related to a decline in the anabolic activity of chondrocytes (35,36). The expression of miR-140 was reduced in OA cartilage, and, in the same samples, expression of the proteinase *ADAMTS5* increased, and *COL2A1* expression decreased. Thus, the abnormal expression pattern of miR-140 correlates with the imbalance of anabolic–catabolic responses in OA. Our observations of abnormal miR-140 expression in OA are consistent with the findings of a recent study (37). IL-1β is one of the most prominent mediators of cartilage degradation and joint inflammation (38,39). IL-1β induces a cascade of inflammatory and catabolic events in chondrocytes. It also changes chondrocyte anabolism by suppressing the synthesis of proteoglycans and collagens and by enhancing the production of MMPs (27,28). The expression of miR-140 was down-regulated by IL-1β stimulation of chondrocytes in vitro. These data suggest that IL-1β may be a mediator that is involved in the suppression of miR-140 in OA.

Our studies using dsRNA mimicking miR-140 suggest that miR-140 suppresses *ADAMTS5* mRNA expression. This observation is supported by preliminary observations of increased *ADAMTS5* expression in miR-140–knockout mice (Miyaki S, et al: unpublished observations). The pathogenesis of OA is associated with abnormal activation and differentiation of chondrocytes that overexpress inflammation mediators and matrix-degrading enzymes (3–6). Previously examined mechanisms in these abnormal cellular responses include chondrocyte stimulation by extracellular stimuli such as cytokines, growth factors, mechanical stress, and matrix-degradation products. Intracellularly, these stimuli activate signaling cascades that lead to changes in gene expression (23,40). Alteration of miR-140 by IL-1β represents a novel mechanism to explain such aberrant changes in chondrocyte gene expression.

The present study was focused on miR-140, because it was shown to be the most cartilage-specific miRNA. We performed searches in 3 databases (TargetScan [http://www.targetscan.org/vert_50/], PicTar [http://pictar.mdc-berlin.de/], and miRanda [http://microrna.sanger.ac. uk/]), and this yielded 223–975 potential miR-140 targets. Only 9 potential targets were identified in all 3 databases, and, notably, this did not include *ADAMTS5*. Uncertainty remains regarding the rules for in silico miRNA target identification (41). At present, the most conclusive target validation is the demonstration of changes in protein expression, cell function, or phenotype in knockout or transgenic mice. Future studies are needed to determine the consequences of changes in the complete set of miR-140 targets for cartilage development and homeostasis. Currently, ongoing studies with miR-140–knockout mice and miR-140–transgenic mice will provide information in this regard.

In conclusion, the results of this study suggest that miR-140 is a chondrocyte differentiation–related miRNA. It may be a novel regulator of cartilage homeostasis, and changes in its expression and function play an important role in diseases affecting articular cartilage. Further studies of miR-140 have the potential to reveal important new regulatory pathways that control cartilage development and homeostasis and provide new insights into disease mechanisms and therapeutic interventions for OA.

AUTHOR CONTRIBUTIONS

All authors were involved in drafting the article or revising it critically for important intellectual content, and all authors approved the final version to be published. Dr. Asahara 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. Miyaki, Asahara.

Acquisition of data. Miyaki, Nakasa, Otsuki, Grogan, Higashiyama, Inoue.

Analysis and interpretation of data. Miyaki, Nakasa, Otsuki, Grogan, Inoue, Kato, Sato, Lotz.

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Smad3 activates the Sox9-dependent transcription on chromatin

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ABSTRACT

Transforming growth factor (TGF)-β has an essential role for the Sry-type high-mobility-group box (Sox)-regulated chondrogenesis. Chondrogenic differentiation is also controlled by chromatin-mediated transcription. We have previously reported that TGF-β-regulated Smad3 induces chondrogenesis through the activation of Sox9-dependent transcription. However, the cross-talk between TGF-β signal and Sox9 on chromatin-mediated transcription has not been elucidated. In the present study, we investigated the activity of Smad3, Sox9, and coactivator p300 using an in vitro chromatin assembly model. Luciferase reporter assays revealed that Smad3 stimulated the Sox9-mediated transcription in a TGF-β-dependent manner. Recombinant Sox9 associated with phosphorylated Smad3/4 and recognized the enhancer region of type II collagen gene. In vitro transcription and S1 nuclease assays showed that Smad3 and p300 cooperatively activated the Sox9-dependent transcription on chromatin template. The combination treatment of phosphorylated Smad3, Sox9, and p300 were necessary for the activation of chromatin-mediated transcription. These findings suggest that TGF-β signal Smad3 plays a key role for chromatin remodeling to induce chondrogenesis via its association with Sox9.

1. Introduction

Chondrogenesis is the fundamental process to form bones and articular surfaces. Mesenchymal condensation and the following chondrocyte differentiation are strictly regulated by several transcription factors and growth factors, such as Sry-type high-mobility-group box (Sox) genes and the transforming growth factor (TGF)-β superfamily, respectively. Sox5, 6, and 9 cooperatively regulate the sequential differentiation steps of chondrogenesis (Akiyama et al., 2002, 2004; Stricker et al., 2002). In these transcription factors, Sox9 has an essential role to initiate mesenchymal condensation and to maintain chondrogenic potential in early stages. The expression of α1 chain of type II collagen (Col2a1), a major component of cartilage extracellular matrix, is controlled by Sox9 through the Sox9-binding site on the Col2a1 enhancer region (Bell et al., 1997) and closely parallels that of Sox9 (Ng et al., 1997). The TGF-β superfamily including the two major families (TGF-β and bone morphogenetic protein) is a multifunctional growth factor for many cellular responses such as differentiation and proliferation (Heldin et al., 1997; Shi and Massagué, 2003). In chondrogenesis, TGF-β stimulation is necessary for primary chondrogenesis derived from mesenchymal stem cells (Pittenger et al., 1999). We previously described that TGF-β signal Smad3 promotes the early chondrogenesis through the activation of Sox9 (Furumatsu et al., 2005a). However, the precise mechanisms of Sox9 and TGF-β in the epigenetic regulation for initiating chondrogenesis are still unclear.

The epigenetic regulation is another dynamic system to control gene expression and other fundamental cellular processes, such as proliferation and differentiation (Li, 2002; Felsenfeld and Groudine, 2003; Jaenisch and Bird, 2003). Chromatin remodeling system including histone modification is the representative mechanism of epigenetics. The eukaryotic DNA and histones are packaged into chromatin as the nucleosome-repeated structure. Accesses of transcription factors and other regulators to DNA are highly restricted by chromatin structure. Many molecules have been revealed as important factors to form chromatin. Nucleosome assembly protein-1 (NAP-1) acts as a histone-shuttling protein (Ito

Abbreviations: AcCoA, acetyl-coenzyme A; ACF, ATP-utilizing chromatin assembly and remodeling factor; Col2a1, α1 chain of type II collagen; EMSA, electrophoretic mobility shift assay; MNase, micrococcal nuclease; MAPK, mitogen-activated protein kinase; NAP-1, nucleosome assembly protein-1; si-, small interfering; Sox, Sry-type high-mobility-group box; TβR-I(TD), constitutively active form of TβR-I; TGF, transforming growth factor.

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et al., 1996; Nakagawa et al., 2001). ACF (ATP-utilizing chromatin assembly and remodeling factor), consisting of Acf1 and ISWI subunits, assembles periodic nucleosome arrays on histone-attached DNA in an ATP-dependent process (Ito et al., 1999; Nakagawa et al., 2001). On the other hand, histone modification on chromatin, such as acetylation, enables transcription regulators to access to DNA sequences. DNA-binding transcription factors, such as CREB and MyoD, exert their transcriptional potential on histone-acetylated chromatin (Asahara et al., 2001; Dilworth et al., 2004). However, the relationship between chromatin-mediated transcription and signaling molecules is not elucidated. We previously reported that p300, which has an intrinsic histone acetyltransferase activity, directly associates with Sox9 (Tsuda et al., 2003) and activates the Sox9-dependent transcription on chromatin (Furumatsu et al., 2005b). In this study, we further analyzed the cross-talk between the Sox9-dependent transcription and TGF-β receptor-regulated Smad3 on chromatin using an in vitro chromatin assembly model.

The present study demonstrates that TGF-β-stimulated Smad3 activates the Sox9-dependent transcription on chromatin. This is the first report to explain the importance of TGF-β treatment in chromatin-mediated chondrogenesis.

2. Materials and methods

2.1. Cells, plasmids, si-RNA, and antibodies

A human chondrosarcoma cell line (SW1353) was used as an immature chondrogenic cell line. A plasmid encoding full-length of rat Sox9 and a small interfering (si-) RNA against Smad3 were used (Furumatsu et al., 2005a). p300 was a gift from Tso-Pang Yao. FLAG-tagged Smad3/4 and the constitutively active form of TβR-I [TβR-I(TD)] were generous gifts from Takeshi Imamura. pGL3-585E, which contains a mouse Col2a1 promoter and enhancer, was constructed with a pGL3-Basic (Promega) vector and used as a native Col2a1 reporter gene. 12 × 48-pGL3-P containing 12 sets of a 48-bp Col2a1 enhancer element was used as a reporter plasmid. PCR fragments of FLAG-tagged Sox9, FLAG-tagged Smad3, and Smad4 were subcloned into baculovirus expression vector pENTR3C (Invitrogen) as described (Furumatsu et al., 2005b). The following antibodies were used: FLAG M2, FLAG M2 affinity gel (Sigma), phospho-Smad2/3 (Santa Cruz), Smad2/3 (Upstate), Smad4 (Cell Signaling), and Sox9 (Chemicon).

2.2. Luciferase reporter assay

pGL3-585E and 12 × 48-pGL3-P were used as reporter genes for investigating the Sox9-dependent transcriptional activity. These reporter plasmids were different from our previous constructs (Furumatsu et al., 2005a). Appropriate plasmids (50 ng) and si-Smad3 (200 nM) were transiently transfected into SW1353 cells using FuGENE6 (Roche). pRL-CMV (10 ng, Promega) was used as an internal control. The cells were harvested for 24 h, and then the luciferase activities were analyzed using Dual-Luciferase Reporter Assay System (Promega). The assays were performed in triplicate.

2.3. Nuclear extract and immunoprecipitation

Nuclear extracts of SW1353 cells were prepared in 2× buffer D [20 mM HEPES (pH 7.9), 20% glycerol, 0.1 M KCl, 0.2 mM EDTA, 0.5 mM PMSF, 0.5 mM DTT]. Protein concentrations were measured by BCA protein assay kit (Bio-Rad). Immunoprecipitation analyses using purified recombinant proteins were performed with anti-Sox9 or Smad2/3 antibody in 1× buffer D as described previously (Furumatsu et al., 2005b). Briefly, indicated amounts of recombinant proteins and/or nuclear extracts were incubated for 1 h at 25 °C. Ten percent volume of reaction mixture was loaded as an input fraction. Half of the mixture was incubated with each antibody and protein A beads (Sigma) for 1 h at 4 °C. Remaining mixture was incubated with rabbit IgG as a control.

2.4. Purification of histones and recombinant proteins

Core histones were purified from HeLa nuclear pellets and dialyzed in HEG buffer [10 mM HEPES (pH 7.6) 10% glycerol, 50 mM KCl, 0.1 mM EDTA]. Baculovirus of histidine-tagged NAP-1, FLAG-tagged ISWI, and Acf-1 were kindly gifts from Takashi Ito and used as chromatin assembling molecules (Ito et al., 1999, 2000). The baculovirus expression vectors carrying Sox9 and Smad3/4 were constructed using BaculoDirect Systems according to the manufacturer's protocol (Invitrogen). Recombinant NAP-1, recombinant ACF complex (FLAG-tagged ISWI and untagged Acf-1), FLAG-tagged p300, FLAG-tagged Sox9, and Smad3/4 complex (FLAG-tagged Smad3 and untagged Smad4) were produced in Sf9 cells (Invitrogen) and prepared as described previously (Furumatsu et al., 2005b). Recombinant Smad3/4 was purified after 30-min-treatments of TGF-β3 (R&D). Purified proteins were assessed by silver stain (BioRad) and Western blotting analyses.

2.5. Electrophoretic mobility shift assay (EMSA)

The Col2a1 enhancer probe containing the Sox9-binding site (in capital letters) was generated by annealing the following oligonucleotides: 5′-gcgcttgagaaaagccccATTCATgagaggc-3′ and 5′-gcctctcATGAATGgggctttttctcaagcgc-3′. Probes were ^{32}P end-labeled using T4 polynucleotide kinase (Invitrogen). Purified Sox9 (30 ng) was incubated with the labeled probe (0.8 pmol). The unlabeled Col2a1 enhancer probe (16 pmol) was used as a competitor. In supershift analysis, 15 min treatment with anti-Sox9 antibody (0.2 μg) was performed before protein–DNA binding reaction.

2.6. Chromatin assembly and micrococcal nuclease (MNase) assay

Chromatin assembly and MNase digestion analyses were performed as described (Asahara et al., 2002) by using 12 × 48-pGL3-P. For chromatin reconstitution, standard reactions (20 μl) containing plasmid (150 ng), histones (100 ng), NAP-1 (500 ng), ISWI/Acf-1 (0.65 ng each), ATP (3 mM), and ATP regeneration systems (30 mM phosphocreatine and 20 ng creatine phosphokinase) were incubated at 30 °C for 4 h. In MNase assay, chromatinized plasmids (300 ng) were digested with MNase (0, 0.02, and 0.04 U/15 μl) for 5 min at 37 °C.

2.7. In vitro transcription and S1 nuclease assay

After chromatin assembly, standard reactions (12 × 48-pGL3-P, 150 ng) were incubated with Sox9 (10 ng), Smad3/4 (100 ng), p300 (40 ng), and acetyl-coenzyme A (AcCoA, 5 μM) for 30 min at 30 °C. For in vitro transcription, nuclear extracts from SW1353 cells (30 μg) were added and incubated with rNTPs at 30 °C for 40 min. In vitro-transcribed RNAs were recovered and subjected to S1 nuclease analyses using the specific primer (49 bp) against 12 × 48-pGL3-P luciferase gene as described (Furumatsu et al., 2005b). RNAs were annealed with ^{32}P end-labeled primers (0.2 pmol each) for 12 h, and then digested with 50 units of S1 nuclease (Invitrogen) for 30 min at 37 °C. The protected fragments were run on 8% denaturing polyacrylamide gels and visualized by autoradiography. Each experiment was performed at least three times.

3. Results

3.1. Smad3 stimulates the Sox9-mediated transcription in a TGF-β-dependent manner

To assess the fundamental role of Smad3 in chromatin remodeling during early chondrogenesis, we first analyzed the effect of Smad3 in the Sox9-regulated transcription using newly constructed reporter plasmids. Overexpressed Smad3 stimulated the transcriptional activity of Col2a1 reporter gene (Fig. 1A, pGL3-585E) in a Sox9-depedent manner (Fig. 1B). In addition, the effect of Smad3 was enhanced by the cotransfection of constitutively active form of TGF-β receptor I [TβR-I(TD)]. Twelve copies of the Sox9-binding fragment dramatically induced the Sox9-regulated transcription in reporter assays (Fig. 1C, 12 × 48-pGL3-P). Smad3 also activated the transcription of 12 × 48-pGL3-P in Sox9- and TGF-β-dependent manners. These findings suggest that Smad3 may act as a chromatin remodeling factor in chondrogenesis.

3.2. TGF-β and Smad3 are necessary for the activation of Sox9-dependent transcription

To investigate the effect of Smad3 itself in this reporter assay system, we used a si-RNA fragment against Smad3 as an inhibitor. The activities of Sox9-regulated transcription were stimulated by the addition of Smad3 in a dose-dependent fashion (Fig. 2A and B). si-Smad3 decreased the effect of activated TGF-β receptor and overexpressed Smad3 in Sox9-regulated reporters to the basal levels. However, si-Smad3 did not inhibit the Sox9-induced transactivation. These results prompted us to analyze the function of TGF-β-stimulated Smad3 and Sox9-related transcriptional apparatus on chromatin in chondrogenesis.

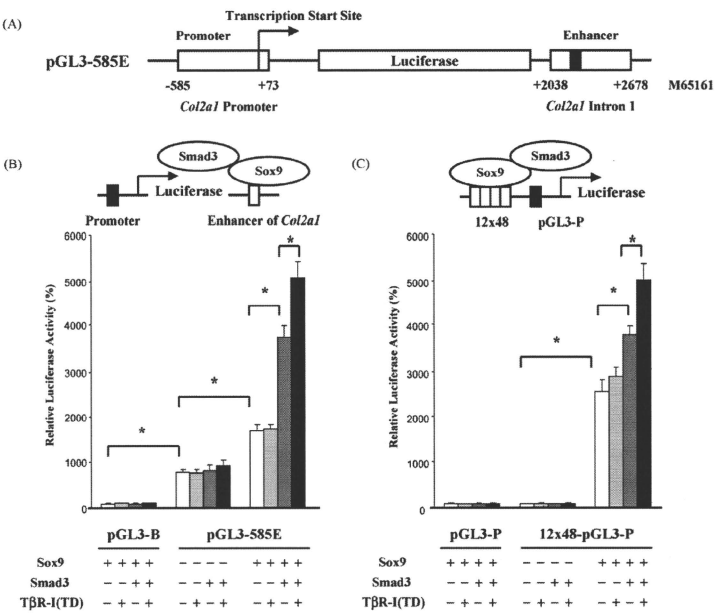

Fig. 1. Smad3 enhances the Sox9-mediated transcription in a TGF-β-dependent manner. (A) A schematic characterization of pGL3-585E which contains a native promoter and enhancer of mouse Col2a1 gene. Numbers indicate the distance from the transcription start site on mouse Col2a1 gene (National Center for Biotechnology Information, M65161). Black box denotes the SOX9-binding site on the enhancer region of Col2a1 intron 1. (B) Transient transfections of Sox9, Smad3, and TβR-I(TD) did not increase luciferase activities of pGL3-B plasmids in SW1353 cells (pGL3-B). In pGL3-585E systems, Sox9 enhanced a relative luciferase activity to a level as high as 2.2-fold over the control. Cotransfection of Smad3 augmented a luciferase activity up to 2.3-fold higher level of Sox9-transfected cells. The additional transfection of constitutively active form of TβR-I(TD) induced an approximately 36% increase of the activity in Sox9- and Smad3-transfected SW1353 cells. Luciferase activities of pGL3-585E were not increased in the absence of Sox9. Note that Smad3 and TβR-I(TD) synergistically activated the native Col2a1 reporter-mediated transcription in a Sox9-dependent manner. (C) The activity of 12 × 48 pGL3-P was enhanced by the addition of Sox9 up to 27.5-fold levels of the control. Smad3 increased the 12 × 48 pGL3-P-based luciferase activity up to 1.5-fold higher level in the presence of Sox9. TβR-I(TD) also induced 33% increase of the activity of Smad3-transfected cells in the presence of Sox9. However, the additional increase of luciferase activity was not observed in pGL3-P-transfected cells. Relative luciferase activities were calculated using the activity of pGL3-P as a control (100%). A schematic illustration of each reporter assay system is placed on the top of each figure (B and C). *Statistical significances ($p < 0.05$) were observed between the indicated bars with the Mann–Whitney *U*-test. Error bars, S.D.

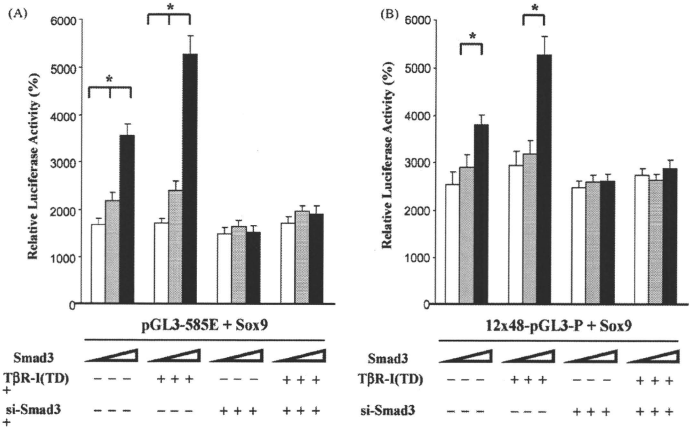

Fig. 2. Smad3 has an essential role for TGF-β-stimulated transactivation in the Sox9-regulated gene expression. (A) Smad3 enhanced the Sox9-dependent transcription in a dose-dependent manner. Smad3 and TβR-I(TD) synergistically increased the luciferase activity in pGL3-585E reporter systems. si-RNA against Smad3 (si-Smad3) totally inhibited the synergistic effects of Smad3 and TβR-I(TD). Note that si-Smad3 did not inhibit the Sox9-induced transactivation of reporter genes. (B) In 12 × 48 pGL3-P reporter systems, Smad3 and TβR-I(TD) cooperatively stimulated the relative luciferase activity up to 1.7-fold higher level in the presence of Sox9. A dose-dependent effect of Smad3 was observed. However, the increase of luciferase activity was suppressed by si-Smad3 in Smad3-transfected cells. Relative luciferase activities were calculated using the activity of pGL3-B (A) or pGL3-P (B) as a control (100%). Triangular boxes denote the transfection volume of Smad3 expression plasmid (0, 25, and 50 ng). *Statistical significances ($p < 0.05$) were observed between the indicated bars with the Mann–Whitney *U*-test. Error bars, S.D.

3.3. Recombinant Sox9 associates with p300 and binds to the Col2a1 enhancer in vitro

To examine the role of Sox9-associated transcriptional complex (Sox9, p300, and Smad3) on chromatin, we purified histones from HeLa cells, chromatin assembly-related molecules (NAP-1 and ACF complex), Sox9, p300, and Smad3 as described in Section 2. Purified NAP-1 and ACF sufficiently assembled chromatin under histone-containing conditions. Chromatin assembling abilities of these molecules were estimated by MNase digestion assays (Fig. 3A). Recombinant Sox9 purified from Sf9 cells associated with recombinant p300 in vitro (Fig. 3B). Recombinant Sox9 also bound with high affinity to the Col2a1 enhancer probe, which contains the Sox9-binding sequence, in EMSA (Fig. 3C).

3.4. TGF-β-stimulated Smad3 and p300 cooperatively activate the Sox9-dependent transcription on chromatin

For in vitro transcription analyses after chromatin assembly (Fig. 4A), we assessed the complex formation of Smad3 and Smad4. Smad3 purified from the nuclear fraction of TGF-β-treated Sf9 cells was a phosphorylated form of Smad3 (Fig. 4B). Smad4 was also detected in the same coimmunoprecipitated fraction using anti-FLAG M2 affinity gel (Fig. 4B). This result demonstrated that phosphorylated Smad3 was transferred into the nucleus with Smad4 by TGF-β treatment. In addition, purified Smad3/4 associated with recombinant Sox9 and p300 in vitro (Fig. 4C). Here we investigated the effect of phosphorylated Smad3 in the Sox9-dependent transcription on chromatin. In vitro transcription analyses on chromatinized templates revealed that the combination of Sox9, Smad3/4, and p300 were necessary for the activation of chromatin-mediated transcription (Fig. 4D). These findings suggest that the Sox9-dependent chondrogenesis might be strictly controlled by TGF-β signal Smad3 and chromatin remodeling factor p300.

4. Discussion

The present study indicates that TGF-β receptor-regulated Smad3 and p300 cooperatively activate the Sox9-dependent transcription on chromatin. The TGF-β signal plays an essential role to induce primary chondrogenesis (Pittenger et al., 1999; Heng et al., 2004). However, the differentiation of chondrocyte is regulated by the conflictive effects of TGF-β. TGF-β3 enhances the early chondrogenesis derived from mesenchymal stem cells (Fan et al., 2008). The short-term treatment with TGF-β3 has been reported to maintain a chondrogenic phenotype (Mehlhorn et al., 2006). On the other hand, TGF-β inhibits chondrocyte maturation at the late stage (Ballock et al., 1993; Ferguson et al., 2000). We previously described that TGF-β signal Smad3 promotes the early chondrogenesis through the activation of Sox9 (Furumatsu et al., 2005a). However, the cross-talk between TGF-β signal and Sox9 in the epigenetic regulation for initiating chondrogenesis is still unclear. Here, we further analyzed a crucial role of Smad3 in the Sox9-dependent chondrogenesis on chromatin. In this study, Smad3 enhanced the Sox9-mediated transcription in luciferase reporter assay systems (Fig. 1B and C). The increase of relative luciferase activity with Smad3 was higher in pGL3-585E, which contains a native set of Col2a1 promoter and enhancer, than in 12 × 48-pGL3-P systems. These findings might be caused by the binding affinity of Sox9 against each reporter plasmid. The activity of 12 × 48-pGL3-P containing high copies of Sox9-binding site might be already excited by the cotransfection of Sox9. A dose-dependent transactivation by Smad3 was observed in both systems,

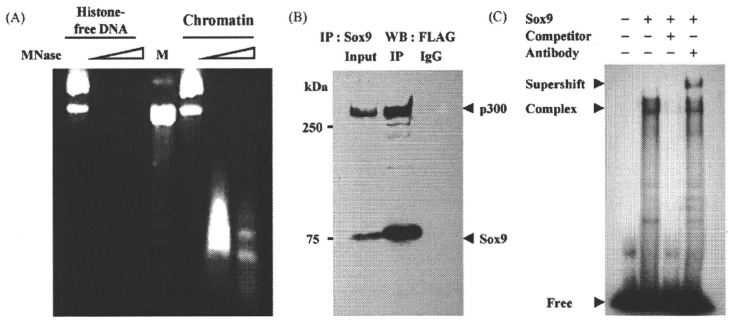

Fig. 3. MNase digestion analyses after chromatin assembly. Purified Sox9 form a complex with p300 or DNA probe containing the Sox9-binding site. (A) Closed circular 12 × 48-pGL3-P (300 ng) was used as a template. Chromatin assembling steps were performed as shown in Fig. 4A. Plasmid DNAs were completely digested by MNase (0.02 and 0.04 U/15 μl) in the absence of histones, NAP-1, and ACF (Histone-free DNA). Chromatinized plasmids were protected from complete digestion (Chromatin). Nucleosome-repeated pattern (approximately 165 bp) was observed in chromatin template after MNase treatment (0.04 U/15 μl). M, 123-bp ladder (Invitrogen). (B) Purified p300 was coimmunoprecipitated with recombinant Sox9 using anti-Sox9 antibody. Western blotting was performed with anti-FLAG M2 antibody. Sox9 (30 ng) was incubated with p300 (30 ng), and then the 10% of reaction was loaded as an input. Immunoprecipitation using rabbit IgG was performed as a control. Numbers indicate molecular weight (kDa). (C) Purified Sox9 associated with the Col2a1 enhancer probe in EMSA. The unlabeled competitor decreased the signal of Sox9–DNA complex. Supershifted band was observed in the presence of anti-Sox9 antibody.

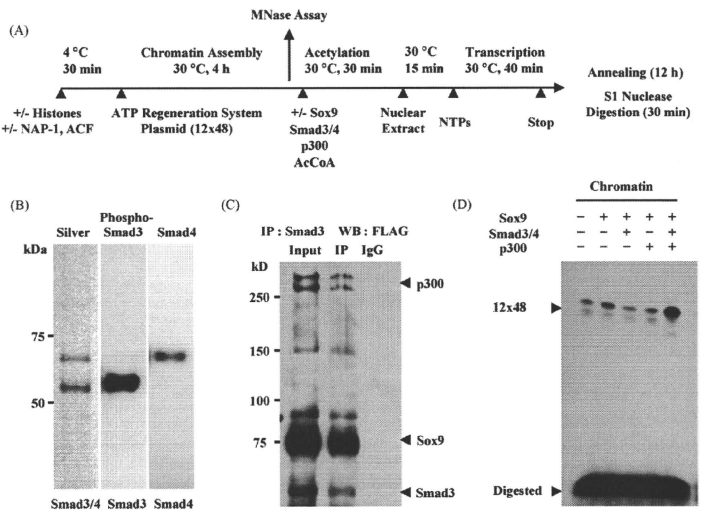

Fig. 4. Phosphorylated Smad3 and p300 cooperatively activate the Sox9-dependent transcription on chromatin. (A) The sequential steps for chromatin assembly and in vitro transcription are illustrated. MNase assays were performed after chromatin assembly (Fig. 3A). To estimate the amounts of RNAs transcribed from chromatinized plasmid, S1 nuclease assays were performed as described in Section 2. S1 nuclease digests a single-stranded part of RNA and excessive primers. Remaining double-stranded fragments (49-bp), which are annealed with ^{32}P end-labeled specific primers, represent transcriptional activities on chromatin. (B) Recombinant Smad3/4 were prepared using baculovirus expression systems. The details are described in Section 2. Smad3/4 complex were visualized with silver staining (left lane). Phosphorylated Smad3 were obtained after TGF-β treatments (middle lane). Smad4 was coimmunoprecipitated with FLAG-tagged Smad3 (right lane). (C) Protein–protein interactions among recombinant proteins. Purified Sox9 (50 ng), p300 (50 ng), and Smad3/4 (50/15 ng) were incubated, and then immunoprecipitated with anti-Smad2/3 antibodies. Sox9 and p300 were coimmunoprecipitated with Smad3 (IP). Western blotting analyses were performed with anti-FLAG M2 antibodies. (D) Sox9, Smad3/4, and p300 cooperatively enhanced the transcriptional activities of chromatinized 12 × 48-pGL3-P (12 × 48, upper bands). Chromatin-mediated transcription was not fully activated by the combined treatment with Sox9 and Smad3/4 (or p300). Note that the synergistic effect of triple combination with Sox9, Smad3/4, and p300 was observed (right lane). Digested denotes non-annealed probes, which were digested by S1 nuclease treatments (lower bands).

and was totally suppressed by the cotransfection of si-RNA against Smad3 itself (Fig. 2). We previously demonstrated that si-Smad3 completely decreased the Col2a1 expression in a mesenchymal stem cell-derived chondrogenic model (Furumatsu et al., 2005a). These results suggest that Smad3 is the major transducer of TGF-β signal in the Sox9-regulated early chondrogenesis.

The Sox9-dependent transcription is synergistically activated by p300 on chromatin (Furumatsu et al., 2005b). Transcriptional coactivator p300 has an important role for gene expression and cellular differentiation (Dilworth et al., 2004; Espinosa and Emerson, 2001; Kitagawa et al., 2003). The effect of p300 is exerted through several mechanisms. p300 acts as a protein scaffold and a bridging factor for forming transcriptional complexes. In addition, the intrinsic histone acetyltransferase activity of p300 has a potential to facilitate the transcriptional activity by modulating chromatin structure (Chan and La Thangue, 2001; Korzus et al., 1998; Utley et al., 1998). Several authors have reported that p300 plays a critical role for the activation of cAMP response element-binding protein-, MyoD-, p53-, or vitamin D receptor-dependent transcription on reconstituted chromatin (Asahara et al., 2001; Dilworth et al., 2004; Espinosa and Emerson, 2001; Kitagawa et al., 2003). In previous studies, we described that p300 and Smad3 enhanced the Sox9-dependent transcription by associating with Sox9 (Tsuda et al., 2003; Furumatsu et al., 2005a). However, the precise effect of the third associating factor, such as Smad3, on chromatin is still unclear. To analyze the additional effect of the third factor in a chromatin assembly model is considered to be hard. This study revealed the additional effect of phosphorylated Smad3 in the Sox9- and p300-mediated transcription using 12 × 48-pGL3-P-based chromatin assembly model (Fig. 4D). However, the synergistic effect of Smad3 was not observed in a different balance of Sox9-associating molecules (data not shown). In pGL3-585E systems, we could not detect a significant effect of Smad3 on chromatin-derived transcription, either (data not shown). These findings suggest that the balance of Sox9-associating factors and the accessibility to chromatinized promoter might be important for the epigenetic regulation of chondrogenesis. In addition, the discrepancy of Smad3-induced transactivation between reporter assays (Figs. 1 and 2) and chromatin-derived transcription (Fig. 4D) might be caused by the following reasons: (i) the chromatinized status of Sox9-reactive plasmid was different in each analysis, (ii) the influence of Sox9 and p300 was more critical on chromatin-assembled plasmid, and (iii) unknown factors in SW1353 nuclear extracts might have important roles in the Sox9-dependent transcription on chromatin. Several transcription partners such as Sox-5/6, PGC-1α, Barx2, and TRAP230 can modify the Sox9-dependent transcription during chondrogenesis (Ikeda et al., 2004; Kawakami et al., 2005; Lefebvre et al., 2001; Meech et al., 2005; Zhou et al., 2002). Further analyses to identify the other unknown partners of Sox9-based transcriptional complex will be required.

Animal models for a loss of Smad3 function have revealed the importance of Smad3 in physiological systems. Smad3 null mice show skeletal defects including osteoarthritis (Datto et al., 1999). Haploinsufficiency of Smad2 and Smad3 causes an embryonic lethality due to endodermal defects and exhibits craniofacial defects (Liu et al., 2004). We previously reported that Smad3 had an important role for primary chondrogenesis (Furumatsu et al., 2005a). In addition to the Smad3 pathway, TGF-β activates mitogen-activated protein kinase (MAPK) pathway during chondrogenic differentiation (Stanton et al., 2003). Several authors have shown that MAPK pathway modulates Col2a1 and Sox9 expression in chondrogenesis (Murakami et al., 2000; Nakamura et al., 1999; Tuli et al., 2003). These reports suggest that TGF-β-stimulated MAPK pathway would also be involved in chondrogenesis with modifying the Sox9-dependent transcription. Further studies to analyze the relationships between MAPK pathway and the Sox9-mediated transcription on chromatin are required.

In conclusion, the present study demonstrates that Smad3 enhances the Sox9-dependent transcription on chromatin. Our findings suggest that the potential molecular mechanism how TGF-β signals induce early chondrogenesis via chromatin regulation.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.biocel.2008.10.032.

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ORIGINAL ARTICLE

A combination of biochemical markers of cartilage and bone turnover, radiographic damage and body mass index to predict the progression of joint destruction in patients with rheumatoid arthritis treated with disease-modifying anti-rheumatic drugs

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Abstract The aim of this study was to evaluate the predictive value of biological, radiological and clinical parameters for the progression of radiographic joint damage in rheumatoid arthritis (RA) patients treated with conventional disease-modifying anti-rheumatic drugs (DMARDs). We analyzed the 145 patients with active RA for less than 5 years who were participating in the prospective 1-year randomized controlled trial of tocilizumab (SAMURAI trial) as a control arm treated with conventional DMARDs. Progression of joint damage was assessed by sequential radiographs read by two independent blinded X-ray readers and scored for bone erosion and joint space narrowing (JSN) using the van der Heijde-modified Sharp method. Multivariate analysis revealed that increased urinary levels of C-terminal crosslinked telopeptide of type II collagen (U-CTX-II), an increased urinary total pyridinoline/total deoxypyridinoline (U-PYD/DPD) ratio and low body mass index (BMI) at baseline were independently associated with a higher risk for progression of bone erosion. In addition to these three variables, the JSN score at baseline was also significantly associated with an increased risk of progression of the JSN score and total Sharp score. High baseline U-CTX-II levels, U-PYD/DPD ratio and JSN score and a low BMI are independent predictive markers for the radiographically evident joint damage in patients with RA treated with conventional DMARDs.

Keywords BMI · CTX-II · Joint destruction · PYD/DPD ratio · Rheumatoid arthritis

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Introduction

Although rheumatoid arthritis (RA) has features of a systemic disease and capable of exhibiting a variety of extra-articular manifestations, it is predominantly characterized by structural destruction of the joints, leading to functional disability [1–4]. Joint destruction often progresses early in the disease process [5–8], but the process is highly variable from patient to patient [9–12]. The identification of patients with rapid joint destruction very early in the disease process is of critical importance to clinicians wanting to optimize treatment strategies. Indeed, although new biological therapies are highly effective in preserving joint structure, they are expensive and may have side effects.

Thus, targeting these treatments to RA patients manifesting rapid progression of the disease may be beneficial.

Several prospective studies have been performed to identify predictive factors indicative of a worse radiological progression of RA [13–31]. The earlier investigations revealed the importance of the rheumatoid factor (RF), inflammation markers or radiographic damage at baseline [13, 14, 16–18, 20, 21], while more recent ones have identified biochemical markers of bone, cartilage and synovial tissue metabolism and catabolic enzymes as being associated with progression in RA [15, 19, 22, 24, 27–29]. Alternatively, RA is also associated with accelerated atherosclerosis and increased cardiovascular mortality and, recently, it has been shown that macrophage inhibitory cytokine 1 (MIC-1), which is linked to clinical events in atherosclerosis, may be involved in the pathological process of erosive joint destruction [32]. The body mass index (BMI) has also been reported to be associated with the radiographic progression of RA, independent of inflammation markers [23, 30, 31], and recent new information suggests the potential involvement of adipokines as regulators of inflammation in RA [33]. These new findings have lead to the recognition of RA as a disease involving a variety of pathological conditions related with joint destruction and made clinicians aware of the fact that RA is a systemic disease in terms of the pathology of the bone and destruction of cartilage. However, to date, there has been no study that has analyzed concomitantly in the same population the independent contribution of these various anthropometric, clinical, laboratory and radiological features to the prediction of disease progression in RA.

The aims of the study reported here were to determine which combination of a few risk factors identified among a panel of clinical, biological and radiological parameters would be powerful in predicting the radiological progression of bone erosion and joint space narrowing (JSN) in RA patients treated with conventional disease-modifying antirheumatic drugs (DMARDs).

Methods

Patients and protocol

The patient cohort consists of 148 patients with RA receiving conventional DMARDs who participated in the control arm of the SAMURAI trial described in a recent publication [34]. The aim of the SAMURAI, which was a 52-week-long multi-center clinical trial, was to evaluate the effect of tocilizumab on radiological joint damage. Three hundred and six patients with RA diagnosed according to the American College of Rheumatology criteria [35] were randomly assigned to tocilizumab monotherapy (8 mg/kg intravenously every 4 weeks) or conventional DMARDs. For the DMARDs group, the dose, type and combination of DMARDs and/or immunosuppressants could vary according to disease activity at the discretion of the treating physician. The study protocol was approved by the Ministry of Health, Labor and Welfare of Japan, and by the ethical committee at each participating site, and patients gave their written informed consent.

Radiographic assessment

Posteroanterior radiographs of hands and anteroposterior radiographs of feet were performed at baseline and at weeks 28 and 52 or at the last visit for patients who withdrew from the study prior to week 52. Radiographs were scored using the van der Heijde-modified Sharp method [36, 37] for bone erosion, joint space narrowing (JSN) and total sharp score (TSS) independently by two readers who were well trained and competent to score radiographs in accordance with the method. The readers were blinded to the treatment group and chronological order of the films.

Clinical assessment

The Disease Activity Score on 28 joints (DAS28), clinical improvement in signs and symptoms of RA, tender joint count, swollen joint count, and modified health assessment questionnaire (MHAQ) [38] were assessed at baseline.

Laboratory examinations

Fasting blood samples and the second morning urine samples were obtained from all subjects at clinical visits. C-reactive protein (CRP) and erythrocyte sedimentation rate (ESR) were measured in the local clinical test laboratory of each investigation site.

To assess bone formation, we measured serum intact-osteocalcin (OC) using a two-site immunoradiometric assay (Mitsubishi Kagaku Iatron, Japan) and serum bone alkaline phosphatase (bone ALP) by an enzyme-linked immunosorbent analysis (ELISA; Quidel, San Diego, CA). Markers of bone resorption included urinary N-terminal crosslinked telopeptide of type I collagen (U-NTX-I), which was measured by an ELISA (Ostex Int, Seattle, WA), and urinary total deoxypyridinoline (U-DPD) and total pyridinoline (U-PYD), measured by a high-performance liquid chromatography (HPLC) assay. Markers of cartilage synthesis included the N-terminal propeptide of type IIA collagen (PIIANP; Linco, St. Louis, MO) and the C-terminal propeptide of type II collagen (PIICP; IBEX Diagnostics, Montreal, Canada). Cartilage degradation was assessed by the urinary excretion of the C-terminal

crosslinked telopeptide of type II collagen (CTX-II Cartilaps ELISA; NORDIC Biosciences, Herlev, Denmark). Synovial tissue metabolism was assessed by measuring the urinary excretion of glucosyl–galactosyl–pyridinoline (Glc–Gal–PYD) by HPLC, serum matrix metalloproteinase-3 (MMP-3) by ELISA (Daiichi Pure Chemical, Japan) and serum amyloid protein A (SAA) by a latex immunoassay (LIA; Eiken Chemical, Japan). Other measures included serum interleukin-6 (IL-6) using a chemiluminescent enzyme immunoassay (CLEIA) (Fujirebio Japan), RF by LIA (Mitsubishi Kagaku Iatron, Japan), and immunoglobulin G (IgG) by LIA (Eiken Chemical, Japan).

Statistical analysis

For analyzing the correlation between markers at baseline and at the 52-week radiological progression of joint damage, we normalized the markers by logarithmic transformation when needed. First, the markers were selected by Pearson correlation coefficient with TSS, erosion score, and JSN score ($|r| > 0.15$). Then, the predictive factors were selected based on the multivariate regression analysis using the backward elimination method, the forward selection method, and the best-subset selection procedure using Mallows' Cp- adjusted R^2.

The odds ratio of progression in TSS, bone erosion and JSN score according to the levels of these baseline factors were estimated by logistic regression analysis with a 95% confidence interval (95% CI). The progression of joint damage was defined as an increase of TSS of 0.5 or more at 52 weeks.

All statistical analyses were two-sided, and p values <0.05 were considered to be significant. All statistical analyses were carried out using SAS ver. 8.2, TS2MO (SAS Institute, Cary, NC).

Results

One hundred and forty-five patients were included in the intent to treatment (ITT) analyses. Demographics and baseline disease characteristics are shown in Tables 1 and 3. At baseline, the mean age and the disease duration were 53.1 and 2.4 years, respectively. Patients had very active disease, as indicated by a DAS28 score of 6.4 and CRP of 4.9 mg/dl at baseline. The kinds of DMARDs and immunosuppressants used for RA treatment during the study and the number of patients are shown in Table 2.

Bivariate linear correlation analyses showed that baseline values of U-PYD, the ratio U-PYD/DPD, U-CTX-II, U–Glc–Gal–PYD, TSS, erosion score, JSN score, age and BMI were associated significantly with the 1-year increase in all three radiological indices of joint damage, i.e. bone erosion score, JSN score and TSS (Table 3). The baseline levels of U-DPD, S-PIIANP, triglyceride, ferritin also had a significant association with one or two variables among these three radiographic progression parameters (Table 3). None of the clinical indices of disease activity nor the biological parameters of inflammation were associated significantly with radiological progression. In the

Table 1 Baseline demographics, clinical and laboratory characteristics of the patient cohort

Baseline demographics, clinical and laboratory characteristics	Values
Number of patients	145
Age, years (mean)	53.1 ± 12.5
Female, *n* (%)	119 (82.1)
BMI (kg/m^2)	21.8 ± 3.0
RA duration (years)	2.4 ± 1.3
Number of previous DMARDs	2.8
Tender joint count	14.4 ± 7.5
Swollen joint count	11.8 ± 5.8
CRP (mg/dl)	4.9 ± 2.9
DAS28	6.4 ± 0.9
Radiological total Sharp score	30.6 ± 42.0
Radiological bone erosion score	13.9 ± 21.7
Radiological joint space narrowing (JSN) score	16.7 ± 21.8

Values are given as the mean ± standard deviation, unless otherwise indicated

RA Rheumatoid arthritis, *DAS28* Disease Activity Score based on 28 joint counts, *CRP* C-reactive protein, *BMI* body mass index, *DMARDs* disease-modifying anti-rheumatic drugs

Table 2 Number of patients using concomitant drugs related to rheumatoid arthritis during the study

Variables	Number of patients[a]
Corticosteroids	145 (100%)
Methotrexate	123 (84.8%)
Mizoribine	11 (7.6%)
Azathioprine	7 (4.8%)
Ciclosporin	5 (3.4%)
Tacrolimus hydrate	3 (2.1%)
Sulfasalazine	60 (41.4%)
Bucillamine	33 (22.8%)
Sodium aurothiomalate	4 (2.8%)
D-Penicillamine	11 (7.6%)
Actarit	6 (4.1%)
Lobenzarit disodium	2 (1.4%)
Cyclophosphamide	2 (1.4%)
Minocycline hydrochloride	2 (1.4%)

[a] Values are given as the number of patients taking a drug; patients can take more than one drug

Table 3 Baseline patient measurements and Pearson correlation coefficient between the levels of candidate factors at baseline and the changes in radiographic score at week 52

Variables	Levels at baseline (mean ± SD)	*r* value between baseline levels and radiological progression at week 52		
		Total sharp score	Bone erosion score	Joint space narrowing (JSN) score
Bone markers				
Intact-osteocalcin (ng/ml)	5.1 ± 2.1	NS	NS	NS
Bone alkaline phosphatase (U/l)	21.5 ± 6.5	NS	NS	NS
S-NTX-I (nmol BCE/l)	15.8 ± 4.8	NS	NS	NS
U-NTX-I (nmol BCE/mmol creatinine)	62.6 ± 31.9	NS	NS	NS
U-DPD (μmol/mol creatinine)	8 ± 4	0.185*	NS	0.187*
Bone or cartilage markers				
U-PYD (μmol/mol creatinine)	55 ± 37	0.278**	0.253**	0.274**
U-PYD/DPD	7.2 ± 1.8	0.190*	0.180*	0.178*
Cartilage markers				
S-PIIANP (ng/ml)	459.8 ± 210.9	NS	−0.188*	NS
S-PIICP (ng/ml)	819.1 ± 311.6	NS	NS	NS
U-CTX-II (ng/mmol creatinine)	902.5 ± 919.2	0.356***	0.321***	0.356***
Radiographic scores				
Total Sharp score	16.7 ± 21.8	0.323***	0.303***	0.307***
Erosion score	30.6 ± 42.0	0.313***	0.308***	0.282**
Joint space narrowing score	13.9 ± 21.7	0.323***	0.291***	0.322***
Symptoms or functions				
DAS28	6.4 ± 0.9	NS	NS	NS
Objective signs				
Tender joint count	14.4 ± 7.5	NS	NS	NS
Swollen joint count	11.8 ± 5.8	NS	NS	NS
Patients reported functional assessment				
MHAQ	0.90 ± 0.58	NS	NS	NS
Inflammation markers				
CRP (mg/dl)	4.9 ± 2.9	NS	NS	NS
ESR (mm/h)	71 ± 25	NS	NS	NS
MMP-3 (ng/ml)	456.5 ± 347.5	NS	NS	NS
SAA (μg/ml)	347 ± 307	NS	NS	NS
Fibrinogen (mg/dl)	490 ± 96	NS	NS	NS
Interleukin-6 (pg/ml)	60.2 ± 64.9	NS	NS	NS
Synovium degradation marker				
U-Glc–Gal–PYD (nmol/mmol creatine)	11.6 ± 9.3	0.255**	0.238**	0.245**
Hematological parameters				
WBC (/μl)	8,923 ± 2,430	NS	NS	NS
RBC (10^4/μl)	397 ± 38	NS	NS	NS
Hemoglobin (g/dl)	11.3 ± 1.4	NS	NS	NS
Platelet (10^4/μl)	37.2 ± 10.1	NS	NS	NS
Lipid parameters				
Total cholesterol (mg/dl)	182 ± 33	NS	NS	NS
HDL cholesterol (mg/dl)	56 ± 14	NS	NS	NS
LDL cholesterol (mg/dl)	108 ± 27	NS	NS	NS
Triglyceride (mg/dl)	90 ± 35	−0.187*	−0.193*	NS
Other biomarkers				
RF (IU/ml)	247 ± 452	NS	NS	NS

Table 3 continued

Variables	Levels at baseline (mean ± SD)	*r* value between baseline levels and radiological progression at week 52		
		Total sharp score	Bone erosion score	Joint space narrowing (JSN) score
IgG (mg/dl)	1,697 ± 492	NS	NS	NS
Albumin (g/dl)	3.7 ± 0.3	NS	NS	NS
Ferritin (ng/ml)	105 ± 116	NS	−0.182*	NS
Age	53.1 ± 12.5	−0.259**	−0.278**	−0.205*
Gender (M:F)	26:119	NS	NS	NS
Duration of disease	2.4 ± 1.3	NS	NS	NS
Anthropometric factor				
BMI (kg/m^2)	21.8 ± 3.0	−0.298***	−0.257**	−0.311***

NS not significant, *S-NTX* Serum type I collagen cross-linked N-telopeptides, *U-NTX* urinary type I collagen cross-linked N-telopeptides, *U-DPD* urinary deoxypyridinoline, *U-PYD* urinary pyridinoline, *S-PIIANP* serum N-terminal propeptide of type IIA collagen, *S-PIICP* serum C-terminal propeptide of type II collagen, *U-CTX-II* urinary C-terminal telopeptide of type II collagen, *MHAQ* modified health assessment questionnaire, *ESR* erythrocyte sedimentation rate, *MMP-3* matrix metalloproteinase-3, *SAA* serum amyloid protein A, *U-Glc–Gal–PYD* urinary glucosyl–galactosyl–pyridinoline, *IgG* immunoglobulin G, *WBC* white blood cell, *RBC* red blood cell, *HDL cholesterol* high-density lipoprotein cholesterol, *LDL cholesterol* low-density lipoprotein cholesterol

* $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$

Table 4 Multivariate regression analysis relating JSN U-CTX-II, U-PYD/DPD, or BMI to changes in the radiographic scores at 52 weeks

Baseline predictor	Parameter estimate		*p* value
Total Sharp score progression			
JSN	4.88		0.04
PYD/DPD	20.81		0.02
CTX-II	9.41		<0.01
BMI	−0.92		<0.01
R^2		0.24	<0.001
Bone erosion progression			
PYD/DPD	11.20		0.04
CTX-II	5.58		<0.01
BMI	−0.48		0.02
R^2		0.17	<0.001
Joint space narrowing progression			
JSN	2.37		0.04
PYD/DPD	9.62		0.02
CTX-II	4.56		<0.01
BMI	−0.46		<0.01
R^2		0.25	<0.001

JSN Joint space narrowing, *PYD/DPD* logarithmic transformed urinary pyridinoline/deoxypyridinoline ratio, *CTX-II* logarithmic transformed urinary C-terminal telopeptide of type II collagen

multivariate analyses, increased levels of U-CTX-II, an increased U-PYD/DPD ratio and decreased BMI were the only independent predictors of the progression of bone erosion (Table 4). Together, these three variables explained 17% of the interindividual variance in the progression of bone erosion. For the progression of JSN and TTS, baseline JSN was also an independent predictor in addition to U-CTX-II, the U-PYD/DPD ratio and BMI (Table 4).

Logistic regression analysis after the categorization of the four predictive variables with the cut-off value of 500 ng/mmol/creatinine in U-CTX-II, median level for the U-PYD/DPD ratio, two cut-off values of 18.5 and 25 kg/m^2, respectively, in BMI and a 0 or >0 score in JSN score at baseline showed that the odds ratio for a yearly increase of TSS >0.5 was 2.6- to 9.9-fold higher risk in the high-risk group than in patients with low risk levels (Fig. 1a); the respective figures for progression in erosion score and for progression in JSN were 2.8–4.8 and 1.8–20.0, respectively (Fig. 1b, c). Baseline levels in the categorized groups are shown in Table 5.

Discussion

Based on our analysis of a panel of several demographical, clinical and laboratory parameters of disease activity, we found that increased urinary CTX-II, a high PYD/DPD ratio and low BMI were independent predictors of radiological progression in bone erosion and TTS in patients with RA receiving conventional DMARDs and that baseline JSN was also an independent predictor of radiological progression in JSN and TTS. These results suggest that these factors should be useful in identifying patients at high risk.

The bivariate analyses revealed that the baseline levels of U-PYD, the U-PYD/DPD ratio, U-CTX-II, TSS, erosion score, JSN score, U-Glc–Gal–PYD, age and BMI were

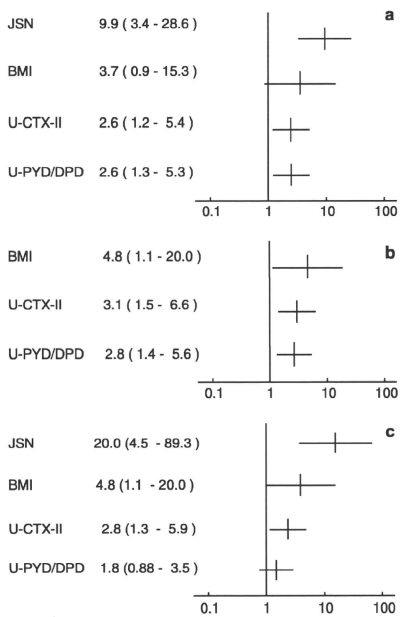

Fig. 1 Odds ratio (95% confidence interval) of radiological progression associated with high baseline joint space narrowing (*JSN*), high urinary C-terminal telopeptide of type II collagen (*U-CTXII*), high urinary total pyridinoline/total deoxypyridinoline (*U-PYD/DPD*), or low body mass index (*BMI*). Progression of joint damage over 1 year was defined as an increase >0.5 U of the total Sharp score (**a**), bone erosion (**b**) or JSN (**c**)

Table 5 Baseline levels in the categorized groups

Variables	Cut-off value	*n*	Mean of baseline value ± SD
JSN	0	30	0
	0<	115	21.1 ± 22.5
U-CTX-II (ng/mmol/creatinine)	<500	53	327.2 ± 104.6
	500≤	88	1,249.0 ± 1,014.9
U-PYD/DPD	<median (6.8)	72	5.8 ± 0.7
	Median (6.8)≤	73	8.6 ± 1.4
BMI (kg/m^2)	<18.5	20	17.5 ± 1.2
	18.5≤, <25	102	21.5 ± 1.6
	25≤	21	27.1 ± 1.7

significantly associated with the 1-year increase in all three indices of TSS, erosion score and JSN score and that the baseline levels of U-DPD, S-PIIANP, triglycerides and ferritin were significantly associated with one or two variables among these three radiographic progression parameters. However, there was no significant association with radiographic progression in the baseline levels of inflammation markers, MMP-3, hematological parameters, patients-reported functional assessments, such as MHAQ, and objective symptomatic scores. Although several previous studies showed that MMP-3 was predictive of radiological progression [22, 29, 39, 40] in RA, our data and those of Cunnane et al. [41] failed to reveal a significant association. Circulating MMP-3 levels have been reported to be significantly decreased after treatment with methotrexate or sulfasalazine or both together [29, 41–44]. These findings suggest that levels of MMP-3 are dependent on the type, duration and intensity of the pharmacotherapy. It is thus possible that differences in the therapeutic regimen between studies may explain some of the inconsistencies in the relation of MMP-3 to progression. Additional factors may include differences in disease duration and activity and variation in assay characteristics, which are not standardized between studies. Consistent with the results of a recent study [29], we confirmed that patient-reported functional assessments and clinical symptomatic indices were not useful in predicting radiological progression.

Inflammation markers, such as CRP and ESR, have been regarded as useful predictors of joint damage in RA. However, our study confirmed the recent findings of Young-Min [29], showing that when novel and more specific markers of joint tissue metabolism were included in the model, these unspecific laboratory tests were no longer predictive. Among these novel tissue turnover markers, the strongest and most consistent association with progression was observed for urinary CTX-II, a biochemical marker of cartilage degradation, a finding consistent with several previous studies involving patients with early RA receiving MTX or etanercept [19], very early RA receiving the COBRA combination therapy or sulfasalazine alone [45] or late RA treated with conventional DMARDs [29]. Taken together, the results from these previous studies and the current one suggest that urinary CTX-II is predictive of radiological progression across patient populations and independent of the type of therapy. We also found that urinary-Glc–Gal–PYD, a specific biochemical marker of synovial tissue metabolism, was associated significantly with radiographical progression in bivariate analysis. This result was consistent with that of a previous study [19] of early RA patients receiving methotrexate or etanercept. However, urinary-Glc–Gal–PYD did not remain in the final panel of predictors after multivariate analysis, confirming

the recent study of Young-Min [29] who showed that Glc–Gal–PYD was predictive in bivariate, but not in multivariate analyses when CTX-II was included in the model. This lack of independent predictive value is likely to be due to the high correlation of Glc–Gal–PYD with CTX-II ($r = 0.61$, $p < 0.001$) and suggests that in early active RA, degradation of cartilage is closely linked to synovitis. Whether urinary Glc–Gal–PYD could be an independent predictor of progression in late RA or in patients receiving biological therapies remains to be determined.

Previously published cross-sectional studies found an increased urinary PYD/DPD ratio in patients with RA [46–49]. Our study, however, is the first showing that U-PYD/DPD ratio is an independent predictor of radiological progression. Both PYD and DPD are non-reducible cross-links of mature collagen molecules, and they are believed to be important factors for maintaining the structure of the collagen fibril network in the matrix of the various tissues, including bone and cartilage. In healthy tissues, the PYD/DPD ratio is highest in cartilage (ratio: 50), intermediate in synovial tissue and tendons (ratio: 15–16) and lowest in bone (ratio: 3.5) [50–52]. The tissue PYD/DPD ratio can be altered in RA tissue, with the latter showing a higher ratio than healthy synovium [23, 51]. In addition, a high tissue PYD/DPD ratio in bone caused by the overhydroxylation of Lys at the helical cross-linking sites in type I collagen has been observed in the hip fracture cases [53] and osteoporosis [54]. Thus, the PYD/DPD ratio may theoretically provide some indication of the type of articular tissue that is predominantly degraded in RA. In our study, this ratio, but not PYD and DPD separately, was associated with radiological progression of bone erosion and JSN independently of CTX-II, which is a specific marker of cartilage degradation and of Glc–Gal–PYD (a specific marker of synovial metabolism), suggesting indeed the added value of this parameter. One possibility is that this ratio partially reflects structural alterations of bone tissue matrix associated with increased bone fragility, as suggested by some ex vivo biochemical studies [53, 54].

We found that high BMI was correlated negatively with the progression of joint erosion and JSN and that patients with lower values (<18.5), defined as underweight, had a 4.8-fold (95% CI 1.1–20) higher risk than the patients with higher BMI (>25) who were defined as overweight. Previously published reports showed a body weight loss due to disease activity [55–58] in RA, although no significant correlation between BMI and inflammation markers was observed at baseline in our study (data not shown). Our results agree with studies published previously by Kaufmann [23], Westhoff [31] and van der Helm-van Mil [30] which showed that high BMI was protective against the radiological progression in early RA. It has been suggested that the relationships between BMI and joint damage are mediated in part by the adipocytokines secreted by fat tissues. Interestingly, we recently reported that increased serum levels of adiponectin—which is negatively associated with BMI—are associated with a greater overall joint destruction in patients with RA [59]. Using a bivariate analysis, we found that triglycerides, but not total cholesterol and its subfractions were negatively correlated with radiological progression. However, in the multiple variable model, triglycerides were not an independent predictors, possibly because of its positive association with BMI ($r = 0.29$, $p < 0.001$).

Previously published data showed that high initial radiographical damage evaluated with TSS or the Larsen score was associated with subsequent radiological progression [16, 17] and that the initial erosion score in particular has a predicting value for radiological prognosis [14, 18, 23]. These data were analyzed without biochemical markers of joint tissue turnover as the initial factors; however, we found that baseline radiological joint damage of the extent of JSN was strongly and independently predictive of biochemical markers of joint tissue turnover associated with progression.

We believe that the four independent predictors of radiological progression we identified in this study may reflect different and complementary information of the various pathophysiological processes involved in joint destruction. The baseline Sharp score provides an estimation of the amount of joint destruction that has occurred, on average, during 2.3 years of disease duration before the start of the follow-up. Urinary CTX-II is a dynamic indicator of the rate at which cartilage tissue will deteriorate during the course of the disease. The PYD/DPD ratio may be related to increased bone fragility, and the BMI may provide integrated information on contribution of adipose tissue metabolism to maintain joint tissues health. These four independent predictors were statistically selected using those patients with high disease activity who were participating in the control arm of the SAMURAI study and who had >6 tender joints (of 49 evaluated), >6 swollen joints (of 46 evaluated joints), ESR of >30 mm/h and CRP of >2 mg/dl. These predictors may therefore be beneficial for targeting new biological therapies to patients with rapid progression of joint destruction.

Although our study covered one of the largest ranges of predictive variables for the progression of joint damage ever investigated concomitantly in the same population, due to sample volume limitation we could not analyze a number of the biochemical markers that have been reported to be associated with joint damage in RA, including anti-CCP antibody, cartilage oligomeric matrix protein (COMP) [25, 26, 60], osteoprotegerin (OPG) and Receptor Activator of Nuclear Factor-kappa B Ligand (RANKL) [61]. Our

study included patients with RA within 5 years of disease duration, so it remains to be determined whether the same set of predictive factors will also perform similarly in patients with earlier RA. Furthermore, our study could not clarify the prognostic factors in the each type of DMARDs treatment nor whether CTX-II, the PYD/DPD ratio, the JSN score and BMI predict progression independent of the type of DMARDs treatment, since the dose, type and combination of DMARDs and/or immunosuppressants was varied and changed according to disease activity at the discretion of the treating physician in our study. However, our data could provide the prognostic values of CTX-II, PYD/DPD ratio, JSN score and BMI in the actual clinical practice of RA treatment.

In summary, among of a panel of 40 different variables, we identified baseline joint damage, urinary CTX-II, the PYD/DPD ratio and BMI as strong and independent factors of radiological progression in patients with RA receiving conventional DMARDs. If confirmed in other studies, this set of few variables may be useful to identify patients with RA who are at high risk for disease progression.

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CASE REPORT

Pharmacokinetic study and Fcγ receptor gene analysis in two patients with rheumatoid arthritis controlled by low-dose infliximab

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Abstract The main aim of this study is to investigate the pharmacokinetics of infliximab and Fcγ receptor (FcγR) polymorphism in two patients with rheumatoid arthritis (RA) who were well controlled by low-dose infliximab. A 57-year-old woman (Patient 1) and a 67-year-old woman (Patient 2) had active RA despite methotrexate and prednisolone treatments. They improved after the addition of infliximab (3 mg/kg), but developed pneumonia and sepsis, respectively. Although the infliximab doses were reduced to 1.5 mg/kg and 1 mg/kg, respectively, clinical improvements were maintained. Blood samples were obtained at 1 h after infliximab administration and at eight weeks (just before the next dose). The elimination half-life was determined by the serum concentration of infliximab. We also analyzed the polymorphisms of FcγRIIA, FcγRIIIA, and FcγRIIIB for the genomic DNA samples from the two patients and three controls. Amplification of the FcγR-genomic regions in allotype-specific polymerase chain reactions was used to distinguish the genotypes. Decresed clearance of infliximab was proven by a pharmacokinetic study of these patients under low-dose infliximab therapy. 131H/H (FcγRIIA) and 176F/F (FcγRIIIA) were detected in both patients. NA1/NA2 and NA2/NA2 (FcγRIIIB) were detected in Patients 1 and 2, respectively. These patients were well controlled over the long term by low-dose infliximab. The mechanism of the reduced clearance of infliximab might possibly be explained in part by the FcγR polymorphisms.

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Introduction

Rheumatoid arthritis (RA) is a chronic inflammatory disease that eventually causes the destruction of cartilage and/or bone [1]. The pathogenesis of RA is considered to be related to several proinflammatory cytokines, including interleukin-1 (IL-1), tumor necrosis factor-α (TNF-α), and interleukin-6 (IL-6) [2]. TNF-α inhibitors have become available in recent years and are reported to prevent or alleviate inflammation and joint destruction in RA patients [3–5]. The TNF-α inhibitor infliximab is a chimeric anti-human TNF-α monoclonal antibody composed of the variable region of a mouse anti-human TNF-α monoclonal antibody and the constant regions of human IgG1, including the Fc region [6]. It is reported to be effective for RA, and a dose of 3 mg/kg or more is usually administered every four or eight weeks [3].

When human IgG binds to a target antigen and forms an immune complex, it is degraded through Fcγ receptor (FcγR)-mediated phagocytosis [7]. The FcγR is categorized into subclasses I, II, and III, and then these subclasses are further categorized into a number of subtypes. Polymorphisms of various FcγR subtypes have already been reported [8]. The affinity of FcγR binding to the Fc region of IgG differs between these polymorphisms, and differences in the binding of IgG to the Fc region may affect the clearance of immune complexes. This suggests that the clearance of antibody preparations (including infliximab) from the blood will vary between FcγR polymorphisms.

Here we report on two patients with RA who were well controlled for a long period by low doses of infliximab.