCL2, CXCL13 and IL10. Moreover, other genes were found to be enhanced by IL-4, such as the cytokines CCL3, CCL7, IL1B, the growth factors VEGFA and CSF1, the metalloproteinase MMP1, the coagulation factor F13A1, and the mannose receptor MRC1.

The expression of 4 genes, namely CCL23, IL10, MRC1 and RELA, was significantly changed according to ANOVA analysis, but only 5 samples proved to be statistically significant at some dilutions according to T-test comparing *Arnica m.* with the respective control solvent (CCL23 at 15c, IL10 at 3c, MRC1 at 3c and 9c, RELA at 2c). The significance of RELA down-regulation by *Arnica m.* 2c was affected by high skewness of data and therefore is not reliable. After 24 h of treatment (Table 2B), no significant effects were done by *Arnica m.* 2c, while a trend to down-regulation - significant by the Wilcoxon test - was observed in the dilutions 3c ($p < 0.01$) , 5c ($p < 0.01$), and 9c ($p < 0.05$). With the dilution 15c a trend to up-regulation was found ($p < 0.01$). According to ANOVA, the expression of 6 genes – CCL3, IL1B, IL10, TNFA, RELA and IKBKB - was significantly changed, but only in 8 samples the differences were statistically significant with T-test (CCL3 at 5c, IL1B at 9c, IL10 at 15c, TNFA at 3c and 5c, RELA at 3c and IKBKB at 3c and 15c). All these changes but IL10 at 15c were in the direction of gene down-regulation.
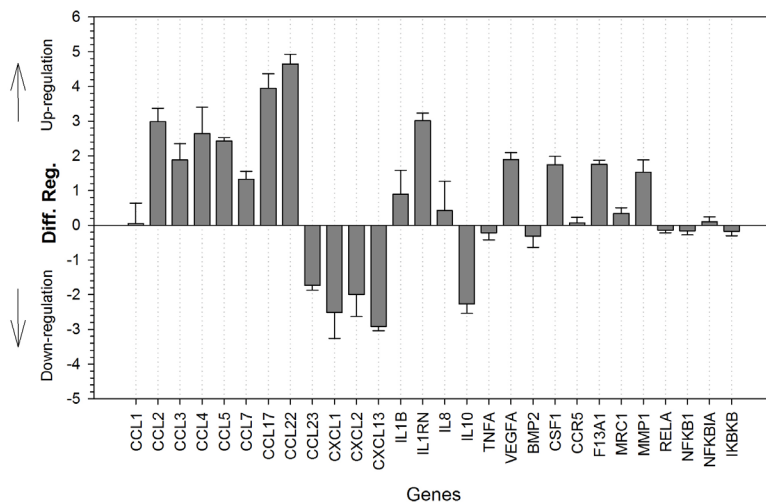
Figure 2. Changes of gene expression induced by IL-4 treatment of THP-1. Cells were incubated for 26 h in the absence and in the presence of 50 ng/ml of IL-4 and the extent of RNA transcripts of the indicated genes was determined. Differential regulation (Diff. Reg.) of IL-4 Mac versus Normal Mac is expressed as Log₂(Fold Change) ± SE.

Table 2. Differential regulation (Diff. Reg.) and statistical evaluations of the effects of *Arnica m.* dilutions on a panel of inflammatory genes of THP-1 Normal Mac treated for 2 h (2A) or 24 h (2B). Diff. Reg. is calculated by the difference between normalized PCR cycles (ΔCq) of control solvent and *Arnica m.* dilutions ± SE as described in Methods. The genes resulted significant with ANOVA are highlighted.

Table 2A (2 h of *Arnica m.* treatment)

| Gene	Statistics homogeneity	ANOVA	*Arnica m.* 2c (n=6)					*Arnica m.* 3c (n=6)					*Arnica m.* 5c (n=6)					*Arnica m.* 9c (n=6)					*Arnica m.* 15c (n=6)				
			Diff. Reg.	SE	Skewness	T - test	p	Diff. Reg.	SE	Skewness	T - test	p	Diff. Reg.	SE	Skewness	T - test	p	Diff. Reg.	SE	Skewness	T - test	p	Diff. Reg.	SE	Skewness	T - test	p
CCL1	0.224	0.086	-0.13	0.16	0.027	-	-	-0.24	0.10	-1.098	-	-	-0.18	0.08	0.483	-	-	0.09	0.14	0.403	-	-	-0.01	0.11	-1.114	-	-
CCL2	0.824	0.884	-0.26	0.45	1.213	-	-	-0.21	0.22	1.028	-	-	-0.32	0.28	0.416	-	-	-0.24	0.38	-0.084	-	-	-0.31	0.30	0.842	-	-
CCL3	0.918	0.859	-0.05	0.17	1.052	-	-	0.08	0.11	0.128	-	-	-0.06	0.12	0.185	-	-	0.04	0.10	0.338	-	-	-0.06	0.18	0.311	-	-
CCL4	0.984	0.617	-0.13	0.13	0.399	-	-	-0.09	0.13	-0.898	-	-	-0.12	0.08	0.420	-	-	-0.04	0.10	0.540	-	-	-0.16	0.14	-0.292	-	-
CCL5	0.999	0.312	0.10	0.04	-0.247	-	-	0.08	0.05	-1.014	-	-	0.04	0.02	0.360	-	-	0.04	0.02	1.248	-	-	0.03	0.04	-0.508	-	-
CCL7	0.466	0.228	-0.17	0.47	1.397	-	-	-0.54	0.21	0.091	-	-	-0.53	0.35	1.519	-	-	0.07	0.43	0.722	-	-	-0.35	0.46	1.036	-	-
CCL17	0.805	0.083	-0.51	0.39	-0.255	-	-	0.51	0.52	-0.348	-	-	0.46	0.22	-1.265	-	-	0.08	0.23	-0.313	-	-	0.69	0.27	0.175	-	-
CCL22	0.072	0.120	-0.24	0.10	-0.390	-	-	0.03	0.18	-0.561	-	-	0.08	0.09	-0.035	-	-	0.06	0.06	-0.444	-	-	-0.01	0.09	-0.342	-	-
CCL23	0.972	**0.027**	-0.05	0.04	0.504	1.240	ns	0.06	0.06	-0.428	-1.060	ns	0.04	0.04	0.638	-1.059	ns	-0.05	0.05	0.178	1.181	ns	0.11	0.04	-0.174	-3.174	**<0.05**
CXCL1	0.944	0.720	-0.14	0.19	-0.538	-	-	0.00	0.11	-1.306	-	-	0.05	0.06	-0.083	-	-	0.09	0.12	-0.050	-	-	-0.07	0.17	0.739	-	-
CXCL2	0.973	0.806	-0.07	0.18	0.722	-	-	-0.07	0.11	-1.074	-	-	-0.11	0.13	-0.264	-	-	-0.11	0.08	0.320	-	-	0.00	0.13	1.338	-	-
CXCL13	0.671	0.340	0.03	0.15	0.668	-	-	0.29	0.14	-0.071	-	-	0.16	0.12	0.074	-	-	0.05	0.04	-0.560	-	-	0.15	0.10	1.168	-	-
IL1B	0.957	0.805	-0.16	0.32	0.702	-	-	-0.21	0.16	0.436	-	-	-0.26	0.25	0.395	-	-	-0.10	0.22	0.800	-	-	-0.19	0.27	0.549	-	-
IL1RN	0.948	0.878	-0.07	0.11	0.993	-	-	-0.10	0.10	-1.309	-	-	-0.09	0.10	0.433	-	-	-0.01	0.10	0.769	-	-	-0.04	0.13	0.259	-	-
IL8	0.983	0.945	0.03	0.17	0.022	-	-	0.03	0.14	0.761	-	-	-0.04	0.14	0.234	-	-	-0.04	0.13	0.555	-	-	-0.10	0.18	0.100	-	-
IL10	0.109	**0.027**	-0.22	0.14	0.355	1.698	ns	-0.27	0.10	-0.020	3.005	**<0.05**	-0.21	0.24	0.128	0.956	ns	0.07	0.11	0.477	-0.706	ns	0.07	0.11	-0.330	-0.749	ns
TNFA	0.975	0.633	-0.15	0.12	0.145	-	-	-0.07	0.07	0.681	-	-	-0.06	0.10	0.048	-	-	-0.02	0.09	0.221	-	-	-0.08	0.13	0.089	-	-
VEGFA	1.000	0.822	0.02	0.08	1.241	-	-	0.12	0.06	0.138	-	-	0.07	0.09	0.570	-	-	0.09	0.14	1.277	-	-	0.00	0.15	0.517	-	-
BMP2	0.683	0.607	0.02	0.17	0.476	-	-	0.13	0.09	-0.518	-	-	-0.02	0.10	-0.537	-	-	-0.04	0.11	-0.453	-	-	-0.02	0.13	0.395	-	-
CSF1	0.921	0.163	-0.33	0.21	-0.061	-	-	-0.21	0.15	-0.235	-	-	-0.08	0.14	0.749	-	-	0.07	0.10	0.345	-	-	-0.08	0.17	-0.201	-	-
CCR5	0.277	0.153	-0.07	0.18	0.180	-	-	-0.03	0.13	-0.672	-	-	0.19	0.08	-0.252	-	-	0.01	0.08	-0.177	-	-	0.14	0.14	-0.164	-	-
F13A1	0.233	0.337	-0.04	0.13	0.676	-	-	0.00	0.11	0.503	-	-	0.11	0.08	0.591	-	-	0.17	0.09	0.243	-	-	0.15	0.14	-1.221	-	-
MRC1	0.545	**0.045**	-0.22	0.13	-0.155	1.844	ns	-0.47	0.13	0.568	3.950	**<0.01**	-0.24	0.18	1.212	1.457	ns	-0.26	0.13	0.692	2.160	**<0.05**	-0.08	0.09	-0.072	1.004	ns
MMP1	0.948	0.194	-0.12	0.08	-0.550	-	-	-0.05	0.12	-0.892	-	-	-0.02	0.08	0.366	-	-	0.10	0.05	-1.081	-	-	0.09	0.09	0.554	-	-
RELA	0.767	**0.006**	-0.16	0.07	-1.433	2.498	(<0.05)	-0.04	0.08	-0.209	0.532	ns	0.04	0.05	0.569	-0.843	ns	0.08	0.06	0.381	-1.375	ns	0.05	0.05	0.303	-1.037	ns
NFKB1	0.853	0.074	-0.16	0.10	-0.867	-	-	-0.17	0.10	0.039	-	-	-0.08	0.10	0.496	-	-	0.00	0.05	-0.732	-	-	0.00	0.09	0.404	-	-
NFKBIA	0.808	0.258	-0.15	0.10	-0.161	-	-	-0.03	0.09	0.087	-	-	-0.03	0.09	0.944	-	-	0.06	0.05	-0.597	-	-	-0.01	0.09	0.689	-	-
IKBKB	0.065	0.411	-0.08	0.12	-0.323	-	-	-0.01	0.14	0.274	-	-	0.05	0.08	1.005	-	-	0.11	0.11	0.074	-	-	0.05	0.07	0.408	-	-
Mean Differential regulation			-0.12					-0.05					-0.04					0.01					0.00				
Median Differential regulation			-0.13					-0.04					-0.04					0.05					-0.01				
N. of up-regulated			5					11					11					17					12				
N. of down-regulated			23					17					17					11					16				
Wilcoxon (p-value)			**<0.001**					0.139					0.187					0.151					0.600				

Table 2B (24 h of *Arnica m.* treatment)

Gene	Statistics homogeneity	ANOVA	Arnica m. 2c						Arnica m. 3c						Arnica m. 5c						Arnica m. 9c						Arnica m. 15c					
			n	Diff. Reg.	SE	Skewness	T-test	p	n	Diff. Reg.	SE	Skewness	T-test	p	n	Diff. Reg.	SE	Skewness	T-test	p	n	Diff. Reg.	SE	Skewness	T-test	p	n	Diff. Reg.	SE	Skewness	T-test	p
CCL1	0.720	0.651	6	0.34	0.37	-0.915	-	-	6	0.20	0.22	0.021	-	-	6	0.35	0.20	0.036	-	-	6	0.24	0.44	-0.408	-	-	6	0.59	0.23	2.363	-	-
CCL2	0.433	0.080	9	0.13	0.20	0.584	-	-	10	-0.27	0.13	0.005	-	-	10	-0.14	0.21	0.357	-	-	6	0.09	0.15	0.898	-	-	11	0.16	0.14	1.305	-	-
CCL3	0.867	0.005	9	0.07	0.12	0.372	-0.602	ns	10	-0.18	0.10	0.834	1.847	ns	10	-0.18	0.10	-0.145	1.878	<0.05	11	-0.26	0.18	0.994	1.475	ns	11	0.18	0.12	-0.049	-1.515	ns
CCL4	0.988	0.298	6	-0.05	0.15	0.025	-	-	6	-0.30	0.14	-0.853	-	-	6	-0.25	0.16	0.285	-	-	6	-0.45	0.35	1.549	-	-	6	0.13	0.23	-0.493	-	-
CCL5	0.999	0.147	6	0.10	0.05	0.450	-	-	6	0.02	0.02	-0.051	-	-	6	0.09	0.03	1.716	-	-	6	0.06	0.05	-1.160	-	-	6	0.05	0.03	-0.190	-	-
CCL7	0.917	0.950	6	0.09	0.55	0.924	-	-	6	0.14	0.51	0.026	-	-	6	-0.09	0.50	1.316	-	-	6	0.31	0.62	0.368	-	-	6	0.32	0.49	0.871	-	-
CCL17	0.470	0.651	9	-0.57	0.28	-0.388	-	-	10	-0.27	0.23	-0.361	-	-	10	-0.50	0.27	-0.951	-	-	11	-0.41	0.47	-0.263	-	-	11	0.19	0.41	0.452	-	-
CCL22	0.739	0.835	6	0.10	0.13	0.193	-	-	6	0.07	0.15	0.637	-	-	6	0.06	0.09	-0.131	-	-	6	0.09	0.09	-0.820	-	-	6	0.16	0.13	-0.071	-	-
CCL23	0.993	0.220	6	-0.12	0.07	0.835	-	-	6	-0.07	0.07	1.445	-	-	6	-0.05	0.02	-1.215	-	-	6	-0.04	0.02	-0.204	-	-	6	-0.06	0.03	-1.346	-	-
CXCL1	0.939	0.408	6	-0.12	0.06	-0.179	-	-	6	-0.12	0.11	-0.735	-	-	6	-0.24	0.15	0.118	-	-	6	-0.30	0.35	1.527	-	-	6	0.23	0.22	-1.319	-	-
CXCL2	0.918	0.274	6	-0.24	0.14	0.435	-	-	6	-0.12	0.14	-0.105	-	-	6	-0.18	0.09	-0.654	-	-	6	-0.34	0.32	1.604	-	-	6	0.25	0.22	-1.349	-	-
CXCL13	0.880	0.513	6	-0.02	0.19	0.578	-	-	6	0.10	0.23	1.173	-	-	6	-0.17	0.11	-0.741	-	-	6	-0.19	0.11	0.200	-	-	6	0.01	0.11	0.748	-	-
IL1B	0.991	0.044	9	-0.21	0.13	-0.166	1.683	ns	10	-0.16	0.13	0.395	1.338	ns	10	-0.16	0.11	0.531	1.498	ns	11	-0.36	0.17	0.536	2.275	<0.05	11	0.06	0.15	-1.058	-0.436	ns
IL1RN	0.991	0.849	6	0.01	0.04	-0.322	-	-	6	0.00	0.05	-0.088	-	-	6	0.00	0.03	-0.052	-	-	6	-0.04	0.03	0.287	-	-	6	-0.04	0.03	-0.277	-	-
IL8	0.963	0.201	9	0.05	0.06	2.456	-	-	10	-0.10	0.07	0.532	-	-	10	-0.11	0.07	0.641	-	-	11	-0.22	0.19	1.715	-	-	11	0.10	0.15	-0.637	-	-
IL10	0.836	0.002	9	0.05	0.10	2.456	0.981	ns	10	-0.09	0.10	0.339	0.982	ns	10	-0.16	0.09	-0.763	1.767	ns	11	0.07	0.08	0.195	-0.970	ns	11	0.17	0.05	-0.342	-3.698	<0.01
TNFA	0.943	0.017	9	-0.06	0.10	2.428	1.099	ns	10	-0.14	0.05	-0.041	3.038	<0.01	10	-0.14	0.08	0.128	1.920	<0.05	11	-0.18	0.11	0.274	1.787	ns	11	0.10	0.08	-1.660	-1.244	ns
VEGFA	0.678	0.179	9	-0.05	0.09	2.425	-	-	10	-0.08	0.08	0.073	-	-	10	-0.09	0.08	0.253	-	-	11	-0.01	0.07	1.081	-	-	11	0.03	0.08	-0.368	-	-
BMP2	0.689	0.546	9	0.10	0.09	2.439	-	-	10	0.05	0.08	0.376	-	-	10	0.03	0.07	-0.639	-	-	11	0.07	0.05	-0.141	-	-	11	0.08	0.06	0.280	-	-
CSF1	0.979	0.237	6	-0.05	0.09	0.610	-	-	6	-0.07	0.06	0.480	-	-	6	-0.08	0.06	-0.111	-	-	6	-0.01	0.04	-0.323	-	-	6	0.09	0.06	-0.080	-	-
CCR5	0.874	0.109	9	-0.17	0.14	2.264	-	-	10	-0.08	0.16	2.230	-	-	10	0.14	0.06	-0.711	-	-	11	0.13	0.07	-0.125	-	-	11	-0.06	0.09	0.685	-	-
F13A1	0.992	0.481	6	-0.11	0.13	0.361	-	-	6	-0.12	0.09	0.065	-	-	6	0.00	0.04	-0.385	-	-	6	0.00	0.05	0.818	-	-	6	0.16	0.08	-1.077	-	-
MRC1	0.956	0.091	6	0.07	0.09	-0.634	-	-	6	-0.21	0.10	-0.212	-	-	6	-0.13	0.09	0.323	-	-	6	-0.04	0.07	0.199	-	-	6	-0.02	0.11	0.250	-	-
MMP1	0.971	0.419	6	0.00	0.22	-0.110	-	-	6	-0.07	0.18	0.326	-	-	6	0.10	0.11	0.256	-	-	6	-0.08	0.13	0.009	-	-	6	0.23	0.15	-0.054	-	-
RELA	0.983	0.037	6	-0.03	0.05	0.158	0.641	ns	6	-0.12	0.05	-0.565	2.444	<0.05	6	-0.06	0.04	-0.006	1.808	ns	6	0.01	0.03	-1.205	-0.281	ns	6	0.00	0.03	-0.689	-0.122	ns
NFKB1	0.875	0.182	6	-0.03	0.10	0.811	-	-	6	-0.09	0.05	-0.786	-	-	6	-0.11	0.06	0.684	-	-	6	-0.09	0.08	0.976	-	-	6	0.10	0.08	-0.437	-	-
NFKBIA	0.943	0.122	6	0.01	0.05	0.026	-	-	6	-0.08	0.05	-0.812	-	-	6	-0.16	0.06	-0.633	-	-	6	-0.11	0.16	1.503	-	-	6	0.15	0.09	-0.941	-	-
IKBKB	0.683	0.007	6	0.00	0.08	0.439	-0.020	ns	6	-0.14	0.07	-0.218	2.120	<0.05	6	-0.17	0.08	-1.246	2.423	(<0.05)	6	-0.04	0.06	-0.900	0.788	ns	6	-0.11	0.05	-0.062	2.267	<0.05
Mean Differential regulation				-0.02						-0.08						-0.09						-0.08						0.11				
Median Differential regulation				-0.01						-0.09						-0.11						-0.04						0.10				
N. of up-regulated				14						7						7						8						22				
N. of down-regulated				14						21						21						20						6				
Wilcoxon (p-value)				0.186						0.002						0.003						0.031						0.005				

Figure 3 reports the most interesting findings extracted from the general dataset of Normal Mac, considering only those genes where ANOVA revealed some statistically significant difference and where the direction of effect was consistent at different times (2h and 24h) and for different dilutions. A slight down-regulation of IL1B, TNFA and MRC1 was caused by 2c, 3c, 5c and 9c test solutions in almost all conditions. However, only 9c on IL1B at 24h, 3c and 5c on TNFA at 24h and 3c and 9c on MRC1 at 2h reached the statistically significant threshold.
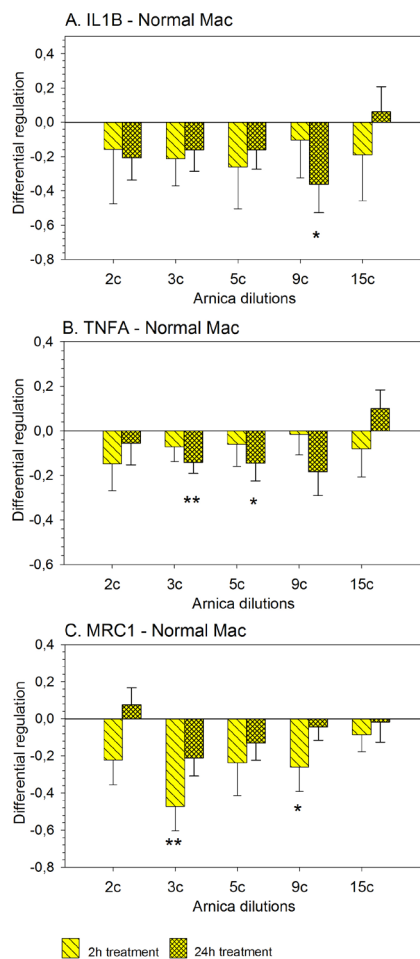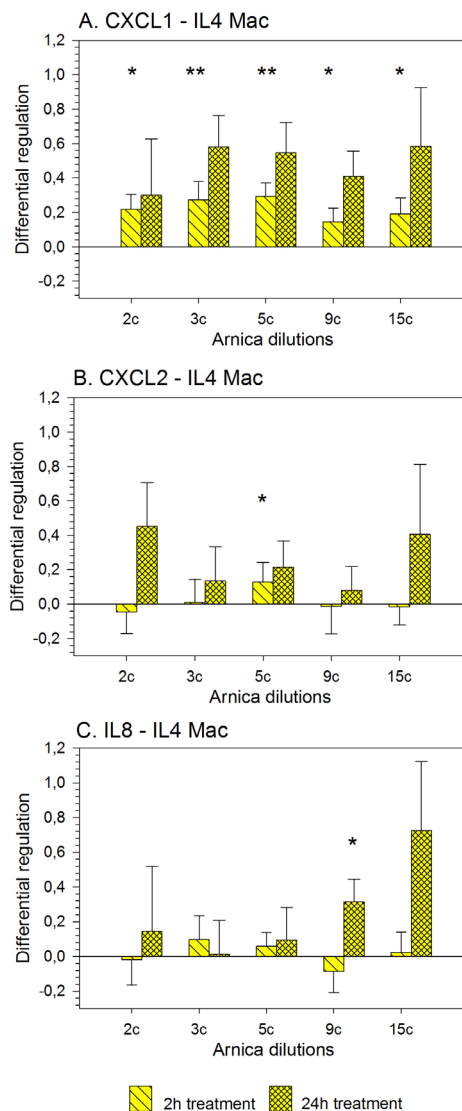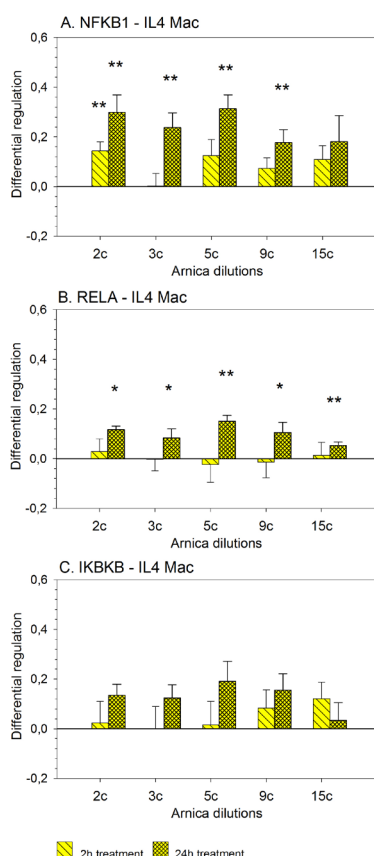

Figure 3. Effects of *Arnica m.* on Normal Mac IL1B (A), TNFA (B) and MRC1 (C) gene expression after 2 h and 24 h of treatment. * = p < 0.05, ** p < 0.01. Differential regulation is expressed as Log$_2$(Fold Change) ± SE.

Arnica m. effects on IL-4 Macrophages

The effects of *Arnica m.* on IL-4 Mac at 2h and 24h are reported in Tables 3A and 3B respectively. In general, ANOVA analysis showed that a higher number of genes was modified in macrophages differentiated towards the wound healing phenotype: after 2h of treatment (Table 2A), 10 genes were significantly affected – CCL1, CCL4,CCL5, CCL17, CXCL1, CXCL2, TNFA, CCR5, MMP1, NFKB1 – with a total of 15 samples statistically significant at the T-test.

Table 3. Differential regulation (Diff. Reg.) and statistical evaluations of the effects of *Arnica m.* dilutions on a panel of inflammatory genes of THP-1 IL-4 Mac treated for 2 h (3A) or 24 h (3B). Diff. Reg. is calculated by the difference between normalized PCR cycles (ΔCq) of control solvent and *Arnica m.* dilutions ± SE as described in Methods. The genes resulted significant with ANOVA are highlighted.

Table 3A (2 h of *Arnica m.* treatment)

Gene	Statistics homogeneity	ANOVA	*Arnica m.* 2c (n=6)					*Arnica m.* 3c (n=6)					*Arnica m.* 5c (n=6)					*Arnica m.* 9c (n=6)					*Arnica m.* 15c (n=6)				
			Diff. Reg.	SE	Skewness	T - test	p	Diff. Reg.	SE	Skewness	T - test	p	Diff. Reg.	SE	Skewness	T - test	p	Diff. Reg.	SE	Skewness	T - test	p	Diff. Reg.	SE	Skewness	T - test	p
CCL1	0.742	**0.001**	-0.06	0.20	1.145	0.940	ns	**-0.28**	0.17	0.505	2.760	**<0.05**	-0.23	0.09	0.322	2.049	ns	0.16	0.12	-0.447	-0.842	ns	0.18	0.13	0.808	-0.942	ns
CCL2	0.916	0.659	0.09	0.23	0.022	-0.171	-	-0.19	0.21	0.378	0.717	-	-0.31	0.06	0.812	4.665	-	-0.04	0.32	-0.672	-0.410	-	-0.17	0.10	-0.396	0.549	-
CCL3	0.963	0.099	-0.01	0.11	0.502	0.486	-	-0.05	0.10	0.333	2.026	-	0.01	0.07	0.528	-0.501	-	-0.03	0.10	-0.009	0.726	-	0.02	0.09	0.659	0.292	-
CCL4	0.899	**0.033**	-0.10	0.09	0.755	1.304	ns	-0.16	0.13	-0.085	3.794	**<0.01**	-0.10	0.07	0.333	1.834	ns	-0.10	0.07	-0.677	1.729	ns	-0.05	0.09	0.647	1.033	ns
CCL5	0.978	**0.049**	-0.04	0.03	-0.715	1.275	ns	-0.06	0.04	-0.114	3.697	**<0.01**	-0.04	0.05	0.397	1.283	ns	-0.07	0.04	0.466	2.968	**<0.05**	0.02	0.04	0.537	0.067	ns
CCL7	0.952	0.283	0.06	0.24	0.057	-0.200	-	-0.42	0.10	0.454	2.746	-	-0.36	0.08	-0.857	2.426	-	0.24	0.32	-1.212	-0.648	-	0.09	0.22	0.296	-0.509	-
CCL17	0.919	**0.036**	-0.01	0.16	0.045	-0.018	ns	0.07	0.10	0.436	-1.284	ns	0.36	0.23	0.389	-1.693	ns	0.02	0.17	0.877	-0.188	ns	0.40	0.09	-0.588	-4.200	**<0.01**
CCL22	0.989	0.312	0.11	0.07	0.000	-1.361	-	0.18	0.10	-0.448	-0.928	-	0.07	0.08	-0.391	-0.310	-	0.01	0.06	-0.302	2.929	-	0.08	0.07	-0.451	-0.837	-
CCL23	0.731	0.326	0.06	0.05	0.129	-2.328	-	-0.01	0.04	1.049	0.116	-	0.08	0.09	0.316	-1.084	-	-0.05	0.09	0.475	0.440	-	0.06	0.11	0.326	-0.556	-
CXCL1	0.957	**0.038**	0.22	0.09	0.129	-3.242	**<0.05**	0.27	0.11	-0.710	-4.165	**<0.01**	0.29	0.08	0.482	-5.867	**<0.01**	0.15	0.08	-0.036	-2.077	**<0.05**	0.19	0.09	0.474	-2.110	**<0.05**
CXCL2	0.739	**0.038**	-0.05	0.12	0.418	0.210	ns	0.01	0.13	-0.466	-0.642	ns	0.13	0.11	-0.200	-2.298	**<0.05**	-0.01	0.16	-0.412	-0.315	ns	-0.01	0.11	0.209	0.267	ns
CXCL13	0.992	0.080	0.09	0.11	0.729	-0.750	-	0.15	0.07	-1.012	-3.006	-	0.23	0.05	0.937	-0.131	-	-0.23	0.16	0.306	1.771	-	0.12	0.10	-0.060	-1.306	-
IL1B	0.939	0.413	0.19	0.11	-0.151	-1.606	-	0.10	0.05	-0.401	-1.225	-	0.07	0.03	0.034	-3.338	-	0.05	0.12	-0.110	0.163	-	0.13	0.10	0.508	-0.819	-
IL1RN	0.948	0.517	0.05	0.06	-0.253	-0.705	-	0.04	0.07	-0.486	1.181	-	0.02	0.04	0.084	-0.123	-	0.00	0.06	-0.318	0.426	-	0.07	0.07	0.196	-0.767	-
IL8	0.912	0.159	-0.02	0.15	0.553	1.173	-	0.10	0.14	0.226	-0.181	-	0.06	0.08	0.953	-0.717	-	-0.09	0.12	-0.206	1.165	-	0.02	0.12	1.248	0.068	-
IL10	0.616	0.481	-0.13	0.19	0.948	0.400	-	-0.14	0.11	1.063	0.951	-	-0.17	0.10	-0.570	1.741	-	0.16	0.15	-0.301	-1.122	-	0.02	0.16	-0.311	-0.124	-
TNFA	0.644	**0.048**	-0.11	0.09	-0.338	1.815	ns	-0.10	0.07	-0.258	2.047	**<0.05**	-0.07	0.07	0.303	0.708	ns	0.03	0.10	0.185	-0.112	ns	0.07	0.06	0.017	-0.715	ns
VEGFA	0.896	0.200	-0.09	0.10	0.300	0.962	-	-0.06	0.09	0.046	2.333	-	-0.06	0.07	-0.032	0.150	-	0.00	0.07	0.147	-0.075	-	0.03	0.05	-0.909	-0.661	-
BMP2	0.480	0.353	0.05	0.14	0.695	0.379	-	-0.01	0.14	-0.019	1.270	-	-0.07	0.13	0.131	1.558	-	0.19	0.09	0.206	-0.508	-	0.15	0.09	0.132	-0.391	-
CSF1	0.877	0.228	0.00	0.11	0.288	0.227	-	-0.10	0.09	0.217	3.379	-	-0.08	0.10	-0.124	0.727	-	-0.02	0.12	-0.638	0.727	-	0.06	0.12	0.805	-0.125	-
CCR5	0.820	**0.028**	0.05	0.12	-0.027	-0.671	ns	-0.08	0.09	0.372	0.713	ns	-0.01	0.08	0.565	-0.096	ns	0.00	0.05	0.254	0.607	ns	0.16	0.06	-0.394	-4.916	**<0.01**
F13A1	0.961	0.114	-0.11	0.07	-0.068	3.065	-	-0.08	0.10	0.846	2.226	-	-0.07	0.09	0.358	3.215	-	-0.10	0.11	0.392	2.208	-	0.01	0.06	0.179	0.475	-
MRC1	0.977	0.089	0.07	0.11	0.106	0.080	-	-0.15	0.19	-0.260	0.396	-	0.12	0.10	-0.246	-1.057	-	-0.24	0.13	-0.059	1.466	-	0.17	0.06	-0.043	-2.448	-
MMP1	0.986	**0.000**	-0.07	0.06	-0.008	1.295	ns	-0.28	0.18	-0.114	4.416	**<0.01**	-0.10	0.10	0.195	1.827	ns	-0.04	0.09	0.133	1.967	ns	0.04	0.05	0.024	0.265	ns
RELA	0.699	0.675	0.03	0.05	-0.078	-0.376	-	0.00	0.05	0.238	0.859	-	-0.02	0.07	0.106	0.342	-	-0.01	0.06	0.100	1.116	-	0.01	0.05	-0.271	0.707	-
NFKB1	0.102	**0.005**	0.14	0.04	0.142	-3.992	**<0.01**	0.00	0.05	-0.156	1.199	ns	0.12	0.06	0.017	-1.711	ns	0.07	0.04	-0.764	-1.395	ns	0.11	0.05	0.183	-1.533	ns
NFKBIA	0.447	0.584	-0.01	0.05	-0.579	0.049	-	-0.04	0.05	0.012	0.835	-	-0.02	0.06	0.218	0.136	-	0.01	0.06	-0.234	-0.117	-	0.06	0.03	0.717	-2.045	-
IKBKB	0.361	0.311	0.02	0.09	-0.443	-0.217	-	0.00	0.09	-0.044	1.047	-	0.02	0.10	-0.035	-0.355	-	0.08	0.07	-0.122	-1.107	-	0.12	0.07	-0.912	-1.457	-
Mean Differential regulation			0.02					-0.05					0.00					0.01					0.08				
Median Differential regulation			0.01					-0.05					-0.02					0.00					0.06				
N. of up-regulated			15					10					13					13					25				
N. of down-regulated			13					18					15					15					3				
Wilcoxon (p-value)			0.716					**0.016**					0.219					0.495					**0.004**				

Table 3B (24 h of *Arnica m.* treatment)

Gene	Statistics homogeneity	ANOVA	*Arnica m.* 2c (n=5)					*Arnica m.* 3c (n=6)					*Arnica m.* 5c (n=6)					*Arnica m.* 9c (n=6)					*Arnica m.* 15c (n=6)				
			Diff. Reg.	SE	Skewness	T - test	p	Diff. Reg.	SE	Skewness	T - test	p	Diff. Reg.	SE	Skewness	T - test	p	Diff. Reg.	SE	Skewness	T - test	p	Diff. Reg.	SE	Skewness	T - test	p
CCL1	0.934	0.060	-0.24	0.12	-0.197	2.099	-	-0.27	0.18	0.043	1.544	-	-0.05	0.17	0.475	0.292	-	0.05	0.14	0.216	-0.351	-	0.14	0.15	-0.085	-0.910	-
CCL2	0.802	**0.028**	0.21	0.12	0.206	-1.975	ns	-0.11	0.15	-0.376	0.704	ns	-0.19	0.16	0.513	1.158	ns	0.20	0.22	-0.640	-0.915	ns	0.33	0.12	-0.152	-2.709	**<0.05**
CCL3	0.816	0.053	-0.08	0.18	-0.167	0.517	-	-0.13	0.12	-0.116	1.063	-	0.09	0.13	-0.160	-0.710	-	-0.02	0.13	-0.254	0.186	-	0.30	0.20	-0.352	-1.484	-
CCL4	0.967	0.121	-0.22	0.24	-0.242	1.013	-	-0.16	0.14	0.098	1.132	-	0.00	0.17	-0.134	-0.002	-	0.04	0.15	-0.504	-0.277	-	0.27	0.32	-0.499	-0.844	-
CCL5	0.997	**0.001**	-0.22	0.05	-0.174	4.983	**<0.01**	-0.12	0.04	-0.467	3.102	**<0.05**	-0.05	0.05	0.544	1.033	ns	-0.02	0.03	1.042	0.593	ns	-0.09	0.05	-0.280	1.705	ns
CCL7	0.805	0.069	0.21	0.17	-0.076	-1.383	-	-0.09	0.15	0.095	0.643	-	-0.08	0.23	0.135	0.347	-	0.29	0.20	-0.761	-1.424	-	0.27	0.15	-0.279	-1.780	-
CCL17	0.983	**0.009**	-0.26	0.21	-0.009	1.330	ns	0.04	0.08	0.357	-0.459	ns	0.28	0.15	-0.066	-1.838	ns	0.09	0.11	0.055	-0.747	ns	-0.10	0.07	-0.429	1.480	ns
CCL22	0.524	0.153	-0.07	0.14	-0.120	0.570	-	0.10	0.10	-0.017	-1.044	-	0.22	0.08	-0.267	-2.660	-	0.10	0.10	0.407	-0.957	-	0.03	0.13	-0.880	-0.256	-
CCL23	0.940	0.358	0.16	0.20	0.102	-0.896	-	0.14	0.14	0.411	-1.005	-	0.14	0.10	0.738	-1.438	-	0.04	0.15	1.244	-0.248	-	0.22	0.08	-0.360	-2.595	-
CXCL1	0.980	0.222	0.30	0.33	-0.071	-1.009	-	0.58	0.18	0.342	-3.197	-	0.55	0.17	0.357	-3.151	-	0.41	0.14	0.642	-2.840	-	0.59	0.34	-0.999	-1.726	-
CXCL2	0.960	0.450	0.45	0.25	-0.105	-1.946	-	0.13	0.20	-0.558	-0.678	-	0.22	0.15	0.519	-1.420	-	0.08	0.14	0.207	-0.572	-	0.41	0.41	-1.138	-1.000	-
CXCL13	0.468	0.375	0.40	0.19	-0.045	-2.324	-	0.43	0.18	0.124	-2.439	-	0.17	0.21	0.896	-0.817	-	0.15	0.22	0.854	-0.694	-	0.07	0.19	0.618	-0.379	-
IL1B	0.964	0.499	-0.09	0.24	-0.160	0.395	-	0.11	0.15	-0.041	-0.712	-	0.14	0.16	0.120	-0.871	-	0.04	0.13	0.483	-0.281	-	0.18	0.26	-0.526	-0.662	-
IL1RN	0.704	0.179	-0.27	0.16	-0.210	1.836	-	-0.13	0.12	-0.043	1.049	-	-0.03	0.13	-0.270	0.246	-	0.02	0.12	-0.291	-0.157	-	0.00	0.16	-0.706	0.026	-
IL8	0.991	**0.033**	0.14	0.18	-0.152	-0.421	ns	0.01	0.15	-0.578	-0.074	ns	0.09	0.19	-0.754	-0.506	ns	0.31	0.14	-0.458	-2.378	**<0.05**	0.72	0.40	-0.815	-1.820	ns
IL10	0.693	0.649	0.11	0.14	0.051	-0.878	-	-0.03	0.17	-0.254	0.157	-	0.03	0.14	-0.583	-0.256	-	0.04	0.15	-0.476	-0.261	-	0.10	0.14	-0.473	-0.709	-
TNFA	0.890	**0.022**	-0.18	0.14	-0.037	2.749	**<0.05**	-0.21	0.14	0.189	2.384	**<0.05**	-0.11	0.14	1.149	1.091	ns	0.03	0.10	-0.103	-0.328	ns	0.05	0.10	-0.557	-0.446	ns
VEGFA	0.160	0.226	-0.17	0.12	-0.060	1.617	-	-0.09	0.11	0.250	0.844	-	-0.04	0.09	-0.403	0.414	-	0.06	0.08	0.502	-0.654	-	-0.08	0.11	0.473	0.664	-
BMP2	0.803	**0.003**	0.28	0.12	0.239	-2.475	**<0.05**	0.05	0.12	0.549	-0.431	ns	0.11	0.14	0.400	-0.754	ns	0.11	0.12	0.118	-0.977	ns	0.33	0.14	0.317	-2.336	**<0.05**
CSF1	0.701	0.461	-0.17	0.23	-0.183	0.824	-	0.01	0.19	-0.302	-0.081	-	0.14	0.18	-0.371	-0.750	-	0.16	0.18	-1.034	-0.914	-	0.25	0.31	-0.957	-0.798	-
CCR5	0.834	0.178	0.21	0.16	0.176	-1.429	-	-0.13	0.20	0.770	0.676	-	0.08	0.06	0.183	-1.378	-	0.00	0.08	0.369	0.059	-	0.13	0.03	0.112	-3.872	-
F13A1	0.839	0.329	0.19	0.19	0.161	-1.120	-	0.07	0.12	0.115	-0.571	-	0.08	0.15	0.831	-0.536	-	-0.03	0.11	1.245	0.256	-	0.12	0.05	-0.163	-2.597	-
MRC1	0.737	**0.003**	0.18	0.11	0.118	-2.853	**<0.05**	0.14	0.07	0.241	-1.998	ns	0.18	0.09	-0.509	-1.993	ns	0.05	0.09	-0.111	-0.637	ns	0.32	0.11	0.161	-2.890	**<0.05**
MMP1	0.997	**0.008**	-0.30	0.13	-0.032	2.545	**<0.05**	-0.23	0.15	0.364	1.529	ns	0.13	0.09	0.346	-1.430	ns	-0.14	0.18	1.177	0.772	ns	-0.19	0.10	0.846	1.867	ns
RELA	0.968	**0.004**	0.12	0.10	0.551	-8.737	**<0.001**	0.08	0.04	0.519	-2.265	**<0.05**	0.15	0.02	-0.328	-6.529	**<0.001**	0.11	0.04	0.215	-2.572	**<0.05**	0.05	0.01	-0.454	-3.890	**<0.01**
NFKB1	0.873	**0.001**	0.30	0.07	0.084	-4.644	**<0.01**	0.24	0.06	-0.647	-4.041	**<0.01**	0.31	0.06	0.380	-5.638	**<0.01**	0.18	0.05	0.530	-3.378	**<0.01**	0.18	0.10	-0.523	-1.735	ns
NFKBIA	0.892	0.140	0.00	0.08	-0.163	0.025	-	-0.04	0.08	-0.118	0.438	-	0.09	0.08	0.218	-1.074	-	0.08	0.06	0.393	-1.468	-	0.13	0.10	-0.252	-1.351	-
IKBKB	0.909	0.085	0.13	0.04	0.086	-3.303	-	0.12	0.05	0.726	-2.331	-	0.19	0.08	-0.196	-2.364	-	0.16	0.07	0.417	-2.352	-	0.03	0.07	0.567	-0.479	-
Mean Differential regulation			0.04					0.02					0.10					0.09					0.17				
Median Differential regulation			0.12					0.01					0.10					0.07					0.13				
N. of up-regulated			15					15					21					23					23				
N. of down-regulated			13					13					7					5					5				
Wilcoxon (p-value)			0.054					0.946					**0.001**					**<0.0001**					**<0.0001**				

Considering the whole panel as a gene-set, statistically significant at Wilcoxon test indicated a prevalent down-regulation of genes in cells treated with 3c (p = 0.016) and prevalent

up-regulation of genes in cells treated with 15c (p =0.004). After 24h of treatment (Table 3B), 10 genes were significantly affected - CCL2, CCL5, CCL17, IL8, TNFA, BMP2, MRC1, MMP1, RELA and NFKB1 – with a total of 20 samples statistically significant according to the T-test. In IL-4 Mac, after 24 h of treatment, most changes were in the direction of up-regulation and at the dilutions 5c, 9c and 15c the Wilcoxon test was highly significant. The genes TNFA, CCL5 and MMP1 were down-regulated by low dilutions of *Arnica m.* (2c and 3c).

The histograms in Figures 4 to 6 show the results for some genes where ANOVA was significant and where the direction of effect was consistent for different dilutions. This category includes three important chemokines of CXC type (CXCL1, CXCL2 and IL8) (Figure 4).

Figure 4. Effects of *Arnica m.* on IL-4 Mac CXCL1 (A), CXCL2 (B), IL8 (C) gene expression after 2 h and 24 h of treatment. * = p < 0.05, ** p < 0.01. Differential regulation is expressed as Log₂(Fold Change) ± SE.

The most consistent findings concerned the CXCL1 gene whose expression was increased in all conditions, with statistically significant values at the 2 h time point and with higher values also at the 24 h time point, where ANOVA (p=0.222) did not reach the statistical threshold probably due to high variance of data. The CXCL2 and IL8 genes also showed quantitatively higher stimulating effects of *Arnica m,* but only after 24 h of treatment. Broadly, the effects were scattered for the different dilutions, without a clear dose-dependence. Furthermore, *Arnica m.* exhibited a remarkable tendency to increase BMP2 and to decrease MMP1 gene expression in IL-4 Mac (Figure 5), with different effect sizes in different dilutions without dose-

dependence for BMP2 and with higher effects at lower dilutions for MMP1. Figure 6 reports the results of the NF-kappaB complex genes modified by *Arnica m.* in IL-4 Mac. These genes were consistently up-regulated, especially after 24h of treatment.
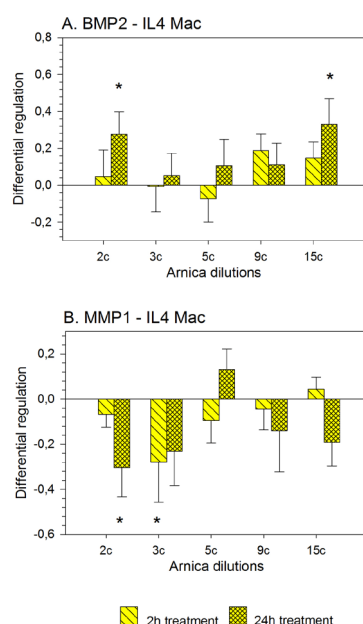
Figure 5. Effects of *Arnica m.* on IL-4 Mac BMP2 (A) and MMP1 (B) gene expression after 2 h and 24 h of treatment. * = p < 0.05. Differential regulation is expressed as Log$_2$(Fold Change) ± SE.

Figure 6. Effects of *Arnica m.* on IL-4 Mac NFKB1 (A), RELA (B) and IKBKB (C) gene expression after 2 h and 24 h of treatment. * = p < 0.05, ** p < 0.01. Differential regulation is expressed as Log$_2$(Fold Change) ± SE.

A summary of the major findings concerning the pharmacological effects of *Arnica m.* on both types of macrophages and their possible dealings with the functional changes of connective tissue during the processes of inflammation and tissue repair is shown in Figure 7.
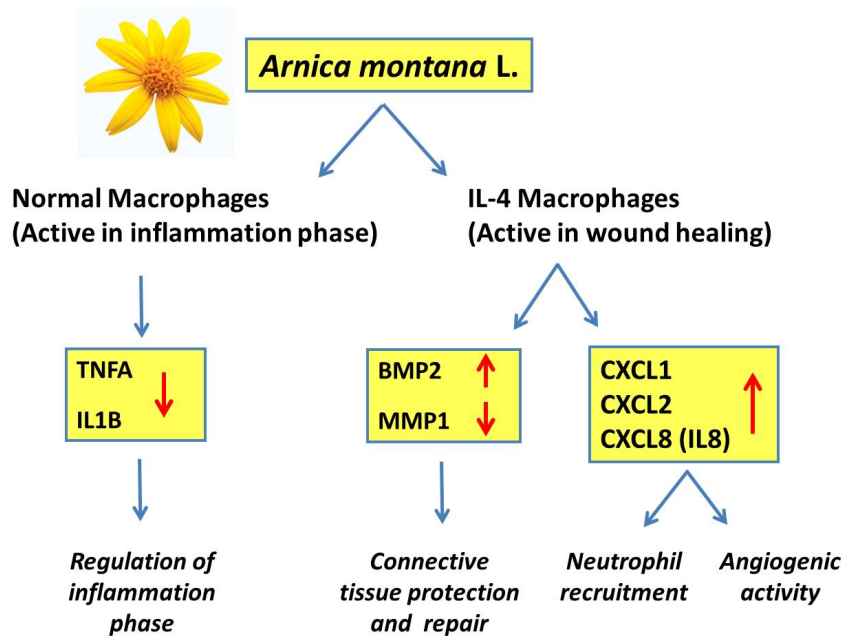
Figure 7. Most important functions of genes whose expression is adjusted by *Arnica m.* on macrophages at two stages of differentiation/polarization.

Discussion

The use of complementary medicines is currently widespread in the population for treating various kinds of ailments, in the hope of getting better whilst reducing the use of conventional drugs which may cause adverse effects. Among herbal medicines, those containing extracts of *Asteraceae* (*Compositae*) are especially popular in the primary-care setting. However, there remains a gap between the growing acceptance of these remedies and the lack of data concerning their action mechanism.

Several efforts have been made to understand the molecular mechanism(s) of biological responses of homeopathic drugs,[35-37] but many aspects remain to be clarified. Recent research has demonstrated the anti-inflammatory effects of *Arnica m.* plant extract and one of its active principles, helenalin. Furthermore, this plant is widely employed for another therapeutic property that plays a central role for human health, i.e. the promotion of wound healing. In a randomized double-blind study conducted on humans, *Arnica m.* at low homeopathic dilution (4x) reduced wound irritation (redness, swelling and heat) after hallux valgus surgery and ameliorated postoperative conditions in fewer days than did diclofenac.[1] An anti-inflammatory effect of *Arnica m.* (6c dilution) on carrageenan-induced foot oedema in rats has been reported by some authors[10] and a complex homeopathic product based on *Arnica m.* plus other compounds at low dilutions (4x-6x) was effective for blood-induced experimental oedema.[38]

To better investigate the targets and mechanisms of *Arnica m.* action at cell level, we used a molecular biology approach, testing several dilutions of the plant extract on a panel of genes possibly involved in the function of human macrophages during inflammation and tissue repair. Based on the literature, human and mouse macrophages can be polarized by IL-4 into a wound-healing type,[22,33] and we confirmed this effect both morphologically and transcriptionally. Our cells were profoundly changed by IL-4 treatment, as shown the by differential expression of many genes (CCL4, CCL17, CCL 22, F13A1, and MMP1) that others have previously described as markers of a polarization typical of 'wound healing' macrophages.[23] The two

functional and genetic states of the cell were well differentiated as described in literature and responded in different ways to *Arnica m.* treatment.

The evaluation of gene expression by inflammatory cells provides a means of probing the effects of a drug using up-to date and reliable assay tools. In fact, analysis of gene expression by microarrays just 5 hours after an arterial injury showed that the most differentially expressed genes were primarily associated with inflammation, cell proliferation, migration, and adhesion.[39] Similarly, internal damage such as traumatic brain injury can exhibit a significant overrepresentation of genes belonging to the inflammation, stress, and signalling categories, such as CCL3, CXCL1, IL1B.[40] Being key-cells of inflammatory processes, macrophages are involved in both tissue damage and repair, and their pharmacological regulation may have a profound impact on the progression of wound healing.

The results of the present study suggest a possible regulating role of *Arnica m.*, involving a direct effect on both types of macrophages, with a slight but significant influence on the expression of some relevant genes belonging to inflammatory pathways and connective tissue defence and repair (see a summary in Figure 7). One important and novel finding was the marked difference between the effects of *Arnica m.* in Normal Mac and IL-4 Mac. In the basal state (Normal Mac), the main significant change was a slight down-regulation of the genes of two pro-inflammatory cytokines, namely IL1B and TNFA. This effect can be linked to a decrease in expression of genes of the NF-kappaB complex, in agreement with the claimed anti-inflammatory effect of this plant. IL1B plays a major role in regulating inflammatory mediator production in wounds by stimulating the production of multiple cytokines and chemokines, with important aspects of wound biology.[41]

One of the most striking and unexpected effects of *Arnica m.* on IL-4 Mac was the increase of chemokines of the CXC family (CXCL1, CXCL2, IL8) (Figure 4 A,B,C respectively). The effects were higher after 24 hours of treatment, but generally were visible already after 2 hours, indicating a rapid response of the cellular genome. If confirmed, this finding suggests a new property of this plant in wound-healing processes. Cytokines and chemokines promote inflammation and angiogenesis, facilitate the passage of leukocytes from circulation into the tissue, and contribute to the regulation of epithelialization.[42] Thus, their pharmacological fine-tuning can be regarded as a possible way to regulate this complex series of events. CXCL1 and CXCL2 stimulate the expression of specific integrin proteins on the surface of human neutrophils, which can be rapidly induced to adhere to the extracellular matrix and migrate into injured tissue.[43,44] Besides stimulating neutrophil adhesion and chemotaxis, a positive effect of CXC chemokine up-regulation could also concern angiogenesis. The chemokine-mediated regulation of angiogenesis is highly sophisticated, finely tuned, and involves pro-angiogenic chemokines, including CXCL1,-3,-5,-8 and their receptors, CXCR1 and CXCR2. CXCL1 and CXCR2 are expressed in normal human epidermis and are further induced during the wound healing process of human burn wounds, especially during the inflammatory, epithelialization and angiogenic processes.[42,45,46] The topical application of pantothenic acid (vitamin B5) is widely used in skin care and in treating various dermatological diseases because it stimulates skin regeneration and promotes wound healing. Up-regulation of gene expression of CXCL1, CCL18, IL-6, IL1B and other factors are among the molecular mechanisms responsible for the effect of pantothenic acid in wound healing.[47]

A positive influence on connective tissue reinforcement can be also exercised by the decrease of metalloproteinase (MMP1), coding for an enzyme capable of cleaving extracellular matrix substrates and involved in many pathologic processes.[48] Our finding is in keeping with a previous study showing that *Arnica m.* preparations suppress MMP1 and MMP13 mRNA levels in bovine and human articular chondrocytes.[49] Also the slight increase in bone morphogenetic protein (BMP2) gene expression after treatment with *Arnica m.* is important because BMP2 is required for the initiation of bone repair[25,50] or other regenerative processes

in vitro,[51] and BMP2 gene expression is activated in the wounds caused by tooth extraction in mice treated with alendronate, an antiresorptive agent widely used for the cure of osteoporosis.[52]

The extent of differential regulation by *Arnica m.* on both types of macrophages was generally low and reached statistical significance only in a minority of the considered genes and dilutions. The slight effect in this *in vitro* model does not mean that the modulating effect will also be small *in vivo,* in whole organisms. Whereas conventional anti-inflammatory drugs are designed to suppress the underlying enzymatic mechanism of inflammation (e.g. prostaglandins, cytokines) and act at considerably high doses, homeopathic treatment is designed to regulate only the pathological excess of inflammation, because the phenomenon in itself is seen as an expression of natural healing dynamics. Given the variety of *Arnica m.* effects and the multiplicity of its alkaloids, flavonoids and sesquiterpene lactones,[53] it is conceivable that the picture of its action is much more complex and could involve modulation of further pathways. These aspects can be addressed using "omic" approaches such as total RNA sequencing and proteomic analysis, which are under investigation in our laboratory.

The ability of highly diluted compounds to modulate gene expression in human/animal cells and unicellular organisms has previously been reported by some authors. A complex homeopathic medication (Canova) used as an immunostimulant produced a differential expression in 147 genes of macrophages involved in transcription/translation, cell structure and dynamics, immune response, cytoprotection, enzymatic process, and receptors/ligands;[54] one of the down-regulated transcripts was CCL5, as also observed in this study. In experiments using microbiological models, ultradiluted *Arnica m.* 30c modified the expression of specific genes that are the targets UV irradiation injury.[55] Preethi and co-workers investigated the effects of antitumor homeopathic medicines through the analysis of expression changes in the whole genome using DNA microarray.[56] In human epithelial cell line, highly diluted preparations obtained from *Apis mellifica* (3c, 5c and 7c) modulated hundreds of genes including those involved in cytokine expression, inflammatory processes, and anti-oxidative responses.[57] These findings support the hypothesis that homeopathic remedies could turn some important genes on or off, initiating a cascade of gene actions to correct the gene expression that has gone wrong and so produced the disorder or disease.

A final aspect to be discussed is the unusual dose-effect relations of the effect of *Arnica m.* on the expression of many genes. The statistical evaluation of the set of genes observed in this RT-array panel (Wilcoxon test in Tables 2 and 3) showed that the lower dilutions (2c, 3c, 5c) have a tendency to inhibition of gene expression, while the highest (particularly the 15c) always lead to an up-regulation (statistically significant at 24 hours in the Normal Mac and at 2 hours and 24 hours in IL4 Mac). This observation could be in line with the views that gene expression is modulated by a hormetic effect as recently suggested by others.[58] However, this type of inversion of effects applies on the median behaviour of the gene set and on some genes in particular (CCL3, L1B and TNFA in Table 2B; TNFA in Table 3B), while other important genes (see figures 3 to 6), including CXC chemokines have no hormetic trends, showing remarkable consistency between the responses to higher and lower dilutions. The role of hormesis in homeopathic effects is still a matter of investigation and discussion,[59-62] particularly because in this pharmacologic approach also high dilutions are used, where the conventional dose-response paradigm should be revised in view of physicochemical factors such as water clusters and nanoparticles.[63-65]

Genes of CXC chemokines and NF-kappaB complex were modulated in a non-linear way, and often showed some effects that were higher in higher dilutions (Figures 4A, 4C and 5A). Among the genes that were affected by *Arnica m.* treatment, in 5 cases the 15c was the only significantly active dilution (see CCL23 in Table 2A, IL10 in 2B, CCL17 and CCR5 in 3A, CCL2 in 3B). This kind of non-linearity of homeopathic drugs has previously been observed

by us[66,67] and others.[57,68-74] High sensitivity to external regulations and nonlinear responses are frequently reported also with non-homeopathic dilutions. For example, mouse fibroblasts responded to TNF-α at concentrations as low as few pg/ml (10^{-12} g, corresponding approximately to a 6c dilution) and in a non-linear manner, since early NF-кappaB gene expression was not dependent on the concentration of the inducing signal.[75] Moreover, the cell response was expressed as a dynamical oscillations of NF-kappaB translocations, whose frequency can produce distinct gene expression profiles.[76] On the basis of DNA microarray data, it has been suggested that gene regulatory networks may be regarded as dynamically 'critical' systems poised near the transition phase between order and chaos[77,78] where extreme sensitivity to initial conditions and small perturbations are known to occur. Genetic regulatory networks may be the target of subtle messages by virtue of their flexibility of response to environmental stimuli.[78] In such a situation, a variability of responses to low doses of drugs is also to be expected: if a treatment acts by influencing the cell genetic networks by means of small doses, this action could be highly sensitive to even small changes in experimental conditions.[79,80]

In conclusion, this study surveyed for the first time several *Arnica m.* dilutions on human macrophages, using real-time RT-Array PCR of a panel of cytokines and chemokines. With this technique, a small but significant down-regulation of inflammatory genes was detected in normal macrophages, confirming previous findings, while in IL-4 treated macrophages *Arnica m.* promoted the down-regulation of genes for metalloproteinase-1 and the up-regulation of those for chemokines that are involved in connective tissue healing after injury. These findings lead to new working hypotheses concerning the action of this plant on macrophages, and thus on the complex mechanisms of tissue repair.

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References

1   Karow JH, Abt HP, Frohling M, Ackermann H. Efficacy of Arnica montana D4 for healing of wounds after Hallux valgus surgery compared to diclofenac. *J Altern Complement Med* 2008;**14**:17-25.

2   Reddy KK, Grossman L, Rogers GS. Common complementary and alternative therapies with potential use in dermatologic surgery: risks and benefits. *J Am Acad Dermatol* 2013;**68**:e127-e135.

3   Iannitti T, Morales-Medina JC, Bellavite P, Rottigni V, Palmieri B. Effectiveness and Safety of Arnica montana in Post-Surgical Setting, Pain and Inflammation. *Am J Ther* 2016; 23: e184-197.

4   Stevinson C, Devaraj VS, Fountain-Barber A, Hawkins S, Ernst E. Homeopathic arnica for prevention of pain and bruising: randomized placebo-controlled trial in hand surgery. *J R Soc Med* 2003;**96**:60-65.

5   Barlow T, Downham C, Barlow D. The effect of complementary therapies on post-operative pain control in ambulatory knee surgery: a systematic review. *Complement Ther Med* 2013;**21**:529-534.

6   Cornu C, Joseph P, Gaillard S, Bauer C, Vedrinne C, Bissery A, Melot G, Bossard N, Belon P, Lehot JJ. No effect of a homoeopathic combination of Arnica montana and Bryonia alba on bleeding, inflammation, and ischaemia after aortic valve surgery. *Br J Clin Pharmacol* 2010;**69**:136-142.

7   Cameron M, Chrubasik S. Topical herbal therapies for treating osteoarthritis. *Cochrane Database Syst Rev* 2013;**5**:CD010538.

8   Sharma S, Arif M, Nirala RK, Gupta R, Thakur SC. Cumulative therapeutic effects of phytochemicals in Arnica montana flower extract alleviated collagen-induced arthritis: inhibition of both pro-inflammatory mediators and oxidative stress. *J Sci Food Agric* 2015, doi: 10.1002/jsfa.7252.

9   Macedo SB, Ferreira LR, Perazzo FF, Carvalho JC. Anti-inflammatory activity of Arnica montana 6cH: preclinical study in animals. *Homeopathy* 2004;**93**:84-87.

10   Kawakami AP, Sato C, Cardoso TN, Bonamin LV. Inflammatory Process Modulation by Homeopathic Arnica montana 6CH: The Role of Individual Variation. *Evid Based Complement Alternat Med* 2011;**2011**:917541.

11   Klaas CA, Wagner G, Laufer S, Sosa S, Della LR, Bomme U, Pahl HL, Merfort I. Studies on the anti-inflammatory activity of phytopharmaceuticals prepared from Arnica flowers. *Planta Med* 2002;**68**:385-391.

12   Sutovska M, Capek P, Kocmalova M, Pawlaczyk I, Zaczynska E, Czarny A, Uhliarikova I, Gancarz R, Franova S. Characterization and pharmacodynamic properties of Arnica montana complex. *Int J Biol Macromol* 2014;**69**:214-221.

13   Lyss G, Schmidt TJ, Merfort I, Pahl HL. Helenalin, an anti-inflammatory sesquiterpene lactone from Arnica, selectively inhibits transcription factor NF-kappaB. *Biol Chem* 1997;**378**:951-961.

14   Jeschke E, Ostermann T, Luke C, Tabali M, Kroz M, Bockelbrink A, Witt CM, Willich SN, Matthes H. Remedies containing Asteraceae extracts: a prospective observational study of prescribing patterns and adverse drug reactions in German primary care. *Drug Saf* 2009;**32**:691-706.

15   Craciunescu O, Constantin D, Gaspar A, Toma L, Utoiu E, Moldovan L. Evaluation of antioxidant and cytoprotective activities of Arnica montana L. and Artemisia absinthium L. ethanolic extracts. *Chem Cent J* 2012;**6**:97.

16   de Camargo RA, da Costa ED, Catisti R. Effect of the oral administration homeopathic Arnica montana on mitochondrial oxidative stress. *Homeopathy* 2013;**102**:49-53.

17   Verma N, Tripathi SK, Sahu D, Das HR, Das RH. Evaluation of inhibitory activities of plant extracts on production of LPS-stimulated pro-inflammatory mediators in J774 murine macrophages. *Mol Cell Biochem* 2010;**336**:127-135.

18   Hostanska K, Rostock M, Melzer J, Baumgartner S, Saller R. A homeopathic remedy from arnica, marigold, St. John's wort and comfrey accelerates in vitro wound scratch closure of NIH 3T3 fibroblasts. *BMC Complement Altern Med* 2012;**12**:100.

19   Castro FC, Magre A, Cherpinski R, Zelante PM, Neves LM, Esquisatto MA, Mendonca FA, Santos GM. Effects of microcurrent application alone or in combination with topical Hypericum perforatum L. and Arnica montana L. on surgically induced wound healing in Wistar rats. *Homeopathy* 2012;**101**:147-153.

20   Amsen D, Spilianakis CG, Flavell RA. How are T(H)1 and T(H)2 effector cells made? *Curr Opin Immunol* 2009;**21**:153-160.

21   Wu LC, Scheerens H. Targeting IgE production in mice and humans. *Curr Opin Immunol* 2014;**31**:8-15.

22   Gordon S. Alternative activation of macrophages. *Nat Rev Immunol* 2003;**3**:23-35.

23   Murray PJ, Allen JE, Biswas SK, Fisher EA, Gilroy DW, Goerdt S, Gordon S, Hamilton JA, Ivashkiv LB, Lawrence T, Locati M, Mantovani A, Martinez FO, Mege JL, Mosser DM, Natoli G, Saeij JP, Schultze JL, Shirey KA, Sica A, Suttles J, Udalova I, van Ginderachter JA, Vogel SN, Wynn TA. Macrophage activation and polarization: nomenclature and experimental guidelines. *Immunity* 2014;**41**:14-20.

24   Martinez FO, Helming L, Milde R, Varin A, Melgert BN, Draijer C, Thomas B, Fabbri M, Crawshaw A, Ho LP, Ten Hacken NH, Cobos J, V, Kootstra NA, Hamann J, Greaves DR, Locati M, Mantovani A, Gordon S. Genetic programs expressed in resting and IL-4 alternatively activated mouse and human macrophages: similarities and differences. *Blood* 2013;**121**:e57-e69.

25   Werner S, Grose R. Regulation of wound healing by growth factors and cytokines. *Physiol Rev* 2003;**83**:835-870.

26   Christian LM, Graham JE, Padgett DA, Glaser R, Kiecolt-Glaser JK. Stress and wound healing. *Neuroimmunomodulation* 2006;**13**:337-346.

27   Qin L, Crews FT. NADPH oxidase and reactive oxygen species contribute to alcohol-induced microglial activation and neurodegeneration. *J Neuroinflammation* 2012;**9**:5.

28   Olioso D, Marzotto M, Moratti E, Brizzi M, Bellavite P. Effects of Gelsemium sempervirens L. on pathway-focused gene expression profiling in neuronal cells. *J Ethnopharmacol* 2014;**153**:535-539.

29   Hofbauer R, Pasching E, Moser D, Frass M. Heparin-binding epidermal growth factor expression in KATO-III cells after Helicobacter pylori stimulation under the influence of strychnos Nux vomica and Calendula officinalis. *Homeopathy* 2010;**99**:177-182.

30   Huh YH, Kim MJ, Yeo MG. Homeopathic Rhus toxicodendron treatment increased the expression of cyclooxygenase-2 in primary cultured mouse chondrocytes. *Homeopathy* 2013;**102**:248-253.

31   Sharif O, Bolshakov VN, Raines S, Newham P, Perkins ND. Transcriptional profiling of the LPS induced NF-kappaB response in macrophages. *BMC Immunol* 2007;**8**:1.

32   Takashiba S, Van Dyke TE, Amar S, Murayama Y, Soskolne AW, Shapira L. Differentiation of monocytes to macrophages primes cells for lipopolysaccharide stimulation via accumulation of cytoplasmic nuclear factor kappaB. *Infect Immun* 1999;**67**:5573-5578.

33   Jin C, Wu L, Li J, Fang M, Cheng L, Wu N. Multiple signaling pathways are involved in the interleukine-4 regulated expression of DC-SIGN in THP-1 cell line. *J Biomed Biotechnol* 2012;**2012**:357060.

34   Ishiyama M, Tominaga H, Shiga M, Sasamoto K, Ohkura Y, Ueno K. A combined assay of cell viability and in vitro cytotoxicity with a highly water-soluble tetrazolium salt, neutral red and crystal violet. *Biol Pharm Bull* 1996;**19**:1518-1520.

35   Khuda-Bukhsh AR. Towards understanding molecular mechanisms of action of homeopathic drugs: an overview. *Mol Cell Biochem* 2003;**253**:339-345.

36   Bellavite P, Marzotto M, Olioso D, Moratti E, Conforti A. High-dilution effects revisited. 2. Pharmacodynamic mechanisms. *Homeopathy* 2014;**103**:22-43.

37   Marotti I, Betti L, Bregola V, Bosi S, Trebbi G, Borghini G, Nani D, Dinelli G. Transcriptome Profiling of Wheat Seedlings following Treatment with Ultrahigh Diluted Arsenic Trioxide. *Evid Based Complement Alternat Med* 2014;**2014**:851263.

38   Lussignoli S, Bertani S, Metelmann H, Bellavite P, Conforti A. Effect of Traumeel S, a homeopathic formulation, on blood-induced inflammation in rats. *Complement Ther Med* 1999;**7**:225-230.

39   Fedorov A, Kostareva A, Raud J, Roy J, Hedin U, Razuvaev A. Early changes of gene expression profiles in the rat model of arterial injury. *J Vasc Interv Radiol* 2014;**25**:789-796.

40   Redell JB, Moore AN, Grill RJ, Johnson D, Zhao J, Liu Y, Dash PK. Analysis of functional pathways altered after mild traumatic brain injury. *J Neurotrauma* 2013;**30**:752-764.

41   Hu Y, Liang D, Li X, Liu HH, Zhang X, Zheng M, Dill D, Shi X, Qiao Y, Yeomans D, Carvalho B, Angst MS, Clark JD, Peltz G. The role of interleukin-1 in wound biology. Part II: In vivo and human translational studies. *Anesth Analg* 2010;**111**:1534-1542.

42   Zaja-Milatovic S, Richmond A. CXC chemokines and their receptors: a case for a significant biological role in cutaneous wound healing. *Histol Histopathol* 2008;**23**:1399-1407.

43   Burke SJ, Lu D, Sparer TE, Masi T, Goff MR, Karlstad MD, Collier JJ. NF-kappaB and STAT1 control CXCL1 and CXCL2 gene transcription. *Am J Physiol Endocrinol Metab* 2014;**306**:E131-E149.

44   Stadtmann A, Block H, Volmering S, Abram C, Sohlbach C, Boras M, Lowell CA, Zarbock A. Cross-Talk between Shp1 and PIPKIgamma Controls Leukocyte Recruitment. *J Immunol* 2015;**195**:1152-1161.

45   Yew TL, Hung YT, Li HY, Chen HW, Chen LL, Tsai KS, Chiou SH, Chao KC, Huang TF, Chen HL, Hung SC. Enhancement of wound healing by human multipotent stromal cell conditioned medium: the paracrine factors and p38 MAPK activation. *Cell Transplant* 2011;**20**:693-706.

46   Vries MH, Wagenaar A, Verbruggen SE, Molin DG, Dijkgraaf I, Hackeng TH, Post MJ. CXCL1 promotes arteriogenesis through enhanced monocyte recruitment into the peri-collateral space. *Angiogenesis* 2015;**18**:163-171.

47   Heise R, Skazik C, Marquardt Y, Czaja K, Sebastian K, Kurschat P, Gan L, Denecke B, Ekanayake-Bohlig S, Wilhelm KP, Merk HF, Baron JM. Dexpanthenol modulates gene expression in skin wound healing in vivo. *Skin Pharmacol Physiol* 2012;**25**:241-248.

48   Arakaki PA, Marques MR, Santos MC. MMP-1 polymorphism and its relationship to pathological processes. *J Biosci* 2009;**34**:313-320.

49   Jager C, Hrenn A, Zwingmann J, Suter A, Merfort I. Phytomedicines prepared from Arnica flowers inhibit the transcription factors AP-1 and NF-kappaB and modulate the activity of MMP1 and MMP13 in human and bovine chondrocytes. *Planta Med* 2009;**75**:1319-1325.

50   Chappuis V, Gamer L, Cox K, Lowery JW, Bosshardt DD, Rosen V. Periosteal BMP2 activity drives bone graft healing. *Bone* 2012;**51**:800-809.

51   Lynch KM, Ahsan T. Correlating the effects of bone morphogenic protein to secreted soluble factors from fibroblasts and mesenchymal stem cells in regulating regenerative processes in vitro. *Tissue Eng Part A* 2014;**20**:3122-3129.

52   Tanoue R, Koi K, Yamashita J. Effect of Alendronate on Bone Formation during Tooth Extraction Wound Healing. *J Dent Res* 2015;**194**:1251-1258.

53   Ganzera M, Egger C, Zidorn C, Stuppner H. Quantitative analysis of flavonoids and phenolic acids in Arnica montana L. by micellar electrokinetic capillary chromatography. *Anal Chim Acta* 2008;**614**:196-200.

54   de Oliveira CC, de Oliveira SM, Goes VM, Probst CM, Krieger MA, Buchi DF. Gene expression profiling of macrophages following mice treatment with an immunomodulator medication. *J Cell Biochem* 2008;**104**:1364-1377.

55   Das S, Saha SK, De A, Das D, Khuda-Bukhsh AR. Potential of the homeopathic remedy, Arnica Montana 30C, to reduce DNA damage in Escherichia coli exposed to ultraviolet irradiation through up-regulation of nucleotide excision repair genes. *Zhong Xi Yi Jie He Xue Bao* 2012;**10**:337-346.

56   Preethi K, Ellanghiyil S, Kuttan G, Kuttan R. Induction of apoptosis of tumor cells by some potentiated homeopathic drugs: implications on mechanism of action. *Integr Cancer Ther* 2012;**11**:172-182.

57   Bigagli E, Luceri C, Bernardini S, Dei A, Filippini A, Dolara P. Exploring the effects of homeopathic Apis mellifica preparations on human gene expression profiles. *Homeopathy* 2014;**103**:127-132.

58   Dei A, Bernardini S. Hormetic effects of extremely diluted solutions on gene expression. *Homeopathy* 2015;**104**:116-122.

59   Rattan SI, Deva T. Testing the hormetic nature of homeopathic interventions through stress response pathways. *Hum Exp Toxicol* 2010;**29**:551-554.

60   Bellavite P, Chirumbolo S, Marzotto M. Hormesis and its relationship with homeopathy. *Hum Exp Toxicol (BELLE Newsl)* 2010;**16**:11-18.

61   Bellavite P, Signorini A, Marzotto M, Moratti E, Bonafini C, Olioso D. Cell sensitity, non-linearity and inverse effects. *Homeopathy* 2015;**104**:139-160.

62   Oberbaum M, Frass M, Gropp C. Unequal brothers : are homeopathy and hormesis linked? *Homeopathy* 2015;**104**:97-100.

63   Chikramane PS, Suresh AK, Bellare JR, Kane SG. Extreme homeopathic dilutions retain starting materials: A nanoparticulate perspective. *Homeopathy* 2010;**99**:231-242.

64   Bell IR, Schwartz GE. Enhancement of adaptive biological effects by nanotechnology preparation methods in homeopathic medicines. *Homeopathy* 2015;**104**:123-138.

65   Bellavite P, Marzotto M, Olioso D, Moratti E, Conforti A. High-dilution effects revisited. 1. Physicochemical aspects. *Homeopathy* 2014;**103**:4-21.

66   Chirumbolo S, Brizzi M, Ortolani R, Vella A, Bellavite P. Inhibition of CD203c membrane up-regulation in human basophils by high dilutions of histamine: a controlled replication study. *Inflamm Res* 2009;**58**:755-764.

67   Magnani P, Conforti A, Zanolin E, Marzotto M, Bellavite P. Dose-effect study of Gelsemium sempervirens in high dilutions on anxiety-related responses in mice. *Psychopharmacology (Berl)* 2010;**210**:533-545.

68   Poitevin B, Davenas E, Benveniste J. In vitro immunological degranulation of human basophils is modulated by lung histamine and Apis mellifica. *Br J Clin Pharmacol* 1988;**25**:439-444.

69   Sainte-Laudy J, Belon P. Inhibition of basophil activation by histamine: a sensitive and reproducible model for the study of the biological activity of high dilutions. *Homeopathy* 2009;**98**:186-197.

70   Bigagli E, Luceri C, Bernardini S, Dei A, Dolara P. Extremely low copper concentrations affect gene expression profiles of human prostate epithelial cell lines. *Chem Biol Interact* 2010;**188**:214-219.

71   Endler P, Thieves K, Reich C, Matthiessen P, Bonamin L, Scherr C, Baumgartner S. Repetitions of fundamental research models for homeopathically prepared dilutions beyond 10(-23): a bibliometric study. *Homeopathy* 2010;**99**:25-36.

72   Mannaioni PF, Mastroianni R, Mastrangelo D. Adrenaline inhibits the immunological activation of human basophils at pharmacological and ultra-low doses. *Med Sci Monit* 2010;**16**:BR227-BR232.

73   Venard C, Boujedaini N, Mensah-Nyagan AG, Patte-Mensah C. Comparative analysis of gelsemine and Gelsemium sempervirens activity on neurosteroid allopregnanolone formation in the spinal cord and limbic system. *Evid Based Complement Alternat Med* 2011;**doi: 10.1093/ecam/nep083**:407617.

74   Arora S, Aggarwal A, Singla P, Jyoti S, Tandon S. Anti-proliferative effects of homeopathic medicines on human kidney, colon and breast cancer cells. *Homeopathy* 2013;**102**:274-282.

75   Tay S, Hughey JJ, Lee TK, Lipniacki T, Quake SR, Covert MW. Single-cell NF-kappaB dynamics reveal digital activation and analogue information processing. *Nature* 2010;**466**:267-271.

76   Ashall L, Horton CA, Nelson DE, Paszek P, Harper CV, Sillitoe K, Ryan S, Spiller DG, Unitt JF, Broomhead DS, Kell DB, Rand DA, See V, White MR. Pulsatile stimulation determines timing and specificity of NF-kappaB-dependent transcription. *Science* 2009;**324**:242-246.

77   Ramo P, Kesseli J, Yli-Harja O. Perturbation avalanches and criticality in gene regulatory networks. *J Theor Biol* 2006;**242**:164-170.

78   Balleza E, varez-Buylla ER, Chaos A, Kauffman S, Shmulevich I, Aldana M. Critical dynamics in genetic regulatory networks: examples from four kingdoms. *PLoS ONE* 2008;**3**:e2456.

79   Bellavite P. Complexity science and homeopathy. A synthetic overview. *Homeopathy* 2003;**92**:203-212.

80   Bell IR, Baldwin CM, Schwartz GE. Translating a nonlinear systems theory model for homeopathy into empirical tests. *Altern Ther Health Med* 2002;**8**:58-66.