



# Monocyte-derived dendritic cells from HLA-B27+ axial spondyloarthritis (SpA) patients display altered functional capacity and deregulated gene expression

Alice Talpin, Félicie Costantino, Nelly Bonilla, Ariane Leboime, Franck Letourneur, Sébastien Jacques, Florent Dumont, Sonia Amraoui, Charles-Antoine Dutertre, Henri-Jean Garchon, et al.

## ► To cite this version:

Alice Talpin, Félicie Costantino, Nelly Bonilla, Ariane Leboime, Franck Letourneur, et al.. Monocyte-derived dendritic cells from HLA-B27+ axial spondyloarthritis (SpA) patients display altered functional capacity and deregulated gene expression. *Arthritis Research and Therapy*, BioMed Central, 2014, 16 (4), pp.417. <10.4049/jimmunol.177.3.1932>. <inserm-01122331>

**HAL Id: inserm-01122331**

**<http://www.hal.inserm.fr/inserm-01122331>**

Submitted on 3 Mar 2015

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



RESEARCH ARTICLE

Open Access

# Monocyte-derived dendritic cells from HLA-B27<sup>+</sup> axial spondyloarthritis (SpA) patients display altered functional capacity and deregulated gene expression

Alice Talpin<sup>1,2</sup>, Félicie Costantino<sup>1,2,3</sup>, Nelly Bonilla<sup>4</sup>, Ariane Leboime<sup>3</sup>, Franck Letourneur<sup>4</sup>, Sébastien Jacques<sup>4</sup>, Florent Dumont<sup>4</sup>, Sonia Amraoui<sup>4,5</sup>, Charles-Antoine Dutertre<sup>6</sup>, Henri-Jean Garchon<sup>1,2,3,7</sup>, Maxime Breban<sup>1,2,3</sup> and Gilles Chiochia<sup>1,2\*</sup>

## Abstract

**Introduction:** This study aimed to compare the functional capacity and gene expression profile of monocyte-derived dendritic cells (MD-DCs) in HLA-B27<sup>+</sup> axial spondyloarthritis (SpA) patients and healthy controls.

**Methods:** MD-DCs were differentiated with interleukin 4 (IL-4) and granulocyte-macrophage colony-stimulating factor (GM-CSF) for seven days, starting from purified CD14<sup>+</sup> monocytes and stimulated with lipopolysaccharide (LPS) for six and twenty four hours. Their capacity to stimulate allogeneic CD4<sup>+</sup> T cells from unrelated healthy donor was tested. Transcriptomic study was performed with Affymetrix HuGene 1.0 ST microarrays. Gene expression levels were compared between patients and controls using a multivariate design under a linear model (LIMMA). Real-time quantitative PCR (qRT-PCR) was performed for validation of the most striking gene expression differences.

**Results:** The stimulatory capacity of allogeneic CD4<sup>+</sup> T cells by MD-DCs from SpA patients was decreased. Transcriptomic analysis revealed 81 genes differentially expressed in MD-DCs between SpA patients and controls ( $P < 0.01$  and fold-change  $< 0.66$  or  $> 1.5$ ). Four selected genes were validated by qRT-PCR: *ADAMTS15*, *CITED2*, *F13A1* and *SELL*. Expression levels of *ADAMTS15* and *CITED2*, encoding a metalloproteinase and a transcription factor, respectively, were inversely correlated with each other ( $R = 0.75$ ,  $P = 0.0003$ ). Furthermore, *in silico* analysis identified several genes of the Wnt signaling pathway having expression co-regulated with *CITED2*.

**Conclusion:** This study revealed altered function and gene expression pattern in MD-DCs from HLA-B27<sup>+</sup> axial SpA. Co-expression study showed an inverse correlation between *ADAMTS15* and *CITED2*. Moreover, the Wnt signaling pathway appeared as deregulated in SpA MD-DCs, a finding which may be connected to Th17-driven inflammatory responses.

## Introduction

Spondyloarthritis (SpA) is a chronic inflammatory rheumatic disorder, with a prevalence of around 0.42% in Caucasian populations [1]. Joint inflammation is responsible for pain and stiffness but long-term outcome is mainly determined by new bone formation, which can lead to complete ankylosis. Effective treatments such as

TNF blockers can temporarily suppress inflammation, but none has yet proven to affect long-term disease outcome. Therefore, there is a need to better understand pathological mechanisms controlling both initiation and progression of SpA.

Genome-wide gene expression analysis is a powerful approach to identify molecular mechanisms responsible for a disease. Microarray studies have already been conducted in SpA, most of them focusing on the ankylosing spondylitis (AS) subtype [2-7]. Each of those studies identified several genes differentially expressed between patients and

\* Correspondence: gilles.chiochia@inserm.fr

<sup>1</sup>INSERM U987, Laboratoire d'excellence INFLAMEX, Université Versailles-Saint-Quentin, Versailles 78000, France

<sup>2</sup>UFR des Sciences de la Santé, Simone Veil, Versailles Saint Quentin en Yvelines Université, Montigny-Le-Bretonneux 78180, France

Full list of author information is available at the end of the article

controls but there was very little overlap between their results, maybe due to the variety of protocols.

Several studies support an important role of dendritic cells (DCs) in the pathogenesis of SpA. Indeed, aberrant functions of DCs have been demonstrated in an HLA-B27/human  $\beta$ 2-microglobulin transgenic rat model of SpA [8]. First, DCs from these rats have a decreased capacity to stimulate primary allogeneic or syngeneic T cell responses [9]. Furthermore, the proportion of conjugates formed between HLA-B27 DCs and naïve CD4<sup>+</sup> T cells is reduced. Moreover, mature HLA-B27 molecules expressed by DCs appear to impair the formation of an antigen-independent immunologic synapse with naïve CD4<sup>+</sup> T cells by interfering with the engagement of co-stimulatory molecules [10]. Finally, B27 transgenic rat DCs were shown to favor Th17 expansion [11,12] and to alter regulatory T cell function, resulting in decreased IL-10 and enhanced IL-17 production [13].

On this basis, we hypothesized that DCs also play an important role in human disease, as proposed in the HLA-B27 transgenic rat model. The aim of the current study was to compare functional capacity and the gene expression profile of monocyte-derived DCs (MD-DCs) in patients with HLA-B27<sup>+</sup> axial SpA and healthy controls.

## Methods

### Patients and controls

We studied three different groups of patients and controls: 10 patients and 5 controls for monocyte subset characterization by flow cytometry, 19 patients and 24 controls for mixed lymphocyte reaction and 9 patients and 10 controls for the MD-DC transcriptomic study (6 patients and 4 controls were investigated for the two latter). All the patients were HLA-B27<sup>+</sup> and fulfilled the Assessment of SpondyloArthritis International Society classification criteria for axial SpA [14]. Controls were healthy blood donors.

Patients' and healthy controls' characteristics are summarized in the Additional files (see Additional file 1: Table S1 and Additional file 2: Table S2, respectively). All participants in the study gave written informed consent and the study was approved by local ethics committee of Ile-de-France XI (Saint-Germain-en-Laye France).

### Cell isolation, culture and stimulation

Peripheral blood mononuclear cells (PBMCs) were isolated from 50 mL of blood by gradient separation on Ficoll density gradient centrifugation (STEMCELL Technologies, Grenoble, France). Monocytes used to generate MD-DCs were purified by magnetic cell sorting using anti-CD14 monoclonal antibody (mAb)-coated beads (BD IMag, Le Pont de Claix, France). Sorted monocytes were morphologically homogeneous with 99% of CD14<sup>+</sup> cells, as determined by flow cytometry.

Monocytes were further cultured for 6 days in 24-well plates (400,000 cells/500  $\mu$ L) in Roswell Park Memorial Institute (RPMI) 1640 medium supplemented with 10% heat-inactivated fetal calf serum, 100 U/mL penicillin, 100  $\mu$ g/mL streptomycin, 500 U/mL recombinant human granulocyte-macrophage colony stimulating factor (rhGM-CSF) and 500 U/mL rhIL-4 (AbCys, Paris, France). Then, the MD-DCs were stimulated or not with lipopolysaccharide (LPS) from *Escherichia coli* (LPS, Sigma-Aldrich, St Louis, MO, USA) at a concentration of 100 ng/mL for the last 6 or 24 hours of culture (further referred to as time points H0, H6 and H24).

CD4<sup>+</sup> T cells were purified from PBMCs from two unrelated healthy donors by magnetic cell sorting using anti-CD4 monoclonal antibody (mAb)-coated beads (BD IMag), and stored frozen until used for mixed lymphocyte reaction (MLR).

### Flow cytometry

To characterize monocyte subsets, freshly purified PBMCs were analyzed by six-color flow cytometry on FACS LSRII apparatus. The gating strategy was based on a previous report [15]. Monocytes were subdivided into three major subsets: classical CD14<sup>++</sup>CD16<sup>-</sup>, intermediate CD14<sup>++</sup>CD16<sup>+</sup> and non-classical CD14<sup>+</sup>CD16<sup>++</sup> monocytes. The following anti-human mAbs were used: CD45-Amcyan (BD Biosciences), HLA-DR-PerCP (BD Biosciences), CD19-ECD (Beckman Coulter), CD14-QDot655 (Invitrogen), CD16-APC-H7 (Beckman Coulter, Villepinte, France). The Live/Dead blue Dye (Invitrogen) was used to exclude dead cells.

Samples of the purified monocytes used to generate MD-DCs and of the resulting MD-DCs were routinely stained with the following anti-human mAbs: CD14-FITC, CD11c-APC, CD40-PE, HLA-I-FITC, HLA-DR-PerCP, CD80-PE, CD83-APC and CD86-FITC (all from BD Bioscience) and analyzed by flow cytometry on FACS canto II apparatus (BD Biosciences).

### Mixed lymphocyte reaction (MLR)

Purified allogeneic CD4<sup>+</sup> T cells (10<sup>5</sup> cells per well) from healthy donors were cultured with unstimulated (H0) or LPS-stimulated (H6, H24) MD-DCs (10<sup>4</sup> cells per well), in 96-well flat-bottomed culture dishes in a final volume of 200  $\mu$ L. Proliferation of T cells was assayed by measuring incorporation of <sup>3</sup>H-deoxythymidine added (0.5  $\mu$ Ci per well) after 6 days of culture, using a Microbeta scintillation counter (Wallac, Turku, Finland). Data are expressed as the mean counts per minute (CPM) in triplicate wells. An MLR index (ratio of CPM of MLR on CPM of CD4<sup>+</sup> T cells only) was used to represent CD4<sup>+</sup> T cell proliferation. Two stored CD4<sup>+</sup> T cell batches from different healthy donors were sequentially used for MLR in two sets of experiments, each including equivalent numbers of patient and control MD-DC samples. As there was no statistically significant

difference in the results between both sets of experiments, we pooled them. The Wilcoxon test was used to compare MLR indices between patients and controls at each stimulation time point.

### Transcriptomic study

#### RNA isolation

MD-DCs were disrupted and homogenized using RLT buffer (Qiagen, Valencia, CA, USA). Total RNA was isolated using RNeasy Mini Kit (Qiagen). RNA quantity and quality were assessed using Agilent 2100 Bioanalyzer (Agilent, Santa Clara, CA, USA). Only samples with an RNA integrity number (RIN) above 8 were further processed.

#### Microarray hybridization

RNA was reverse-transcribed, converted to biotinylated complementary RNA using standard Affymetrix protocol (Affymetrix, Santa Clara, CA, USA) and hybridized to the Affymetrix GeneChip Human Gene 1.0 ST Array by the genomic platform of the Cochin Institute.

#### Differential gene expression validation by qRT-PCR

For validation, the relative gene expression levels of candidate genes identified through the foregoing microarray study were further quantified using qRT-PCR. Briefly, RNA treated with DNase I (Invitrogen) was reverse-transcribed using SuperscriptII (Invitrogen) and then quantified using the SYBR green PCR Master Mix (Applied Biosystems) and the 7300 Real-Time PCR System (Applied Biosystems). Primers were purchased from Eurofins MWG (nucleotide sequences of the PCR primers are available in Additional file 3: Table S3). The experiment design included three technical replicates.

#### Statistical analysis

Raw Affymetrix data (.cel files) from 57 arrays (corresponding to H0, H6 and H24 time points of stimulation by LPS for 19 subjects) were transformed by the Robust Multichip Analysis (RMA) method using Bioconductor in R software (library Affy) [16]. This transformation included background correction, normalization and summarization of expression values using Brainarray version 15 custom chip definition (cdf) files generated with the Ensembl annotation set [17]. Before analysis, genes were filtered on annotation and expression level mean with a cut off at 6.11 (corresponding to the mean of expression level of both anti-genomic and intronic probes of housekeeping genes). Gene expression levels were then fitted to a bivariate linear model including disease status and time point after stimulation, using the LLinear Models for Microarray data (LIMMA) package of Bioconductor in R environment to determine differentially expressed genes [18]. The threshold for differential gene expression between patients and controls was

set to a global fold change above or below 1.5 with a nominal  $P$ -value below 0.01.

For qRT-PCR validation, gene expression data were computed with the  $\Delta\Delta Cq$  method, using three house-keeping genes: *RPL30*,  *$\beta$ -ACT* and *GAPDH*. Then, two-way analysis of variance (ANOVA) was used to test differential gene expression among samples from SpA and controls without (baseline; no treatment) and with LPS treatment for 6 and 24 hours. In case of statistical significance ( $P < 0.05$ ), post hoc  $t$ -tests with the Bonferroni correction allowed us to perform pairwise comparisons.

#### Paired genes co-expression study and molecular pathway analysis

Pairwise correlations between gene expression levels were tested using the nonparametric Spearman test. We used the commercial software Genomatix Pathway System [19] to identify significantly enriched pathways and functional themes, among the list of the best correlated genes with genes of interest.

## Results

### Functional impairment of MD-DCs from SpA patients

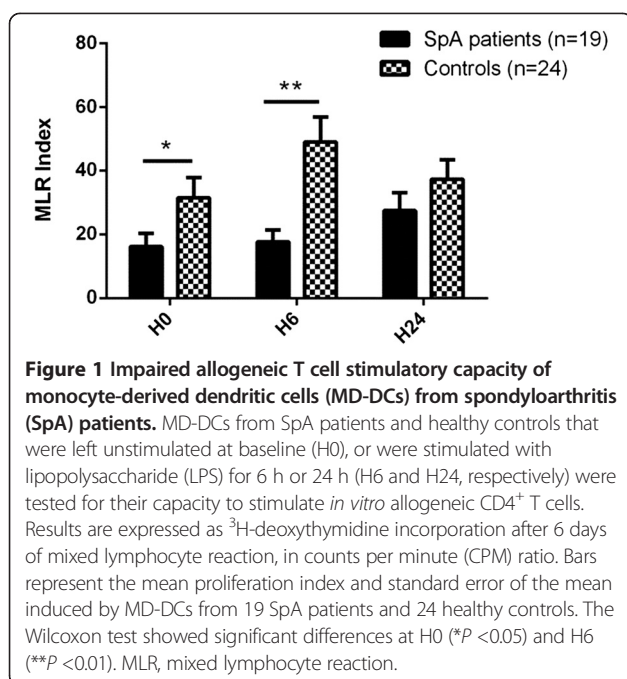
To verify that MD-DCs were differentiated from comparable monocyte populations between SpA patients and controls, we analyzed monocytes subsets in both groups. As shown in an additional file, the distribution of the classical, intermediate and non-classical circulating subsets among CD45<sup>+</sup> PBMCs was similar in patients and controls (see Additional file 4: Figure S1).

The cells obtained after 7 days of differentiation in culture in patients and controls were uniformly CD14<sup>-</sup>, CD11c<sup>+</sup>, CD40<sup>+</sup>, HLA-DR<sup>+</sup>, CD83<sup>dim</sup> and CD86<sup>+</sup>, consistent with a MD-DC phenotype. Moreover, HLA-DR, CD80 and CD86 expression increased and CD83 was induced on MD-DCs after LPS stimulation for 24 hours (Additional file 5: Figure S2).

In the rat model of SpA, HLA-B27 transgenic DCs have a decreased capacity to stimulate allogeneic T cells. Thus, we tested the capacity of MD-DCs from HLA-B27<sup>+</sup> SpA patients to prime allogeneic CD4<sup>+</sup> T cells using an *in vitro* proliferation assay. A weaker proliferation of CD4<sup>+</sup> T cells was observed with SpA MD-DCs as compared to controls, which was statistically significant before and after 6 hours of LPS exposure ( $P < 0.05$  and  $P < 0.01$ , respectively; Figure 1).

### Identification of differentially expressed genes in MD-DCs between patients and controls

To investigate the mechanisms underlying the functional defect of MD-DCs from SpA patients, we then compared gene expression levels in those cells between SpA and healthy donors upon stimulation with LPS. After filtering on gene expression level and gene annotation, 13,021 genes



(57.3% of the genes present in the microarray) were kept for further analysis. Expression data for MD-DCs either left unstimulated or stimulated with LPS for 6 or 24 hours were first globally compared between SpA patients and healthy subjects. Unsupervised hierarchical clustering showed that samples were perfectly grouped according to LPS stimulation time points (Additional file 6: Figure S3) but not to the disease status. Linear modeling nevertheless identified 81 genes differentially expressed between patients and controls at any time point, with a nominal *P*-value <0.01 and a fold change below 0.66 or greater than 1.5 (Additional file 7:

Table S4). Of this set of genes, 61 were downregulated and 20 were upregulated in patients.

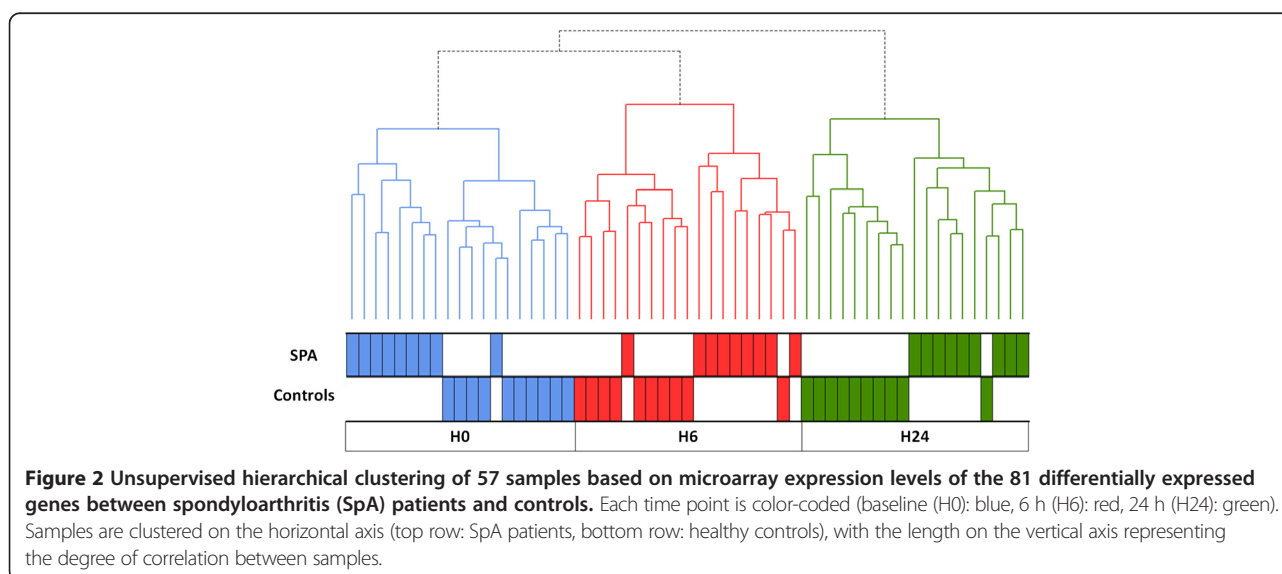
Using the extraction of the dataset corresponding to these 81 genes, LPS stimulation time points were perfectly separated by unsupervised hierarchical clustering. Furthermore, patients and controls were now clearly discriminated, with only four misclassifications (one at H0, two at H6 and one at H24) (Figure 2).

Four candidate genes were chosen for validation study on the basis of their *P*-value, fold change and biological relevance: *ADAMTS15*, *CITED2*, *F13A1* and *SELL*. For all four genes, the qRT-PCR data produced with the RNA samples used for the microarray study confirmed the significant differences in expression and the direction of changes between SpA patients and controls (Table 1, Figure 3): *ADAMTS15*, *F13A1* and *SELL* were significantly upregulated in SpA samples, whereas *CITED2* was downregulated.

#### Co-regulated genes in SpA patients

Examination of gene expression data indicated that some of them displayed similarity in their expression profile, suggesting co-regulation. Indeed, we found a highly significant negative correlation between *ADAMTS15* and *CITED2* expression levels at H6 in both patient and control groups (combined data:  $\rho = -0.75$ ; *P* = 0.0003; Figure 4).

Considering the transcriptional co-activator function of *CITED2* and its downregulation in SpA MD-DCs, we sought whether genes other than *ADAMTS15* shared a similarly co-regulated expression pattern in patient MD-DCs. We tested the correlation of the genome-wide expression matrix of patient MD-DCs with *CITED2* expression in a pairwise fashion. A set of 222 genes was found significantly correlated with *CITED2* (*P* <0.01). They were





**Table 1 qRT-PCR expression analysis of four selected genes in monocyte-derived dendritic cells from spondyloarthritis patients, as compared to controls**

Gene	Microarray P-value	qRT-PCR				
		P-value		Fold change		
		Disease	Disease/time	H0	H6	H24
<i>ADAMTS15</i>	0.0003	<b>0.0005</b>	<b>0.04</b>	2.2	<b>5.63</b>	2.2
<i>CITED2</i>	0.0007	0.21	<b>0.031</b>	0.94	<b>0.51</b>	0.99
<i>F13A1</i>	0.00006	<b>0.019</b>	<b>0.001</b>	1.32	1.25	<b>5.05</b>
<i>SELL</i>	0.006	<b>0.012</b>	0.8	<b>3.57</b>	<b>3.47</b>	2.97

P-value is reported considering the global effect, the effect of the disease status only or the effect of the disease status adjusted for time. Bold text indicates significant P-values and at what time the modulation of gene expression was significantly different between patients and controls.

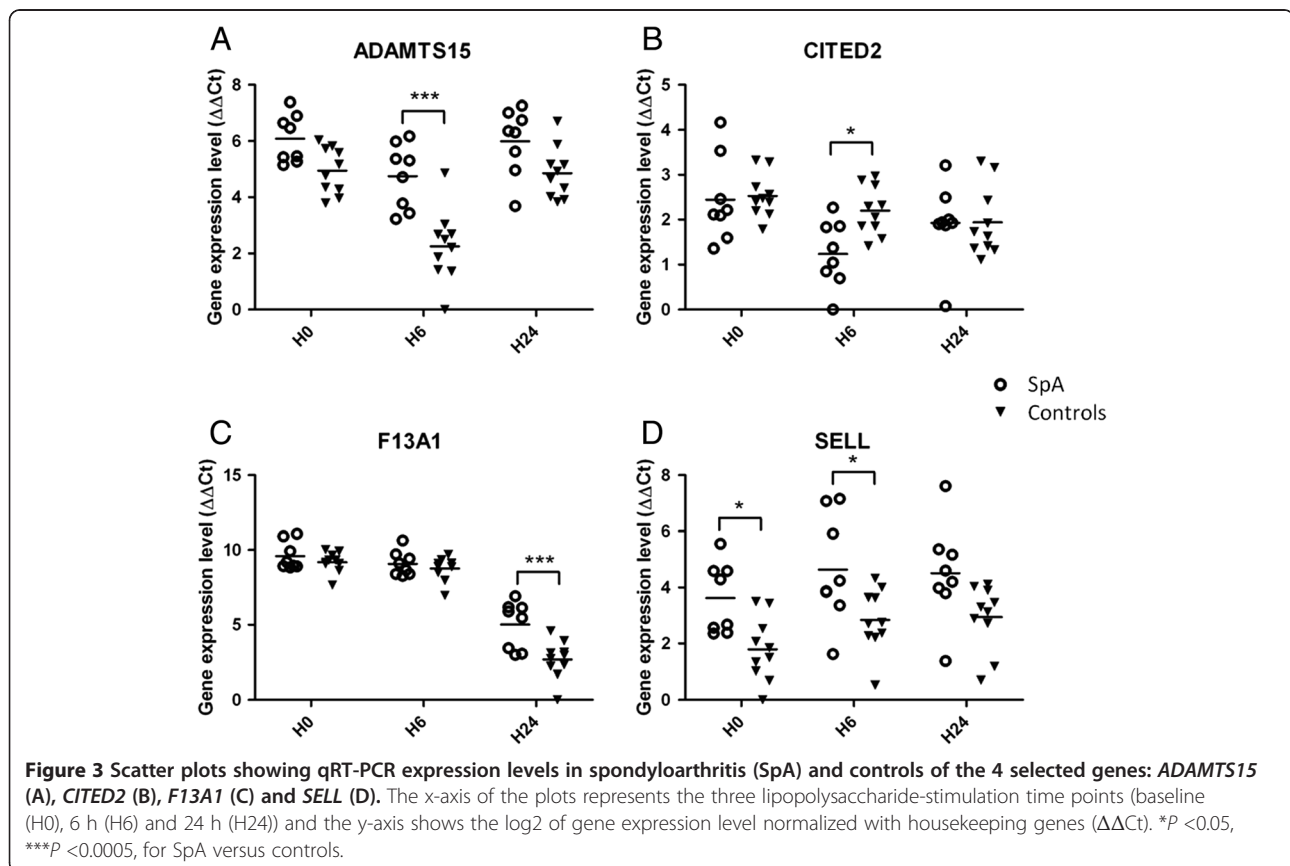
analyzed with the Genomatrix web platform in order to interrogate their biological relevance. This revealed a significant enrichment of genes belonging to the Wnt signaling pathway ( $P = 2.48 \times 10^{-4}$ ) in the SpA group. In the controls, there was no significant correlation between expression levels of *CITED2* and the four genes identified in the Wnt pathway (that is, *WNT1*, *WNT10B*, *FZD4* and *ROR2*) (Figure 5). This co-regulation pattern involving four genes of the Wnt signaling pathway was therefore specifically associated with the disease.

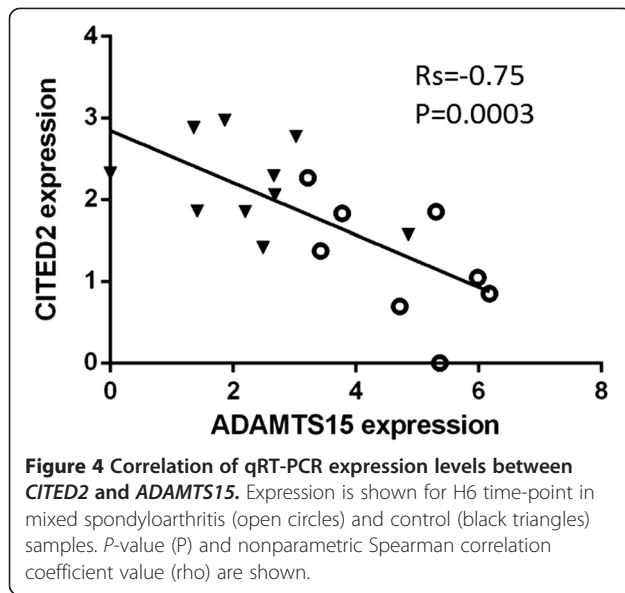
## Discussion

Starting from the hypothesis that aberrant DCs function could play a critical role in the development of SpA, we showed here for the first time that the capacity of MD-DCs to stimulate allogeneic CD4<sup>+</sup> T cell response was impaired in SpA patients compared to controls. The genome-wide transcriptome of these MD-DCs elicited by LPS stimulation revealed 81 genes differentially expressed, 4 of which have been validated by RT-qPCR. Finally, we identified the Wnt signaling pathway as dysregulated in patients.

Our choice to study *in vitro*-differentiated DCs rather than DCs purified from peripheral blood had the advantage to remove those cells from *in vivo* influences, such as non-specific acute inflammation and drug therapy. Therefore, the differences that we observed between DCs from SpA and controls were more likely to be intrinsic to the DC and could be involved in the disease mechanism.

First, we demonstrated that MD-DCs differentiated from similar monocyte populations in both groups. Then, we observed that the ability of SpA MD-DCs to stimulate allogeneic CD4<sup>+</sup> T cell proliferation was markedly defective, as compared to controls, as previously shown in SpA-prone HLA-B27 transgenic rats. The molecular basis for this impaired DC function has yet to be elucidated.





To investigate this impairment, we have studied the time-dependent global transcriptome of MD-DCs in response to LPS stimulation. A number of microarray-based studies have previously been undertaken in AS, on whole blood cells [3-5], PBMCs [6,7] or macrophages [2]. However, no transcriptomic analysis had been conducted on DCs. Of note, as we worked on a homogeneous cell population rather than on cell mixture, our results were not confounded by variations in the composition of the cell populations [20]. The time-dependency of our gene profiling is also a novel aspect, rarely investigated in humans.

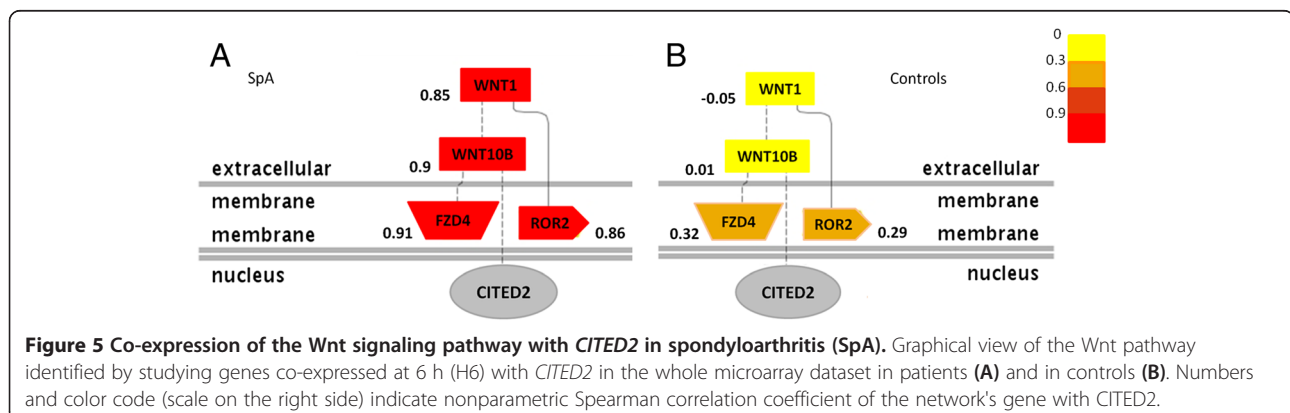
Our analysis revealed 81 genes differentially expressed in resting and/or LPS-stimulated MD-DCs between SpA patients and controls. Of note, we did not identify a reverse interferon signature, such as in HLA-B27 transgenic rat splenic DCs [21] or in SpA patients monocyte-derived macrophages [2]. Such a discrepancy could be explained by differences in culture conditions. Here, we used IL-4 to differentiate MD-DCs, a cytokine that opposes interferon and interferon-induced gene expression

and this might have blunted interferon-related differences between groups. Based on the magnitude of their variation between patients and controls, the level of statistical significance, and their biological relevance, we selected four of these genes that we validated using qRT-PCR.

We found an increased expression of *ADAMTS15* (A Disintegrin And Metalloproteinase with Thrombospondin motif) in SpA. Although the ADAMTS family has not yet been implicated in this disorder, numerous studies have identified a role for metalloproteinases (MMPs) in SpA susceptibility and severity [22-24]. Of note, *ADAMTS15* was shown to be expressed in the joint with decreased expression in osteoarthritis [25]. Thus, *ADAMTS15* could be implicated in the cartilage and/or bone turnover that takes place during joint inflammation, such as in SpA.

*CITED2* functions as a context-dependent transcriptional modulator to up- or downregulate the expression of specific genes [26-28]. Here, the expression of *CITED2* was downregulated in SpA MD-DCs. We further showed an inverse correlation between *CITED2* and *ADAMTS15* expression after 6 hours of LPS treatment. Interestingly, similar inverse correlation has previously been reported between *CITED2* and several MMP family members [29,30]. MMPs constitute a very important group of proteolytic enzymes in joint tissues. Thus, it has been suggested that *CITED2* exerted chondroprotective effects through MMP downregulation [31]. The downregulation of *CITED2* and the inverse correlation between *CITED2* and *ADAMTS15* expression that we observed here suggest that DCs or other phagocytic mononuclear cells, such as macrophages and osteoclasts, could be implicated in SpA joint resorption through heightened metallopeptidase activity.

*In silico* pathway analysis conducted on *CITED2* co-expressed genes highlighted downregulation of several factors belonging to the canonical (that is, *WNT1*, *WNT10B* and *FRZL4*) and non-canonical (*ROR2*) Wnt signaling pathways, of potential relevance for SpA pathogenesis. First, factors of the canonical Wnt pathway were shown to play a crucial role either in bone formation or destruction in inflammatory arthritis [32,33], such as *WNT10b*





[34,35]. On the other hand, activation of canonical Wnt- $\beta$ -catenin signaling in DCs was shown to concur to regulatory T cell differentiation and conversely to inhibit Th17 differentiation [36]. Moreover, ROR2 is a signaling component of the non-canonical Wnt pathway acting on actin cytoskeleton to stimulate cell migration [37,38]. Interestingly, altered T cell stimulation was linked to defective cytoskeleton dynamics in HLA-B27 transgenic rat DCs [39].

*F13A1* encodes the coagulation factor XIII A subunit, a transglutaminase enzyme. It has multiple extra- and intracellular functions, including a role in cartilage and bone development. Hence, increased factor XIII A expression has previously been associated with cartilage ageing and degeneration [40]. Fibrin crosslinking by factor XIII is of crucial importance not only for hemostasis, but also for inflammation. For instance, factor XIII A-subunit genotype was shown to influence C-reactive protein levels during inflammation in rheumatoid arthritis (RA) [41].

Finally, *SELL* encodes the lymphocyte homing receptor L-selectin/CD62L, one of the major adhesion molecules, which regulates entry of neutrophils and monocytes into inflamed tissues and contributes to the severity of joint inflammation in experimental arthritis [42]. Thus, upregulation of *SELL*, as shown here in DCs could well participate in joint inflammation in SpA. Interestingly, this gene was also found to be upregulated in splenic DCs from the HLA-B27/human  $\beta$ 2-microglobulin transgenic rat [21].

## Conclusions

Results of the present study reveal the defective functional capacity of DCs from SpA patients, as compared to controls. Furthermore, our results demonstrate significant changes in MD-DCs gene expression upon LPS stimulation that may be inherent to SpA patients. Some of them (that is, decreased Wnt signaling) could account for the altered DC function that provided a rationale for the present study. Others (that is, upregulation of *ADAMTS15*, *F13A1* and *SELL*) would concur to reinforce tissue inflammation and/or damage. Finally, the co-expression of *CITED2* co-transcriptional factor with several of the foregoing genes (that is, the Wnt signaling pathway and *ADAMTS15*) supports the hypothesis that a coordinated deregulation taking place in DCs may play an important role in SpA pathogenesis.

## Additional files

**Additional file 1: Table S1.** Characteristics of the study patients.\*SpA, spondyloarthritis; BASDAI, Bath Ankylosing Spondylitis Disease Activity Index; NSAID, non-steroidal anti-inflammatory drug; TNF, tumor necrosis factor. ND, not done. \*The registered manifestations correspond to those

present at the time of examination, or retrieved from past-medical history. \*\*Refers to radiographic sacroiliitis  $\geq$  grade II bilateral or grade III unilateral. \*\*\*Six patients are common to both studies. \*\*\*\*Data available for nine patients.

**Additional file 2: Table S2.** Characteristics of the study healthy controls.

**Additional file 3: Table S3.** Nucleotide sequence of the PCR primers.

**Additional file 4: Figure S1.** Comparison of monocyte subsets distribution among peripheral blood mononuclear cells (PBMCs) between spondyloarthritis (SpA) patients and healthy controls (Ctrl) by six-color flow cytometry. Distribution of monocyte subsets among CD45<sup>+</sup> PBMC was studied in five healthy donors (clear boxes) and 10 HLA-B27<sup>+</sup> SpA patients (gray boxes). Results are represented as boxes, bars indicate medians. The mean age of healthy donors was 42 years at the time of the study and 40% of them were men. Characteristics of the patients are shown in Additional file 1: Table S1.

**Additional file 5: Figure S2.** Phenotypic characterization of purified monocytes and monocyte-derived dendritic cells (MD-DCs) by flow cytometry. Results of one healthy donor representative of study subjects are shown. Monocytes (D0) were CD14<sup>+</sup>, CD11c<sup>+</sup>, CD40<sup>+</sup>, HLA-I<sup>+</sup>, HLA-DR<sup>+</sup>, CD80<sup>-</sup>, CD83<sup>-</sup> and CD86<sup>-</sup>. MD-DCs (D7) were CD14<sup>+</sup>, CD11c<sup>+</sup>, CD40<sup>+</sup>, HLA-I<sup>+</sup>, HLA-DR<sup>+</sup>, CD80<sup>-</sup>, CD83<sup>dim</sup>, and CD86<sup>+</sup>. HLA-DR, CD83 and CD86 expression increased, and CD80 was induced on MD-DCs after lipopolysaccharide (LPS) stimulation for 24 h (H24). Clear plot represents control isotype and gray plot the tested antibody.

**Additional file 6: Figure S3.** Unsupervised hierarchical clustering of 57 samples based on whole-genome gene expression levels. Each time point is represented by a color (baseline (H0): blue, 6 h (H6): red, 24 h (H24): green). Samples are clustered on the horizontal axis (top row: spondyloarthritis (SpA) patients, bottom row: healthy controls).

**Additional file 7: Table S4.** List of the genes differentially expressed in monocyte-derived dendritic cells (MD-DCs) between spondyloarthritis (SpA) and controls, ranked by fold change.\*\*The criteria for the inclusion of genes in this table are described in Patients and Methods. Global values are Linear models for microarray data (LIMMA) values. The four genes selected for qRT-PCR validation are in bold text.

## Abbreviations

AS: ankylosing spondylitis; CPM: counts per minute; DC: dendritic cell; EBV: Epstein-Barr virus; GM-CSF: granulocyte-macrophage colony-stimulating factor; IL: interleukin; LIMMA: Linear models for microarray data; LPS: lipopolysaccharide; mAb: monoclonal antibody; MD-DC: monocyte-derived dendritic cell; MLR: mixed lymphocyte reaction; MMP: metalloproteinase; PBMC: peripheral blood mononuclear cell; qRT-PCR: real-time quantitative PCR; SpA: spondyloarthritis; TNF: tumor necrosis factor.

## Competing interests

The authors declare that they have no competing interests.

## Authors' contributions

All authors were involved in drafting the article or revising it critically for important intellectual content, and all authors read and approved the final manuscript. GC had full access to all of the data in the study and takes responsibility for the integrity of the data and the accuracy of the data analysis. Study conception and design: AT, FC, HJG, MB, and GC. Acquisition of data: AT, FC, NB, AL, SJ, and SA. Analysis and interpretation of data: AT, FC, NB, FL, FD, CAD, HJG, MB, and GC. The corresponding author confirms that all the individuals listed as authors fulfil the uniform authorship credit requirements for manuscripts submitted to medical journals, that is, that they all contributed to the manuscript based on (1) substantial contributions to conception and design, acquisition of data, or analysis and interpretation of data; (2) drafting the article or revising it critically for important intellectual content; and (3) final approval of the version to be published.

## Acknowledgements

We gratefully acknowledge the contribution of Pr A Hosmalin (Director of Antigen presentation by Dendritic cell team), for fruitful scientific discussions and providing antibodies for monocyte subset characterization. This work was supported by a grant from *Agence Nationale de la Recherche* (grant ANR

2010 GEMISA) and the financial support of the *Investissements d'Avenir* programme ANR-11-IDEX-0005-02, Sorbonne Paris Cité, Laboratoire d'excellence INFLAMEX. Alice Talpin was supported by a grant from *Arthritis Fondation Courtin*. Félicie Costantino was supported by a grant from the *Société Française de Rhumatologie (SFR)*. Charles-Antoine Dutertre was supported by the *Agence Nationale de Recherche sur le SIDA et les Hépatites Virales (ANRS)*. Sonia Amraoui had a fellowship from Paris-Diderot University.

#### Author details

<sup>1</sup>INSERM U987, Laboratoire d'excellence INFLAMEX, Université Versailles-Saint-Quentin, Versailles 78000, France. <sup>2</sup>UFR des Sciences de la Santé, Simone Veil, Versailles Saint Quentin en Yvelines Université, Montigny-Le-Bretonneux 78180, France. <sup>3</sup>Rheumatology Division, Ambroise Paré Hospital (AP-HP), Boulogne-Billancourt 92100, France. <sup>4</sup>Institut Cochin, INSERM U1016, CNRS (UMR 8104), Université Paris-Descartes, Sorbonne Paris-Cité 75014, France. <sup>5</sup>Antigen Presentation by Dendritic Cell Team; Institut Cochin, INSERM U1016, CNRS (UMR 8104), Université Paris-Descartes, Sorbonne Paris-Cité 75014, France. <sup>6</sup>Duke-NUS Graduate Medical School, Program in Emerging Infectious Disease, Singapore, Singapore. <sup>7</sup>Genetics Division, Ambroise Paré Hospital (AP-HP), Boulogne-Billancourt 92100, France.

Received: 1 April 2014 Accepted: 1 August 2014

Published: 21 August 2014

#### References

- Costantino F, Talpin A, Said-Nahal R, Goldberg M, Henny J, Chiochia G, Garchon H-J, Zins M, Breban M: **Prevalence of spondyloarthritis in reference to HLA-B27 in the French population: results of the GAZEL cohort.** *Ann Rheum Dis* 2013, doi:10.1136/annrheumdis-2013-204436.
- Smith JA, Barnes MD, Hong D, DeLay ML, Inman RD, Colbert RA: **Gene expression analysis of macrophages derived from ankylosing spondylitis patients reveals interferon-gamma dysregulation.** *Arthritis Rheum* 2008, **58**:1640–1649.
- Gu J, Wei Y-L, Wei JCC, Huang F, Jan M-S, Centola M, Frank MB, Yu D: **Identification of RGS1 as a candidate biomarker for undifferentiated spondylarthritis by genome-wide expression profiling and real-time polymerase chain reaction.** *Arthritis Rheum* 2009, **60**:3269–3279.
- Duan R, Leo P, Bradbury L, Brown MA, Thomas G: **Gene expression profiling reveals a downregulation in immune-associated genes in patients with AS.** *Ann Rheum Dis* 2010, **69**:1724–1729.
- Assassi S, Reveille JD, Arnett FC, Weisman MH, Ward MM, Agarwal SK, Gourh P, Bhula J, Sharif R, Sampat K, Mayes MD, Tan FK: **Whole-blood gene expression profiling in immune-associated genes shows upregulation of toll-like receptor 4 and 5.** *J Rheumatol* 2011, **38**:87–98.
- Pimentel-Santos FM, Ligeiro D, Matos M, Mourão AF, Costa J, Santos H, Barcelos A, Godinho F, Pinto P, Cruz M, Fonseca JE, Guedes-Pinto H, Branco JC, Brown MA, Thomas GP: **Whole blood transcriptional profiling in ankylosing spondylitis identifies novel candidate genes that might contribute to the inflammatory and tissue-destructive disease aspects.** *Arthritis Res Ther* 2011, **13**:R57.
- Sharma SM, Choi D, Planck SR, Harrington CA, Austin CR, Lewis JA, Diebel TN, Martin TM, Smith JR, Rosenbaum JT: **Insights in to the pathogenesis of axial spondyloarthritis based on gene expression profiles.** *Arthritis Res Ther* 2009, **11**:R168.
- Breban M, Hacquard-Bouder C, Falgarone G: **Animal models of HLA-B27-associated diseases.** *Curr Mol Med* 2004, **4**:31–40.
- Hacquard-Bouder C, Falgarone G, Bosquet A, Smaoui F, Monnet D, Ittah M, Breban M: **Defective costimulatory function is a striking feature of antigen-presenting cells in an HLA-B27-transgenic rat model of spondylarthritis.** *Arthritis Rheum* 2004, **50**:1624–1635.
- Hacquard-Bouder C, Chimenti M-S, Giquel B, Donnadiu E, Fert I, Schmitt A, André C, Breban M: **Alteration of antigen-independent immunologic synapse formation between dendritic cells from HLA-B27-transgenic rats and CD4+ T cells: selective impairment of costimulatory molecule engagement by mature HLA-B27.** *Arthritis Rheum* 2007, **56**:1478–1489.
- Glatigny S, Fert I, Blaton MA, Lories RJ, Araujo LM, Chiochia G, Breban M: **Proinflammatory Th17 cells are expanded and induced by dendritic cells in spondylarthritis-prone HLA-B27-transgenic rats.** *Arthritis Rheum* 2012, **64**:110–120.
- Utraiainen L, Firmin D, Wright P, Cerovic V, Breban M, McInnes I, Milling S: **Expression of HLA-B27 causes loss of migratory dendritic cells in a rat model of spondylarthritis.** *Arthritis Rheum* 2012, **64**:3199–3209.
- Araujo L, Fert I, Jouhault Q, Labroquère K, Andrieu M, Chiochia G, Breban M: **Increased production of interleukin-17 over interleukin-10 by regulatory T cells implicates ICOS molecule in experimental spondyloarthritis.** *Arthritis Rheum* 2014, doi:10.1002/art.38737.
- Rudwaleit M, van der Heijde D, Landewé R, Listing J, Akkoc N, Brandt J, Braun J, Chou CT, Collantes-Estevez E, Dougados M, Huang F, Gu J, Khan MA, Kirazli Y, Maksymowych WP, Mielants H, Sørensen IJ, Ozgocmen S, Roussou E, Valle-Oñate R, Weber U, Wei J, Sieper J: **The development of Assessment of SpondyloArthritis international Society classification criteria for axial spondyloarthritis (part II): validation and final selection.** *Ann Rheum Dis* 2009, **68**:777–783.
- Dutertre C-A, Amraoui S, DeRosa A, Jourdain J-P, Vimeux L, Goguet M, Degrelle S, Feuillet V, Liovat A-S, Müller-Trutwin M, Decroix N, Deveau C, Meyer L, Goujard C, Loulergue P, Launay O, Richard Y, Hosmalin A: **Pivotal role of M-DC8<sup>+</sup> monocytes from viremic HIV-infected patients in TNF $\alpha$  overproduction in response to microbial products.** *Blood* 2012, **120**:2259–2268.
- Gautier L, Cope L, Bolstad BM, Irizarry RA: **affy-analysis of Affymetrix GeneChip data at the probe level.** *Bioinformatics* 2004, **20**:307–315.
- Dai M, Wang P, Boyd AD, Kostov G, Athey B, Jones EG, Bunney WE, Myers RM, Speed TP, Akil H, Watson SJ, Meng F: **Evolving gene/transcript definitions significantly alter the interpretation of GeneChip data.** *Nucl Acids Res* 2005, **33**:e175–e175.
- Smyth GK: **Linear models and empirical bayes methods for assessing differential expression in microarray experiments.** *Stat Appl Genet Mol Biol* 2004, **3**:Article 3.
- Genomatix - NGS Data Analysis & Personalized Medicine.** [https://www.genomatix.de/]
- Plessy C, Desbois L, Fujii T, Carninci P: **Population transcriptomics with single-cell resolution: a new field made possible by microfluidics: a technology for high throughput transcript counting and data-driven definition of cell types.** *Bioessays* 2013, **35**:131–140.
- Fert I, Cagnard N, Glatigny S, Letourneur F, Jacques S, Smith JA, Colbert RA, Tauroug JD, Chiochia G, Araujo LM, Breban M: **Reverse interferon signature is characteristic of antigen-presenting cells in human and rat spondyloarthritis.** *Arthritis Rheum* 2014, **66**:841–851.
- Zhu J, Yu DTY: **Matrix metalloproteinase expression in the spondyloarthropathies.** *Curr Opin Rheumatol* 2006, **18**:364–368.
- Maksymowych WP, Landewé R, Conner-Spady B, Dougados M, Mielants H, van der Tempel H, Poole AR, Wang N, van der Heijde D: **Serum matrix metalloproteinase 3 is an independent predictor of structural damage progression in patients with ankylosing spondylitis.** *Arthritis Rheum* 2007, **56**:1846–1853.
- Mattey DL, Packham JC, Nixon NB, Coates L, Creamer P, Hailwood S, Taylor GJ, Bhalla AK: **Association of cytokine and matrix metalloproteinase profiles with disease activity and function in ankylosing spondylitis.** *Arthritis Res Ther* 2012, **14**:R127.
- Kevoorkian L, Young DA, Darrah C, Donell ST, Shepstone L, Porter S, Brockbank SMV, Edwards DR, Parker AE, Clark IM: **Expression profiling of metalloproteinases and their inhibitors in cartilage.** *Arthritis Rheum* 2004, **50**:131–141.
- Bragança J, Swingler T, Marques FIR, Jones T, Eloranta JJ, Hurst HC, Shioda T, Bhattacharya S: **Human CREB-binding protein/p300-interacting transactivator with ED-rich tail (CITED) 4, a new member of the CITED family, functions as a co-activator for transcription factor AP-2.** *J Biol Chem* 2002, **277**:8559–8565.
- Lou X, Sun S, Chen W, Zhou Y, Huang Y, Liu X, Shan Y, Wang C: **Negative feedback regulation of NF- $\kappa$ B action by CITED2 in the nucleus.** *J Immunol* 2011, **186**:539–548.
- Goodman RH, Smolik S: **CBP/p300 in cell growth, transformation, and development.** *Genes Dev* 2000, **14**:1553–1577.
- Bai L, Merchant JL: **A role for CITED2, a CBP/p300 interacting protein, in colon cancer cell invasion.** *FEBS Lett* 2007, **581**:5904–5910.
- Lee JY, Taub PJ, Wang L, Clark A, Zhu LL, Maharam ER, Leong DJ, Ramcharan M, Li Z, Liu Z, Ma Y-Z, Sun L, Zaidi M, Majeska RJ, Sun HB: **Identification of CITED2 as a negative regulator of fracture healing.** *Biochem Biophys Res Commun* 2009, **387**:641–645.
- Leong DJ, Li YH, Gu XI, Sun L, Zhou Z, Nasser P, Laudier DM, Iqbal J, Majeska RJ, Schaffler MB, Goldring MB, Cardoso L, Zaidi M, Sun HB: **Physiological loading of joints prevents cartilage degradation through CITED2.** *FASEB J* 2011, **25**:182–191.

32. Goldring SR, Goldring MB: **Eating bone or adding it: the Wnt pathway decides.** *Nat Med* 2007, **13**:133–134.
33. Laine CM, Joeng KS, Campeau PM, Kiviranta R, Tarkkonen K, Grover M, Lu JT, Pekkinen M, Wessman M, Heino TJ, Nieminen-Pihala V, Aronen M, Laine T, Kröger H, Cole WG, Lehesjoki A-E, Nevarez L, Krakow D, Curry CJR, Cohn DH, Gibbs RA, Lee BH, Mäkitie O: **WNT1 mutations in early-onset osteoporosis and osteogenesis imperfecta.** *N Engl J Med* 2013, **368**:1809–1816.
34. Bennett CN, Longo KA, Wright WS, Suva LJ, Lane TF, Hankenson KD, MacDougald OA: **Regulation of osteoblastogenesis and bone mass by Wnt10b.** *Proc Natl Acad Sci U S A* 2005, **102**:3324–3329.
35. Franck H, Meurer T, Hofbauer LC: **Evaluation of bone mineral density, hormones, biochemical markers of bone metabolism, and osteoprotegerin serum levels in patients with ankylosing spondylitis.** *J Rheumatol* 2004, **31**:2236–2241.
36. Manicassamy S, Reizis B, Ravindran R, Nakaya H, Salazar-Gonzalez RM, Wang Y-C, Pulendran B: **Activation of beta-catenin in dendritic cells regulates immunity versus tolerance in the intestine.** *Science* 2010, **329**:849–853.
37. Nishita M, Yoo SK, Nomachi A, Kani S, Sougawa N, Ohta Y, Takada S, Kikuchi A, Minami Y: **Filopodia formation mediated by receptor tyrosine kinase Ror2 is required for Wnt5a-induced cell migration.** *J Cell Biol* 2006, **175**:555–562.
38. Nomachi A, Nishita M, Inaba D, Enomoto M, Hamasaki M, Minami Y: **Receptor tyrosine kinase Ror2 mediates Wnt5a-induced polarized cell migration by activating c-Jun N-terminal kinase via actin-binding protein filamin A.** *J Biol Chem* 2008, **283**:27973–27981.
39. Dhaenens M, Fert I, Glatigny S, Haerinck S, Poulain C, Donnadieu E, Hacquard-Bouder C, André C, Elewaut D, Deforce D, Breban M: **Dendritic cells from spondylarthritis-prone HLA-B27-transgenic rats display altered cytoskeletal dynamics, class II major histocompatibility complex expression, and viability.** *Arthritis Rheum* 2009, **60**:2622–2632.
40. Johnson K, Hashimoto S, Lotz M, Pritzker K, Terkeltaub R: **Interleukin-1 induces pro-mineralizing activity of cartilage tissue transglutaminase and factor XIIIa.** *Am J Pathol* 2001, **159**:149–163.
41. Hoppe B, Häupl T, Skapenko A, Ziemer S, Tauber R, Salama A, Schulze-Koops H, Burmester G-R, Dörner T: **Fibrinogen and factor XIII A-subunit genotypes interactively influence C-reactive protein levels during inflammation.** *Ann Rheum Dis* 2012, **71**:1163–1169.
42. Sarraj B, Ludányi K, Glant TT, Finnegan A, Mikecz K: **Expression of CD44 and L-selectin in the innate immune system is required for severe joint inflammation in the proteoglycan-induced murine model of rheumatoid arthritis.** *J Immunol* 2006, **177**:1932–1940.

doi:10.1186/s13075-014-0417-0

**Cite this article as:** Talpin *et al.*: Monocyte-derived dendritic cells from HLA-B27<sup>+</sup> axial spondyloarthritis (SpA) patients display altered functional capacity and deregulated gene expression. *Arthritis Research & Therapy* 2014 **16**:417.

**Submit your next manuscript to BioMed Central and take full advantage of:**

- Convenient online submission
- Thorough peer review
- No space constraints or color figure charges
- Immediate publication on acceptance
- Inclusion in PubMed, CAS, Scopus and Google Scholar
- Research which is freely available for redistribution

Submit your manuscript at  
[www.biomedcentral.com/submit](http://www.biomedcentral.com/submit)

