Increased expression of CXCL2 in ACPA-positive rheumatoid arthritis and its role in osteoclastogenesis

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Abstract

Background. Anti-citrullinated protein/peptide antibodies (ACPA) play important roles in the pathogenesis of rheumatoid arthritis (RA). ACPA-positive (ACPA+) and ACPA-negative (ACPA-) RA were suggested to be different disease subsets with distinct differences in genetic variation and clinical outcomes. The aims of the present study were to compare gene expression profiles in ACPA+ and ACPA- RA and identify novel candidate gene signatures that might serve as therapeutic targets. Methods. Comprehensive transcriptome analysis of peripheral blood mononuclear cells (PBMCs) from ACPA+ and ACPA- RA patients, and healthy controls was performed via RNA sequencing. A validation cohort was used to further investigate differentially expressed genes via PCR and ELISA. Spearman's correlation test was used to evaluate the correlation of differentially expressed genes and the clinical and laboratory data of the patients. The role of differentially expressed genes in osteoclastogenesis was further investigated. Results. Expression of C-X-C motif chemokine ligand 2 (CXCL2) was significantly increased in ACPA+ RA than in ACPA- RA, which was validated in PBMCs and serum. CXCL2 promoted the migration of CD14+ monocytes and increased osteoclastogenesis in RA patients. RAW264.7 macrophages were used to investigate specific mechanisms, and the results suggested that CXCL2 stimulated osteoclastogenesis via ERK MAPK and NFκB pathways. Conclusion. CXCL2 was highly expressed in ACPA+ RA than in ACPA- RA. CXCL2 promoted osteoclastogenesis and was related to bone erosion in RA, which suggest that the blockade of CXCL2 might be a novel strategy for the treatment of RA.

Introduction

Rheumatoid arthritis (RA) is a systemic autoimmune disease that involves activation of inflammatory cells, synovial hyperplasia, and destruction of cartilage and bone(1). In recent years, anti-citrullinated protein/peptide antibodies (ACPAs) have been used as biomarkers in the diagnosis of RA, and to predict clinical outcomes(2-4). Based on the presence or absence of ACPA, RA can be classified into two subtypes as ACPA-positive (ACPA+) or ACPA-negative (ACPA-). It has been reported that ACPAs are detectable years before the onset of arthritis, and they are strong predictors of progression to classic RA in patients with undifferentiated arthritis(5, 6). Moreover, ACPAs are associated with RA severity. RA patients with ACPAs exhibit more severe radiographic damage than those without ACPAs(7-10). Many studies have suggested that ACPAs play a pathophysiologic role in RA(11). In recent years, a number of candidate genes have been shown to be differentially associated with susceptibility in ACPA+ and ACPA-RA(12-14). With the advent of next-generation sequencing technologies such as RNA sequencing, more comprehensive and accurate transcriptome analysis has become feasible and affordable. In RNA sequencing, short fragments of complementary DNA (cDNA) are sequenced ('reads') then mapped onto the reference genome. RNA sequencing facilitates both the identification of differentially expressed genes and precise quantitative determination of

exon and isoform (alternative splicing) expression, along with the characterisation of transcription initiation sites and new splicing variants(15, 16).

In the present study, comprehensive transcriptome analysis of PBMCs from ACPA+ and ACPA- RA patients was performed to identify novel candidate gene signatures that might be involved in the pathogenesis of different subsets of disease.

Materials and Methods

Patients

Two ACPA+ and two ACPA- RA patients from Peking University Third Hospital who fulfilled the 2010 European League Against Rheumatism/American College of Rheumatology classification criteria for RA(2) were enrolled in the study. All 4 patients were newly diagnosed, treatment naive, menopausal, and non-smoker women from the northern Han population with symptom duration of less than 6 months, and none had any other chronic diseases. Three matched healthy individuals were included in the study.

PBMC collected from 40 ACPA+, 40 ACPA- RA patients, and 40 healthy controls were applied for quantitative PCR to validate candidate genes expression. Serum CXCL2 levels were detected by ELISA in a cohort consisted of 70 ACPA+, 37 ACPA- RA patients, and 40 healthy controls. The clinical and laboratory data of the patients were collected from electronic medical records. In all comparisons mentioned, the groups were age and sex matched. The present study was conducted in accordance with the Declaration of Helsinki. The Ethics Committee of Peking University Third Hospital approved the study. All procedures involving specimens obtained from humans were performed with informed consent from each patient.

RNA extraction, sequencing and analysis

PBMCs were isolated from the blood of RA patients and healthy donors via centrifugation over Ficoll-Paque Plus (GE Healthcare, Sweden). RNA was extracted from PBMCs using Trizol: chloroform, precipitated in isopropanol. Sample quality was assessed using Nanodrop. Total RNA was enriched for mRNA using poly-A selection. In brief, mRNA was fragmented, reverse transcribed, adapted with sequencing primers and sample barcodes, size selected, and PCR enriched. Libraries were sequenced on the HiSeq 2000 platform. RNA sequence reads were aligned to the human reference genome (NCBI, hg19) using TopHat2 aligners. Normalised gene counts were calculated using HTSeq, and differential gene expression between samples was identified via edgeR. Gene expression (RPKM) values were calculated using Cufflinks v2.0.2. Gene Ontology (http://geneontology.org/) associations were determined using Gorilla. Network construction was based on the Ingenuity Pathway Analysis (Qiagen, CA, USA) experimental evidence database.

Cell culture

PBMCs were isolated from the blood of RA patients as described above. CD14+ monocytes were positively selected via magnetic-activated cell sorting (Miltenyi Biotec, Germany) and an anti-CD14 antibody. The isolated CD14+ monocytes (1.5×10^5 cells per well in 48-well plates or 6×10^5 cells per well in 12-well plates) were incubated in RPMI-1640 media containing 10% fetal bovine serum (FBS). Osteoclast differentiation was induced from CD14+ monocytes treated with macrophage colony-stimulating factor (M-CSF, 50 ng/ml) and receptor activator of nuclear factor kappa-B ligand (RANKL, 100 ng/ml). C-X-C motif chemokine ligand 2 (CXCL2, 100 ng/ml or otherwise as indicated) were added to the cultures. The medium was replaced every 3 days.

RAW264.7 macrophages (1.0×10^4 cells per well in 48-well plates or 4.5×10^4 cells per well in 12-well plates) were incubated in DMEM media containing 10% FBS. Osteoclast differentiation was induced by M-CSF (10 ng/ml) and RANKL (50 ng/ml) with or without CXCL2.

Flow cytometry

To identify the expression of C-X-C motif chemokine receptor 2 (CXCR2), CD14+ monocytes were incubated for 45 min at 4°C with anti-human CXCR2 in the dark. Cells were washed twice with staining wash buffer

and centrifuged at 1000 rpm for 5 minutes to pellet the cells. Stained cells were resuspended in 200 μl of PBS then analyzed via flow cytometry. In each case, staining was compared with that of the appropriately labeled isotype control antibody.

Cell migration

Monocyte migration testing was performed with 5μm pore-size polycarbonate membrane transwell tissue culture inserts (Corning, USA). Cells (5×10^4 per well) were seeded into the wells in the top chamber in 10% FBS medium, and CXCL2 was added to the lower chamber in 10% FBS medium. After incubation for 1 hour at 37°C the medium was removed and the filters were fixed with 4% paraformaldehyde for 20 minutes. The filters were then stained with 0.1% crystal violet for 15 minutes. The number of cells that had migrated from the upper surface of the filter to the lower surface of the filter was counted.

Quantitative PCR

Total RNA was extracted using TRIzol reagent (Invitrogen), and 1 μg of total RNA was reverse-transcribed into cDNA using a FastQuant RT Kit (with gDNase) (Tiangen Biotech). RT-PCR was carried out using the QuantStudio 5 Real-Time PCR System (Thermo Fisher Scientific) with Talent qPCR PreMix (SYBR Green) (Tiangen Biotech). Data were normalized to the expression of GAPDH. The primer nucleotide sequences for PCR were obtained from GenBank database and synthesized by Sangon Biotech (China). The primer sequence information used in the study was shown in the supplementary material, Table1.

Enzyme-linked immunosorbent assay

CXCL2 levels in sera from ACPA+ RA, ACPA- RA and healthy controls, as well as levels in the supernatants of CD14+ monocyte cultures were measured using human CXCL2 enzyme-linked immunosorbent assay kits in accordance with the manufacturer's instructions.

TRAP staining

TRAP staining of CD14+ monocytes and RAW264.7 macrophages was performed after culturing with or without CXCL2 in the presence of M-CSF and RANKL. TRAP staining was conducted using the TRAP kit (387A-1KT, Sigma) in accordance with the manufacturer's instructions. TRAP-positive multinucleated cells containing more than 3 nuclei were identified as osteoclasts and counted under a microscope.

F-actin ring immunofluorescence

Cells were fixed with 4% paraformaldehyde and incubated with FITC-conjugated anti-actin antibody for 1 hour at 25°C. After a PBS wash the cells were incubated with DAPI for 5 minutes at 25°C, then analyzed using an Olympus BX51 microscope (Tokyo, Japan).

Scanning electron microscopy

Cells on dentine were fixed in 4% glutaraldehyde, dehydrated via graded alcohol solutions then graded (50% to 100%) hexamethyldisilazane solutions (Sigma-Aldrich, MO, USA), then air-dried. Dentine slices were then mounted onto aluminium stubs (EMS, Hatfield, PA, USA), sputtered with gold, and examined using a scanning electron microscope (Philips SEM 505, Best, Netherlands).

Bone resorption assay

Functional evidence of osteoclast formation was determined via a lacunar resorption assay system using cell cultures on dentine slices as previously described(17). Cells were removed from the dentine slices by treatment with 0.1 M ammonium hydroxide. The dentine slices were washed in distilled water and ultrasonicated to remove adherent cells, then stained with 0.5% (v/v) toluidine blue to reveal areas of lacunar resorption, and examined via light microscopy.

Western blotting

Total protein was extracted using RIPA lysis buffer (Applygen, Beijing, China). A total of 40 μg of protein was loaded into a 10% sodium dodecyl sulphate-polyacrylamide gel and electrophoretically transferred to polyvinylidene fluoride membranes (Merck Millipore, Billerica, MA, USA). After blocking with 5% milk for 1 h, the membranes were incubated with specific antibodies at the indicated dilutions for 12–16 h at 4°C. The membranes were scanned using an Odyssey Sa Imaging System (LICOR Biosciences, Lincoln, NE, USA). The antibody information used in this study was shown in the supplementary material, Table 2.

Statistical analysis

Statistical analysis of RNA sequencing count data was conducted using edgeR with a 5% FDR. All experiments were repeated at least three times and are presented as the mean±standard deviation and the median with interquartile range. Statistical analysis were assessed via Spearman correlation, Mann-Whitney test and one-way analysis of variance followed by Tukey's test for multiple comparisons. p values < 0.05 were considered statistically significant.

Results

Selection of candidate genes using RNA sequencing

Further analysis was conducted on RNA sequencing data from 7 samples; 2 ACPA+ RA patients, 2 ACPA- RA patients and 3 healthy controls. Differentially expressed genes (DEGs) were analyzed in the two different sample types, and three groups of DEGs were identified (ACPA+ vs. control, ACPA+ vs. ACPA-, ACPA- vs. control). We identified 1007 DEGs (522 up-regulated and 485 down-regulated) between ACPA+ and control, 628 DEGs (344 up-regulated and 284 down-regulated) between ACPA+ and ACPA-, and 1097 DEGs (549 up-regulated and 548 down-regulated) between ACPA- and control (Fig. 1A and 1B). All these DEGs exhibited distinct expression patterns in the three sample types (Fig. 1C).

Pathway enrichment analysis/ingenuity pathway analysis of DEGs yielded 19 canonical pathways that were significantly enriched between ACPA+ and control, 24 between ACPA+ and ACPA-, and 35 between ACPA- and control (see supplementary information). Some of these pathways were enriched in more than one comparison (Fig. 1D). The agranulocyte adhesion and diapedesis pathway was particularly enriched in ACPA+ vs. control and ACPA+ vs. ACPA- (Fig. 1D). Different DEGs were involved in the agranulocyte adhesion and diapedesis pathway in two comparisons (Fig. 1E and 1F), and of these, CXCL2 and C-X-C motif chemokine ligand 7 (CXCL7) were exclusively up-regulated in ACPA+ samples (Fig. 1E).

Validation of candidate genes expression in ACPA+ RA patients

To validate the differential expression levels of candidate genes in ACPA+ and ACPA- RA patients, the expression levels of CXCL2 and CXCL7 were measured using real time PCR. CXCL2 levels were higher in ACPA+ RA patients (n=40) than in ACPA- RA patients (n=40) and healthy controls (n=40) (Fig. 2A), confirming that CXCL2 was differentially expressed in ACPA+ RA patients and ACPA- RA patients. However, there was no significant difference in CXCL7 expression between ACPA+ RA patients and ACPA- RA patients.

CXCL2 levels in serum and CD14+ cell supernatant

CXCL2 levels in sera were detected in 70 ACPA+ RA patients, 37 ACPA- RA patients and 40 healthy controls. Age and sex were balanced between the groups, whereas the disease duration, RF positive rate and bone erosion positive rate were significantly different among ACPA+ RA patients and ACPA- RA patients (Table 1).

Median serum CXCL2 in RA patients (1083.43, (586.94,1569.50) pg/ml) was significantly higher than in healthy controls (301.44, (217.62,422.26) pg/ml) ($p < 0.001$; Fig, 2B). And median serum CXCL2 was significantly higher in ACPA+ RA patients than in ACPA- RA patients ($p < 0.05$; Fig. 2C). Correlation analysis showed that CXCL2 was positively correlated with DAS28 ($r=0.4594$, $p < 0.001$), ESR ($r=0.3985$, $p <0.001$) and CRP ($r=0.3726$, $p < 0.001$) (Fig. 2D). However, the CXCL2 level was not related to disease

duration (r=-0.084, p=0.391) and RF titer (r=0.1358, p=0.309). Serum CXCL2 was significantly higher in RA patients with bone erosion than in RA patients without bone erosion ($p < 0.05$; Fig. 2E).

CXCL2 expression was significantly higher in the supernatant of CD14+ monocyte cultures derived from ACPA+ RA patients than from the ACPA- RA patients (Fig. 2F).

CXCL2 promoted migration of CD14+ monocytes from RA patients

Flow cytometry analysis using anti-CXCR2 antibody revealed that CD14+ monocytes from ACPA+ patients expressed CXCR2 at a higher level than those from ACPA- patients, but the difference was not statistically significant (Fig. 3A). In the transwell experiments, CXCL2 significantly increased the number of migrating monocytes in cultures derived from RA patients (Fig. 3B).

CXCL2 increased osteoclast differentiation and enhanced osteoclastic bone resorption

In experiments conducted to evaluate the effects of CXCL2 on osteoclastogenesis, cultures from all groups formed osteoclasts on plastic and the average numbers of osteoclasts were similar in the control cultures and cultures exposed to a low concentration of CXCL2 (10 ng/mL). However, high doses of CXCL2 tended to promote the formation of osteoclasts (Fig. 4A). Formation of the F-actin ring by osteoclasts is a necessary step in bone resorption. Immunofluorescence microscopy of CD14+ monocytes cultured for 14 days treated with CXCL2 (100 ng/ml) in the presence of M-CSF and RANKL revealed that F-actin rings were significantly increased in number (Fig. 4B). CXCL2 stimulation also increased cell fusion, resulting in multinucleated cells (Fig. 4C), which suggested that CXCL2 promoted osteoclast formation.

Functional evidence of osteoclast formation was obtained via the lacunar resorption assay system using cell cultures on dentine slices. The result showed that the resorption area was increased in bone slices exposed to CXCL2 (Fig. 4D). Expression of the osteoclast markers RANK, cathepsin K, and TRAP was significantly increased after 3 days of stimulation with the CXCL2 (100 ng/mL) in the presence of M-CSF (50 ng/ml) and RANKL (100 ng/ml) ($p < 0.05$; Fig. 4E).

Consistent with the results obtained in CD14+ monocytes, the effects of exogenous CXCL2 on osteoclast formation were also observed in RAW264.7 cells. Compared with the control group, much larger multinucleated cells were evident in the CXCL2 groups (Fig. 5A). Expression of osteoclast markers such as cathepsin K and TRAP was also significantly increased in the CXCL2 group after 3 days of stimulation in the presence of M-CSF and RANKL ($p < 0.05$; Fig. 5B). These results suggest that CXCL2 enhances osteoclast formation and bone resorption. In addition, CXCL2 significantly increased the expression of NFATc1 and c-Fos by RAW264.7 cells after 5 days of stimulation with M-CSF (10 ng/ml) and RANKL (50 ng/ml) ($p < 0.05$; Fig. 5C).

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To explore the signal pathways involved in the osteoclastogenesis with the stimulation of CXCL2, RAW264.7 cells were incubated in osteoclast-promoting medium with or without CXCL2, western blotting at different time-points was conducted to detect the phosphorylation of IκBα, p65, ERK1/2 and JNK. The addition of CXCL2 dramatically promoted phosphorylation of p65 and ERK1/2 (Fig. 6A, B), with no effect on the phosphorylation of IκBα or JNK (Fig. 6C, D).

Discussion

RNA sequencing technology has been used to detect differences in gene expression profiles in RA patients for the last few years. Several gene expression profiling studies of synovial tissues and PBMCs from RA patients have revealed marked variation in gene expression profiles that have facilitated the identification of distinct molecular disease mechanisms involved in RA pathology(18-21). The heterogeneity of RA was demonstrated by the presence of distinct autoantibody specificities such as ACPA in serum, differential responsiveness to treatment, and variability in clinical presentation. RA patients can be stratified into two subgroups defined by the presence or absence of ACPA, and ACPA+ patients exhibit more severe inflammation and radiographic damage than ACPA- patients(5-7). In the present study, various genes were compared in

ACPA+ and ACPA- patients via RNA sequencing, and two significantly increased chemokines, CXCL2 and CXCL7 were identified in ACPA+ patients. The next more focused analysis using PCR technology on many more patients found that only CXCL2 was differentially expressed in ACPA+ RA patients and ACPA-RA patients. There was no significant difference in CXCL7 expression between ACPA+ RA patients and ACPA-RA patients.

CXCL2 was first identified as a major chemokine produced by endotoxin-treated macrophages(22), which bind to the G-protein coupled receptor CXCR2 expressed on macrophages, neutrophils, and epithelial cells(23). In previous studies, CXCL2 level was found to be higher expressed in RA patients than in normal controls(24). Xiaokun *et al.* downloaded microarray datasets of GSE1919, GSE12021, and GSE21959 (35 RA samples and 32 normal controls) from the Gene Expression Omnibus database (https://www.ncbi.nlm.nih.gov/geo/) and identified DEGs in RA samples. They found that CXCL2 was strongly associated with DEGs involved in RA progression(24). Jacobs *et al.* (25) performed a microarray analysis to characterize the molecular events underlying pathology in autoantibody-mediated arthritis and reported that CXCL2 was up-regulated in parallel with the disease. Jeongim *et al.* (26) reported that CXCL2 was significantly higher in synovial fluid and sera from RA patients compared with corresponding samples from osteoarthritis patients. In the present study, serum CXCL2 was significantly increased in RA patients compared with healthy controls, and serum CXCL2 was higher in ACPA+ RA patients than in ACPA- RA patients. Compared with ACPA-patients, ACPA+ patients had longer disease duration and higher positive rate of RF. To exclude the impact of these two factors on CXCL2 level, correlation analysis was applied and showed that CXCL2 was irrelevant to disease duration and RF titer.

CXCL2 was involved in various biological progresses, such as angiogenesis, inflammation and cancer biological behaviors(23, 27-30). CXCL2 was also considered to be a proinflammatory factor in RA(24). In line with this, our study showed that CXCL2 was positively correlated with DAS28, ESR and CRP. Moreover, recent studies revealed CXCL2 was also involved in the process of osteoclastogenesis(26, 31). In the present study, we also found serum CXCL2 was significantly higher in RA patients with bone erosion than in RA patients without bone erosion. Thus, we hypothesized that CXCL2 could be one of the key molecules upregulated in RA progression, especially in ACPA+ RA which exhibit more radiographic damage, and focused on the CXCL2 for subsequent analyses.

As the most important osteoclast precursors, CD14+ monocytes were derived from ACPA+ patients and exhibited elevated CXCL2 secretion compared with those derived from ACPA- patients. CXCR2 is known to be the major receptor for CXCL2(32). It has been suggested that CXCL2 acts as a chemoattractant for various types of cells by binding to CXCR2, and monocytes constitutively express CXCR2(32). However, whether there is a difference in the expression of cell surface CXCR2 in CD14+ monocytes from ACPA+ and ACPA- RA patients remains unclear. In the present study, we found that CXCR2 expression was higher on the surfaces of CD14+ monocytes derived from ACPA+ patients than those from ACPA- patients, but the difference was not statistically significant.

ACPA+ RA patients usually develop more severe radiological damage, and enhanced osteoclastogenesis may be involved in the bone erosion(7). Osteoclasts are polykaryocytes formed via the fusion of mononuclear monocytic precursors such as monocytes in peripheral blood. We surmise that elevated CXCL2 may recruit more monocytes to joint sites and augment the formation of osteoclasts. The present study showed that CXCL2 promoted the migration, differentiation, and function of osteoclasts in experiments using CD14+ monocytes isolated from RA patients.

The effects of CXCL2 on activating the signaling pathway during osteoclast differentiation were examined to explore the molecular mechanisms of the observed enhancement effect on osteoclastogenesis. The addition of CXCL2 resulted in dramatically increased phosphorylation of p65 and ERK1/2, while it did not affect the phosphorylation of IκBα or JNK. NFATc1 and c-Fos are critical transcription factors in the regulation of osteoclast differentiation(33). In the current study, NFATc1 and c-fos were increased significantly with stimulation of CXCL2 in the presence of M-CSF and RANKL. NFATc1 is an important regulatory factor in the process of osteoclast differentiation mediated by RANKL-activated MAPK and NFκB signalling

pathways(34). Therefore, it suggests that CXCL2 may promote osteoclast differentiation and bone resorption by regulating NFATc1 expression via interfering with the phosphorylation of NFκB p65 and MAPK ERK1/2.

Jeongim *et al.* (26) reported that RANKL significantly increased the expression of CXCL2 in bone marrow-derived macrophages (BMMs) and that CXCL2 mediated RANKL-dependent differentiation of osteoclasts from BMMs in mice. The osteoclastogenesis-enhancing effects of CXCL2 were further corroborated by their investigation with an in vivo bone resorption model. Notably, CXCL2 alone induced significant bone loss in mice calvarial similar to that induced by RANKL. They also reported that CXCL2 mediated lipopolysaccharide (LPS)-induced osteoclastogenesis in RANKL-primed precursors (i.e. BMMs) (31). LPS stimulated the production of CXCL2 in BMMs, and the conditioned medium from LPS-treated BMMs could enhance the migration of osteoclast precursors, which was blocked by treatment with CXCL2-neutralising antibody or CXCR2 receptor antagonist. Blocking CXCL2 also reduced LPS-induced osteoclastogenesis, and in addition, CXCL2 neutralization prevented bone destruction in mice treated with LPS, suggesting a critical role of CXCL2 in the process of osteoclastogenesis. In the present study, CXCL2 was also evidently involved in the process of osteoclast differentiation in RA patients.

Therapies targeting CXCL2/CXCR2 have been tested in animal models of arthritis with concomitant reduction in neutrophil recruitment and tumor necrosis factor-α production(35, 36), and immunization against CXCL2 was reportedly efficient in delaying the onset of arthritis and reducing disease severity in a murine collagen-induced arthritis model(37). The novel orally-active non-competitive allosteric inhibitor of CXCL2 known as DF 2162 significantly ameliorates AIA in rats, an effect that is quantitatively and qualitatively similar to that of anti-tumor necrosis factor antibody treatment(35). In addition, the CXCR2 antagonist SCH563705 led to a dose-dependent decrease in clinical disease scores and paw thickness measurements, and clearly reduced inflammation and bone and cartilage degradation in a mouse model of arthritis(36). The results of our study imply that targeting CXCL2/CXCR2 as a strategy to treat RA may contribute to protection from bone destruction by directly inhibiting bone resorption, in addition to the already suggested anti-inflammatory effects.

In conclusion, we identified novel pathways associated with ACPA+ RA patients using RNA sequencing, and detected higher CXCL2 expression in ACPA+ RA patients than in ACPA- RA patients. Increased levels of CXCL2 led to NFκB activation in CD14+ monocytes from RA patients during the osteoclastogenic process. These results suggest a previously unreported role of CXCL2 during osteoclastogenesis in RA patients, and indicate that CXCL2 blockade might be a novel therapeutic strategy in RA.

Supplementary data

Supplementary data are available online.

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Authors' contributions

LS, XW, NH, ZA, RY, CL, YL, YL and XL carried out the molecular biochemical studies. LS, XW and NH drafted the manuscript and performed the statistical analysis. XF and JZ participated in the design of the study and helped to draft manuscript. All authors read and approved the final manuscript.

Competing interests

The authors declare no conflicts of interest.

Table 1 Baseline characteristics of the enrolled RA patients

	Total (n=107)	ACPA + (n=70)	ACPA – (n=37)	P Value

	Total (n=107)	ACPA + (n=70)	ACPA – (n=37)	P Value
Age (mean year)	55.94±14.11	55.13±13.64	57.49±15.02	0.414
Gender (male/female)	26/81	16/54	10/27	0.632
Duration (months)	24 (12,108)	60 (17,183)	13 (5,36)	**0.000**
RF-positive	57.94%	82.86%	10.81%	**0.000**
ESR (mm/h)	32 (14,60)	33 (14.5,60)	29 (13.5,57.5)	0.692
CRP (mg/dl)	1.86 (0.51,5.22)	1.565 (0.5,4.37)	2.46 (0.61,7.72)	0.250
DAS28	5.84 (4.41,7.59)	6.62 (4.13,7.77)	5.64 (4.5,6.71)	0.187
Bone erosion	28.95% (n=22/76)	38% (n=19/50)	11.54% (n=3/26)	**0.016**

Data are represented as mean ± SD and median with interquartile range.

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