

1 **Overexpression of hsa-miR-148a promotes cartilage production and inhibits**
2 **cartilage degradation by osteoarthritic chondrocytes.**

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17 Running head: miR-148a promotes cartilage synthesis

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20 Abstract:

21 Objective: Hsa-miR-148a expression is decreased in OA cartilage, but its functional
22 role in cartilage has never been studied. Therefore, our aim was to investigate the
23 effects of overexpressing hsa-miR-148a on cartilage metabolism of OA chondrocytes.

24 Design: OA chondrocytes were transfected with a miRNA precursor for hsa-miR-
25 148a or a miRNA precursor negative control. After 3, 7, 14 and 21 days, real-time

1 PCR was performed to examine gene expression levels of aggrecan (ACAN), type I,
2 II, and X collagen (COL1A1, COL2A1, COL10A1), matrix metalloproteinase 13
3 (MMP13), a disintegrin and metalloproteinase with thrombospondin motifs 5
4 (ADAMTS5) and the serpin peptidase inhibitor, clade H (heat shock protein 47),
5 member 1 (SERPINH1). After 3 weeks, DNA content and proteoglycan and collagen
6 content and release were determined. Type II collagen was analyzed at the protein
7 level by Western blot.

8 Results: Overexpression of hsa-miR-148a had no effect on ACAN, COL1A1 and
9 SERPINH1 gene expression, but increased COL2A1 and decreased COL10A1,
10 MMP13 and ADAMTS5 gene expression. Luciferase reporter assay confirmed direct
11 interaction of miR-148a and COL10A1, MMP13 and ADAMTS5. The matrix
12 deposited by the miR-148a overexpressing cells contained more proteoglycans and
13 collagen, in particular type II collagen. Proteoglycan and collagen release into the
14 culture medium was inhibited, but total collagen production was increased.

15 Conclusion: Overexpression of hsa-miR-148a inhibits hypertrophic differentiation
16 and increases the production and deposition of type II collagen by OA chondrocytes,
17 which is accompanied by an increased retention of proteoglycans. Hsa-miR-148a
18 might be a potential disease-modifying compound in OA, as it promotes hyaline
19 cartilage production.

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21 Keywords: microRNA, osteoarthritis, cartilage, chondrocytes

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1 **Introduction**

2 Osteoarthritis (OA) is a major cause of physical disability due to symptoms as pain,
3 stiffness and loss of mobility. Multiple factors are believed to cause OA, such as
4 trauma, abnormal mechanical loading, failure of nutrient supply and genetic
5 predisposition (1). Available treatments are limited to pain management and in end-
6 stage OA patients, joint replacement surgery is often indicated. OA is characterized
7 by local inflammation, synovitis and proteolytic degradation of cartilage, which
8 correlates with alterations in chondrocyte expression levels of genes involved in
9 synthesis and degradation of cartilage (1-4).

10 Recently, it was proposed that epigenetic mechanisms play a role in modulating cell
11 phenotype in OA (5-10), resulting in permanent changes in DNA transcription. One of
12 the epigenetic mechanisms involved is based on microRNA (miRNA) expression
13 (6,8). MiRNAs are short (19-24 nucleotide long) non-coding RNA molecules that can
14 silence gene expression by binding to complementary sequences on target messenger
15 RNA transcripts, resulting in translational repression or target degradation.
16 Approximately one-third of all mammalian genes are regulated by miRNAs (11).

17 Changes in miRNA expression patterns are found in many pathological conditions,
18 including several malignancies and neurological, cardiovascular and developmental
19 diseases (12-16). The role of miRNAs in joint homeostasis has become evident from
20 studies showing major abnormalities in cartilage development and structure in Dicer-
21 null mice (17). The miRNA expression pattern is also changed in OA and several
22 miRNAs, including hsa-miR-27, 140, 145, 146a and 675 were found to be associated
23 with altered levels of cartilage matrix production and degradation (18-29). Although
24 the involvements of the abovementioned miRNAs in OA were analysed, the effects of
25 modulating these miRNAs on cartilage regeneration, in particular at the protein level,

1 is unknown.

2 Typically, studies on the possible involvement of miRNAs in pathological processes
3 start with miRNA screens to identify potential candidates. Previously, screens of 365
4 and 115 miRNAs, respectively, were profiled in normal and OA cartilage (18,19). In
5 the scope of performing a more extensive miRNA screen, we found that hsa-miR-
6 148a was expressed at 10.6 times lower levels in OA cartilage compared to normal
7 cartilage (unpublished observations), in line with previously published results (19).
8 However, the functional role of hsa-miR-148a in cartilage metabolism or specifically
9 OA has never been studied. Hsa-miR-148a has some predicted targets that are
10 relevant for OA and general chondrocyte biology. Amongst the predicted targets are
11 the messenger RNAs (mRNA) for type II collagen (COL2A1), type X collagen
12 (COL10A1), matrix metalloproteinase 13 (MMP13), A disintegrin and
13 metalloproteinase with thrombospondin motifs 5 (ADAMTS5) and the collagen
14 chaperone serpin peptidase inhibitor, clade H (heat shock protein 47), member 1
15 (SERPINH1) (30). Therefore, the aim of this study was to investigate the effects of
16 overexpressing hsa-miR-148a on cartilage metabolism of OA chondrocytes during
17 regeneration.

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19

20 **Materials and methods**

21

22 *miRNA expression screen*

23 Total RNA was isolated from articular cartilage with the mirVana miRNA isolation
24 kit (Ambion, Austin, Tx) according to the manufacturer's protocol. Healthy human
25 cartilage from femoral condyles of knee joints was obtained post-mortem of 3 male

1 donors and 4 female donors, the mean age was 65 years (range: 47 years – 83 years).
2 OA cartilage was obtained from 3 male and 4 female donors (age 53 to 80, average 69
3 years) undergoing total knee arthroplasty. cDNA was synthesized using TaqMan
4 MicroRNA Reverse Transcription Kit (Applied Biosystems, Life technologies,
5 Poland) with Megaplex RT Primers, Human Pool A and B v3.0 according to the
6 manufacturer's protocol. The TaqMan low-density Arrays A and B (TaqMan Array
7 Human MicroRNA A v3.0 and B v3.0 Card Sets, Applied Biosystems) were used in
8 a ABI Prism 7900HT sequence detection system (Applied Biosystems). The raw Ct
9 values were calculated using RQ manager software and analyzed using DataAssist
10 software (ABI, Applied Biosystems).

11

12 *Cell isolation.*

13 Chondrocytes were isolated from articular cartilage from patients with OA
14 undergoing total knee arthroplasty. The anonymous use of redundant tissue for
15 research purposes is part of the standard treatment agreement with patients in the
16 University Medical Center Utrecht (31). The articular cartilage was minced and
17 digested in 0.15% (w/v) collagenase (CLS-2, Worthington, Lakewood, NJ) in
18 Dulbecco's modified Eagle's medium (DMEM, Gibco, Paisley, UK) supplemented
19 with 10% foetal bovine serum (FBS, HyClone, Logan, UT), 100 U/ml penicillin
20 (Gibco) and 100 µg/ml streptomycin (Gibco) for 16h at 37°C.

21 The cells were filtered through a 100 µm cell strainer (BD Biosciences, San Diego,
22 CA) and washed before culturing or miRNA/mRNA isolation.

23

24 *Cell culture and transfection*

25 Isolated OA chondrocytes were expanded in T175 tissue culture flasks in DMEM

1 supplemented with 10% FBS, 100 U/ml penicillin, 100 µg/ml streptomycin, and 10
2 ng/ml bFGF (R&D, Minneapolis, MN), at 37°C in 5% CO₂. At confluency, the cells
3 were trypsinized using 0.25% trypsin/EDTA (Gibco) and replated.

4 At passage 2, OA chondrocytes were reverse-transfected with a Pre-mir miRNA
5 precursor for hsa-miR-148a-5p or a Pre-mir miRNA precursor negative control
6 (Ambion) using Lipofectamine RNAiMax (Invitrogen, Carlsbad, CA). The reverse-
7 transfection was performed during seeding (density 1.6x10⁶ cells/cm²) on Millicell
8 filters (0.4 µm PFTE (Millipore, Bedford MA) that were precoated with type II
9 collagen (type II collagen from chicken sternal cartilage (Sigma, St. Louis, MO))
10 (32,33). The final concentration of pre-mir miRNA precursor was 10 nM. The cells
11 were retransfected after 1 and 2 weeks of culture on filters.

12 The filters were cultured in DMEM (Gibco) supplemented with 10% FBS, 100 U/ml
13 penicillin, 100 µg/ml streptomycin and 50 µg/ml ascorbate-2-phosphate (Sigma) and
14 culture media were renewed every 3 days.

15

16 *MicroRNA Real-time PCR.*

17 Total RNA was extracted from chondrocytes with the mirVana miRNA isolation kit
18 (Ambion) according to the manufacturer's protocol. The expression of hsa-miR-148a
19 was verified using a TaqMan microRNA assay for hsa-miR-148a (Applied
20 Biosystems). MiRNA expression was normalized to RNU44 small nuclear RNA.

21

22 *Real-time PCR*

23 Total RNA was isolated from the cells immersed in Trizol (Invitrogen) as described
24 by the manufacturer. Total RNA (750 ng) was reverse transcribed using an iScript
25 cDNA Synthesis Kit (Biorad, Hercules, CA).

1 Real-time PCR reactions were performed using the SYBRGreen reaction kit
2 according to the manufacturer's instructions (Roche Diagnostics, Mannheim,
3 Germany) in a LightCycler 480 (Roche Diagnostics). The LightCycler reactions were
4 prepared in 20 μ l total volume with 7 μ l PCR-H₂O, 0.5 μ l forward primer (0.2 μ M), 0.5
5 μ l reverse primer (0.2 μ M), 10 μ l LightCycler Mastermix (LightCycler 480 SYBR
6 Green I Master; Roche Diagnostics), to which 2 μ l of 5 times diluted cDNA was added
7 as PCR template. Primers (Invitrogen) used for real-time PCR are listed in Table 1.
8 Specific primers were designed from sequences available in the data banks, based on
9 homology in conserved domains between human, mouse, rat, dog and cow (34). The
10 amplified PCR fragment extended over at least one exon border (except for 18S).
11 Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta
12 polypeptide (Ywhaz) and 18S were used as housekeeping genes and the gene
13 expression levels were normalized for the normalization factor calculated with the
14 equation $\sqrt{(Ywhaz \times 18S)}$. With the Light Cycler software (version 4), the crossing
15 points were assessed and plotted versus the serial dilution of known concentrations of
16 the standards derived from each gene using Fit Points method. PCR efficiency was
17 calculated by Light Cycler software and the data were used only if the calculated PCR
18 efficiency was between 1.85 and 2.0.

19

20 *Papain digestion*

21 After 3 weeks of culture, filters were digested at 60°C for 18 h in a papain enzyme
22 solution consisting of 5 mM L-cysteine, 50 mM Na₂EDTA, 0.1 M NaAc, pH 5.53
23 with 2% (v/v) papain (Sigma).

24

25 *Proteoglycan analysis*

1 To analyse the proteoglycan content of the regenerated cartilage tissue and the amount
2 released into the culture medium, a dimethylmethylene blue (DMMB)
3 spectrophotometric analysis was performed to determine the content of sulphated
4 glycosaminoglycans (GAGs) (35). DMMB solution and papain digest or medium
5 sample were mixed and the absorbance was read at 540 nm and 595 nm. As reference,
6 chondroitin sulfate C (Sigma) was used. The total amount of proteoglycans produced
7 was defined as the amount of proteoglycans in the papain tissue digest and the amount
8 of proteoglycans released into the culture medium during the entire culture period.

9

10 *DNA content*

11 Total DNA was quantified in papain digests using Quant-iT Picogreen (Invitrogen)
12 according to the manufacturer's instructions. Picogreen reagent was added to papain
13 digest. This was incubated at ambient temperature for 5 min, protected from light. The
14 fluorescence was measured at ~480 nm excitation and ~520 nm emission and DNA
15 content determined using lambda DNA as standard.

16

17 *Hydroxyproline assay*

18 To analyse the collagen content, hydroxyproline content was determined in papain
19 digests or medium samples using a modified colorimetric assay (36). In short, freeze-
20 dried papain digests or medium samples were hydrolyzed and the free
21 hydroxyprolines were oxidized with Chloramine-T for the production of pyrroles. The
22 addition of Ehrlich's reagent resulted in the formation of chromophores that were
23 measured at 550 nm and collagen content was determined using gelatin (Sigma) as
24 standard. The total amount of collagens produced was defined as the amount of
25 collagens found in the papain digest and the amount of collagens released into the

1 culture medium.

2

3 *Type II collagen Western blot*

4 After 3 weeks of culture, filters were digested overnight at 4°C with pepsin
5 (Worthington, 100 µg/ml in 0.2 M NaCl, 0.5 M acetic acid). The digests and 0.05,
6 0.025, and 0.005 µg of type II collagen as reference (chicken sternum, Sigma) were
7 denatured by heating at 95°C for 5 min in NuPage LDS sample buffer (Invitrogen)
8 with NuPage reducing agent (Invitrogen). The digests and collagen standards were
9 resolved by SDS-PAGE (8% resolving gel with 4% stacking gel) and transferred to
10 nitrocellulose membranes (Biorad). The membranes were blocked in 2% (w/v) BSA
11 0.1% Tween in phosphate buffered saline (PBS) for 1 h and were then incubated with
12 the primary antibody for 2 h. Mouse monoclonal anti-type II collagen (MAB1330,
13 Chemicon, Millipore) was used at 1:1000 dilution. After three washes with 0.1%
14 Tween in PBS, the membranes were incubated with horseradish peroxidase-
15 conjugated anti-mouse secondary antibody (DakoCytomation, Glostrup, Denmark) at
16 a 1:5000 dilution for 1 h. Following three washes, immunoreactivity was visualized
17 using Lumi-Light^{plus} (Roche Diagnostics).

18

19 *Luciferase assay*

20 The 3' Untranslated regions (3' UTRs) of type II and type X collagen (COL2A1 and
21 COL10A1), matrix metalloproteinase 13 (MMP13), A disintegrin and
22 metalloproteinase with thrombospondin motifs 5 (ADAMTS5) and serpin peptidase
23 inhibitor, clade H (heat shock protein 47), member 1 (SERPINH1) were amplified by
24 PCR with DNA oligonucleotides flanked by XhoI and NotI restriction sites (DNA
25 oligonucleotide sequences are listed in Table 2). The fragments were cloned

1 downstream of the renilla luciferase gene into the pSICHECK2 vector (Promega,
2 Madison, WI) in sense and antisense orientation.

3 Hela cells were plated into 96-wells plates and cotransfected with the described
4 luciferase reporter constructs and 50 nM Pre-mir miRNA precursor for hsa-miR-148a
5 or a Pre-mir miRNA precursor negative control (Ambion) using Lipofectamine
6 (Invitrogen). Luminescence was measured 48 hours after transfection using Pierce
7 Renilla-Firefly Luciferase Dual Assay Kit (Thermo scientific, Rockford, Il).

8

9 *Collagenase activity assay*

10 To analyse collagenase activity, the Enzcheck Gelatinase/Collagenase Assay Kit
11 (Invitrogen) was used according to the manufacturer's instructions. DQ Collagen
12 Fluorescein conjugate was added to 100 times in reaction buffer (kit component)
13 diluted conditioned medium. This was incubated for 4 hours at ambient temperature,
14 protected from light. The fluorescence was measured at ~480 nm excitation and ~520
15 nm emission and collagenase activity was determined using collagenase type IV from
16 *Clostridium histolyticum* (kit component) as standard.

17

18 *Statistical analysis*

19 Gene expression data are expressed as mean \pm SD of miR-148a transfected versus
20 mock transfected chondrocytes of target gene expression normalized for the equation
21 $\sqrt{(Y_{whaz} \times 18S)}$. Differences in expression ratios were tested with a two-tailed t-test
22 for single group mean and compared to 1 (miR148a transfected / mock transfected =
23 1, no effect). Data from biochemical assays are expressed in dot plots where every dot
24 resembles the value of one donor and the mean value of the samples is indicated by a
25 line. The data were analyzed using a two-tailed paired t-test. The level of significance

1 was set at $p < 0.05$. Normal distribution of the data was confirmed using the Shapiro-
2 Wilk test.

3

4

5 **Results**

6 *hsa-miR-148a regulates COL10A1, MMP13 and ADAMTS5*

7 In the scope of performing an extensive miRNA screen between normal and OA
8 cartilage, we had found that hsa-miR-148a was expressed about ten times less in OA
9 cartilage compared to normal cartilage. By real-time PCR it was confirmed that hsa-
10 miR-148a levels were 9 fold lower in OA cartilage compared to normal cartilage (Fig.
11 1A).

12 TargetScan 6.2 and/or microRNA.org identified COL2A1, COL10A1, MMP13,
13 ADAMRS5 and SERPINH1 amongst the predicted targets of hsa-miR-148a. The gene
14 expression levels of these genes were measured in the same RNA in which hsa-miR-
15 148a levels were determined. The expression level of COL2A1 was decreased in the
16 OA donors (Fig. 1B), the levels of COL10A1, MMP13 and ADAMTS5 were
17 increased in OA donors (Fig. 1C-1E), and for SERPINH1 no difference was observed
18 (Fig. 1F).

19 To investigate the effects of upregulation of hsa-miR-148a, a miRNA precursor (pre-
20 miR) for hsa-miR-148a or a pre-mir negative control was transfected in OA
21 chondrocytes. Real-Time PCR analysis confirmed that transfection of the pre-miR
22 increased the expression of hsa-miR-148a compared to transfection with control non-
23 coding pre-miRNA (Fig. 2). The upregulation of hsa-miR-148a expression was
24 highest 3 days after the initial transfection, with a 5-fold increase compared to the
25 precursor negative control. Just before the re-transfections at day 7 and 14 and at the

1 end of the culture period of 3 weeks, the hsa-miR-148a expression levels were up-
2 regulated about 3.5-fold.

3 Overexpression of hsa-miR-148a resulted in increased COL2A1, decreased
4 COL10A1, MMP13 and ADAMTS5, and unchanged SERPINH1 gene expression
5 levels (Fig. 2).

6 To analyse the miRNA – mRNA interactions of the predicted target genes, a
7 luciferase reporter assay was performed. No difference in luciferase activity was
8 observed between HeLa cells cotransfected with the construct containing the 3' UTR
9 of COL2A1 and SERPINH1 and the miRNA precursor for hsa-miR-148a or a miRNA
10 precursor negative control (Fig. 3). A decrease in luciferase activity was measured in
11 HeLa cells cotransfected with the miRNA precursor for hsa-miR-148a and the
12 luciferase reporter vector containing the 3' UTRs of COL10A1, MMP13 and
13 ADAMTS5 in sense orientation (Fig. 3). No difference was shown when the 3' UTRs
14 of COL10A1, MMP13 and ADAMTS5 were cloned into the luciferase reporter vector
15 in antisense orientation (Fig. 3).

16

17 *Overexpression of hsa-miR-148a increases proteoglycan content and decreases*
18 *proteoglycan release*

19 Overexpression of hsa-miR-148a had no effect on ACAN gene expression levels, but
20 did decrease the gene expression levels of the aggrecanase ADAMTS5 (Fig. 2). The
21 amount of proteoglycans was increased in the tissue generated by hsa-miR-148a
22 overexpressing OA chondrocytes compared to controls (Fig. 4A), while proteoglycan
23 release into the culture medium was decreased (Fig. 4B).

24 No difference was found between chondrocytes overexpressing hsa-miR-148a and
25 controls in terms of the total amount of proteoglycans produced, as determined by

1 adding up the amount found in the deposited matrix at the end of culture period and
2 the total amount released into the medium during culture (Fig. 4C).

3

4 *Overexpression of hsa-miR-148a increases collagen II expression at the mRNA and*
5 *protein level and decreases the expression of type X collagen and MMP-13*

6 However, overexpression of hsa-miR-148a resulted in increased COL2A1 gene
7 expression levels and the gene expression levels of COL10A1 and the collagenase
8 MMP13 were decreased (Fig. 2). No effect was shown on gene expression levels of
9 COL1A1 and the collagen chaperone SERPINH1 (Fig. 2).

10 The amount of collagen was increased in the matrix deposited by hsa-miR-148a
11 overexpressing OA chondrocytes compared to controls (Fig. 5A), while the amount of
12 collagen released into the culture medium was decreased (Fig. 5B).

13 In contrast to the lack of effect on total proteoglycan production, the total amount of
14 collagen produced was increased by hsa-miR-148a overexpressing OA chondrocytes
15 compared to controls (Fig 5C).

16 Collagenase activity was decreased in the culture medium of the hsa-miR-148a
17 overexpressing OA chondrocytes (Fig. 5D).

18 To verify whether type II collagen was also specifically upregulated at the protein
19 level, an immunoblot for type II collagen was performed on the collagen extracted
20 from the cultures, confirming the higher deposition of type II collagen by the hsa-
21 miR-148a overexpressing OA chondrocytes compared to the mock-transfected OA
22 chondrocytes (Fig. 5E).

23

24 **Discussion**

25 In this study hsa-miR-148a, expressed at lower levels in OA cartilage compared to

1 healthy cartilage, is suggested to play an important role in cartilage regeneration.
2 Overexpressing hsa-miR-148a in OA chondrocytes increases extracellular matrix
3 deposition by these cells; not only proteoglycan, but also the collagen and specifically
4 type II collagen content was increased. In addition, matrix degradation was reduced,
5 as reflected by a decreased release of proteoglycans during culture, which was
6 accompanied by downregulation of MMP13, COL10A1 and ADAMTS5, predicted
7 and confirmed targets of miR-148a.
8 Surprisingly, COL2A1, another postulated target gene was found to be increased upon
9 overexpression of hsa-miR-148a in OA chondrocytes. This suggests that COL2A1 is
10 not a direct target of hsa-miR-148a, as miRNAs are by default negative regulators of
11 gene expression. A luciferase reporter assay also showed no interaction between miR-
12 148a and COL2A1. However, hsa-miR-148a might target a repressor of COL2A1 as
13 was also suggested for miR-675 (28).
14 The gene expression patterns for collagen and aggrecan were also reflected at the
15 protein level. The gene expression level of aggrecan, the main proteoglycan in the
16 cartilaginous extracellular matrix, was unchanged. Although an increased
17 proteoglycan content was found after culturing, total proteoglycan production did not
18 increase. The decreased proteoglycan release in combination with the decreased
19 ADAMTS5 expression suggests that the increase in proteoglycan content was caused
20 by a diminished breakdown, resulting in increased retention, rather than an increase in
21 synthetic activity.
22 The increased total collagen and specifically type II collagen production found upon
23 overexpression of miR-148a was in line with the increased gene expression levels of
24 COL2A1. Next to a generalised increase in synthetic activity, a higher portion of
25 collagen was found in the deposited matrix compared to collagen released into the

1 culture medium. This coincided with decreased gene expression of MMP13, the main
2 enzyme involved in cartilage collagen degradation. This is supported by the decreased
3 collagenase activity found in the culture medium of the hsa-miR-148a overexpressed
4 chondrocytes. So, collagen production was not only increased but its degradation was
5 also inhibited. Most likely this increased deposition of collagen was responsible for
6 the increase in proteoglycan content found, as an intact collagen network is required
7 for the retention of proteoglycans inside the cartilage matrix (37).

8 In addition to the stimulatory effects on cartilage matrix formation, the
9 downregulation of COL10A1 gene expression levels by miR-148a overexpression
10 suggests further reversal of the OA chondrocytic phenotype, as hypertrophic
11 differentiation characterised by increased COL10A1 expression levels is a hallmark of
12 OA.

13 In addition to COL2A1 another predicted miR-148a target that was not affected in
14 line with the sequence-based prediction was SERPINH1, a collagen-specific
15 chaperone. This protein is required for proper intracellular protein folding of the
16 collagens and decreased SERPINH1 levels might lead to improper collagen folding
17 resulting in intracellular accumulation and degradation of collagens. However, miR-
18 148a after all did not seem to target SERPINH1 and increased production and
19 deposition of collagens by miR-148a overexpressed OA chondrocytes suggests that
20 are no complications with the intracellular folding of collagens. This was confirmed
21 in a luciferase reporter assay, showing that miR-148a interacts with MMP13,
22 COL10A1 and ADAMTS5, but not with SERPINH1 or COL2A1.

23 In addition to modulating matrix protein expression by binding target mRNA or
24 repressor mRNA of matrix gene expression, another mechanism by which hsa-miR-
25 148a may target cartilage metabolism, is by affecting methylation pathways, as miR-

1 148a directly targets DNA methyltransferase 1 (DNMT1) (38-41). Lower expression
2 of miR-148a could increase DNMT1 expression and attenuate DNA hypomethylation.
3 It was suggested that changes in DNA methylation also play a role in the gene
4 expression patterns observed in OA (10), and thus hsa-miR-148a might also modulate
5 cartilage matrix production through a more general DNA methylation-based way.
6 Besides hsa-miR-148a, several other miRNAs are already found to be differentially
7 expressed in OA (18-21). Hsa-miR-140 is one of the most studied miRNAs with
8 respect to cartilage and its expression is significantly lower in OA cartilage compared
9 to healthy cartilage (22-24). Also hsa-miR-27 and hsa-miR-146a levels are
10 significantly lower in OA cartilage compared to healthy cartilage and they are found
11 to regulate the expression of MMP13 (25-27). The gene expression of type II collagen
12 (COL2A1) is indirectly regulated by hsa-miR-675 and miR-145 directly targets SOX9
13 (28,29).

14 Although the abovementioned miRNAs were functionally analysed, the effects of
15 modulating the expression of these miRNAs on actual cartilage regeneration, in
16 particular at the protein level, are unknown. The current study is the first investigating
17 the effect of modulating the expression of a specific miRNA on the production and
18 degradation of the main components of cartilage, the proteoglycans and collagens.

19 In the current study, cartilage production was shown to be enhanced by
20 overexpression of hsa-miR-148a in OA chondrocytes, which, in addition to providing
21 information on mechanisms in the pathogenesis and maintenance of OA, may render
22 this miRNA a target for a potential therapy for OA or to induce cartilage repair.

23 Several clinical trials are already ongoing for miRNA-based treatment of hepatitis C
24 (42), liver cancer (43,44), and heart failure (45). However, a drawback for miRNA-
25 based treatment for cartilaginous tissues is the relative inaccessibility of chondrocytes.

1 Since cartilage is avascular and the chondrocytes are embedded in a dense and
2 charged extracellular matrix, it may be difficult to transfect chondrocytes in the native
3 tissue. However, many advances in transfection of cartilage in vivo are currently
4 being achieved (46-50), increasing the possibility of application of miRNA in
5 targeting cartilaginous tissues.

6 In conclusion, overexpression of hsa-miR-148a stimulated the production of
7 collagens, specifically type II collagen, and enhanced the retention and deposition of
8 collagen and proteoglycans, respectively, in cartilage matrix deposited by OA
9 chondrocytes. Hsa-miR-148a may be a potential target for the treatment of OA, as it
10 promotes cartilage production and prevents cartilage degradation and hypertrophy.

11

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19

20 **Author contributions**

21 Conception and design: LV, LC, DS

22 Collection and assembly of data: LV, AK

23 Analysis and interpretation of the data: LV, LC

24 Provision of study materials: DS

25 Drafting of the article and reviewing: LV, AK, WD, DS, LC

1 Final approval of submitted version: LV, AK, WD, DS, LC

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4 The funding source had no role in study design, collection, analysis or interpretation
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6

7 **Conflict of interest**

8 The authors declare that they have no competing interests.

9

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1 **Table 1.** Oligonucleotide sequences used for real time PCR

Target gene		Oligonucleotide sequence	Annealing temperature (°C)	Product size (bp)
18S	Fw	5' GTAACCCGTTGAACCCATT 3'	57	151
	Rev	5' CCATCCAATCGGTAGTAGCG 3'		
YWHAZ	Fw	5' GATGAAGCCATTGCTGAACTTG 3'	56	229
	Rev	5' CTATTTGTGGGACAGCATGGA 3'		
ACAN	Fw	5' CAACTACCCGGCCATCC 3'	57	160
	Rev	5' GATGGCTCTGTAATGGAACAC 3'		
COL1A1	Fw	5' TCCAACGAGATCGAGATCC 3'	57	191
	Rev	5' AAGCCGAATTCCTGGTCT 3'		
COL2A1	Fw	5' AGGGCCAGGATGTCCGGCA 3'	56	195
	Rev	5' GGGTCCCAGGTTCTCCATCT 3'		
COL10A1	Fw	5' CACTACCCAACACCAAGACA 3'	56	225
	Rev	5' CTGGTTTCCCTACAGCTGAT 3'		
MMP13	Fw	5' GGAGCATGGCGACTTCTAC 3'	56	208
	Rev	5' GAGTGCTCCAGGGTCCTT 3'		
ADAMTS5	Fw	5' GCCAGCGGATGTGTGCAAGC 3'	57	130
	Rev	5' ACACTCCCCCGGACGCAGA 3'		
SERPINH1	Fw	5' TGATGATGCACCGGACAG 3'	57	212
	Rev	5' GGAGATGGCAACAGCCTTC 3'		

2 Forward (Fw) and reverse (Rev) primers for YWHAZ, tyrosine 3-
3 monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide;
4 ACAN, aggrecan; COL1A1, α 1(I)procollagen; COL2A1, α 1(II)procollagen;
5 COL10A1, α 1(X)procollagen; MMP13, matrix metalloproteinase 13; ADAMTS5, a
6 disintegrin and metalloproteinase with thrombospondin motifs 5; SERPINH1, serpin
7 peptidase inhibitor, clade H (heat shock protein 47), member 1.

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1 **Table 2.** Oligonucleotide sequences used for amplifying 3' untranslated regions

3' UTR of target gene		Oligonucleotide sequence
COL2A1 sense	Fw	CCGCTCGAGAAACCTGAACCCAGAAAC
	Rev	CGTACGCCGGCGGTACTTTCCAATAATCTTTTC
COL2A1 antisense	FW	GCATGCGGCCGCAAACCTGAACCCAGAAACAAC
	Rev	CGTACTCGAGGTACTTTCCAATAATCTTTTC
COL10A1 sense	Fw	CCGCTCGAGGTACACACAGAGCTAATCTAAATC
	Rev	CGTACGCCGGCGCACTTTATTGTCCTACTTTTTTATTAAC
COL10A1 antisense	Fw	GCATGCGGCCGCGTACACACAGAGCTAATCTAAATC
	Rev	CGTACTCGAGCACTTTATTGTCCTACTTTTTTATTAAC
MMP13 sense	Fw	CCGCTCGAGGTGTCTTTTTAAAAATTGTTATT
	Rev	CGTACGCCGGCGCTGTTGAAAATATATTTTTATTATAAAC
MMP13 antisense	Fw	GCATGCGGCCGCGTGTCTTTTTAAAAATTGTTATT
	Rev	CGTACTCGAGCTGTTGAAAATATATTTTTATTATAAAC
ADAMTS5 sense	Fw	CCGCTCGAGCCTGTGGTTATGATCTTATGCAC
	Rev	CGTACGCCGGCGACTTTAACCTAGTTTACAATTTATAT
ADAMTS5 antisense	Fw	GCATGCGGCCGCCCTGTGGTTATGATCTTATGCAC
	Rev	CGTACTCGAGACTTTAACCTAGTTTACAATTTATAT
SERPINH1 sense	Fw	CCGCTCGAGGGCCTCAGGGTGCACACAGGATG
	Rev	CGTACGCCGGCGCCACGCTCCAACAAAATGTCATTGG
SERPINH1 antisense	Fw	GCATGCGGCCGCGGCCTCAGGGTGCACACAGGATG
	Rev	CGTACTCGAGCCACGCTCCAACAAAATGTCATTGG

2 Forward (Fw) and reverse (Rev) primers for COL2A1, α 1(II)procollagen; COL10A1,
3 α 1(X)procollagen; MMP13, matrix metalloproteinase 13; ADAMTS5, a disintegrin
4 and metalloproteinase with thrombospondin motifs 5; SERPINH1, serpin peptidase
5 inhibitor, clade H (heat shock protein 47), member 1.

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1 **Figure legends:**

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3 Figure 1: Real-time PCR was performed for hsa-miR-148a, type II collagen
4 (COL2A1), type X collagen (COL10A1), matrix metalloproteinase 13 (MMP13), a
5 disintegrin and metalloproteinase with thrombospondin motifs 5 (ADAMTS5) and
6 serpin peptidase inhibitor, clade H (heat shock protein 47), member 1 (SERPINH1) on
7 reverse transcribed RNA isolated from osteoarthritic cartilage (7 donors) and normal
8 cartilage (7 donors). The data are presented in a dot plot where every dot resembles
9 the value of one donor. The mean value of the samples is indicated by a line. Data are
10 shown as mean \pm SD. ***: $p < 0.001$.

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12 Figure 2: Real-time PCR was performed on reverse transcribed RNA isolated from
13 OA chondrocytes transfected with a pre-mir miRNA precursor for hsa-miR-148a or a
14 pre-miR miRNA precursor negative control after 3, 7, 14 and 21 days in a
15 regeneration culture. Expression levels of hsa-miR-148a (148a), aggrecan (ACAN),
16 type I collagen (COL1A1), type II collagen (COL2A1), type X collagen (COL10A1),
17 matrix metalloproteinase 13 (MMP13), a disintegrin and metalloproteinase with
18 thrombospondin motifs 5 (ADAMTS5) and serpin peptidase inhibitor, clade H (heat
19 shock protein 47), member 1 (SERPINH1) were measured. The results are presented
20 as expression levels of hsa-miR-148a transfected OA chondrocytes relative to
21 negative control transfected OA chondrocytes. Data are shown as mean \pm SD. **: $p < 0.01$;
22 ***: $p < 0.001$.

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24 Figure 3: HeLa cells were cotransfected with 50 nM pre-mir miRNA precursor for
25 hsa-miR-148a or pre-miR miRNA precursor negative control (mock) and

1 pSICHECK2 containing the 3' untranslated regions (UTR) of type II collagen
2 (COL2A1), type X collagen (COL10A1), matrix metalloproteinase 13 (MMP13), a
3 disintegrin and metalloproteinase with thrombospondin motifs 5 (ADAMTS5) and
4 serpin peptidase inhibitor, clade H (heat shock protein 47), member 1 (SERPINH1) in
5 sense and antisense orientation. Firefly and Renilla luciferase were measured 48 hours
6 after transfection. Data are shown as mean \pm SD. *: $p < 0.05$; **: $p < 0.01$.

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8 Figure 4: Proteoglycan content (A), release (B), and total production (C) (determined
9 as glycosaminoglycans (GAG)) (normalized for the DNA content) were determined
10 after 21 days in cultures of OA chondrocytes transfected with a pre-miR miRNA
11 precursor negative control (mock) or a pre-mir miRNA precursor for hsa-miR-148a
12 (miR-148a). The data are presented in a dot plot where every dot resembles the value
13 of one donor. The mean value of the samples is indicated by a line. *: $p < 0.05$;
14 ***: $p < 0.001$.

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16 Figure 5: Collagen content (A), release (B), and total production (C) (determined as
17 hydroxyproline (normalized for the DNA content)), collagenase activity (D) and type
18 II collagen (E, determined by immunoblot) were determined after 21 days in cultures
19 of OA chondrocytes transfected with a pre-miR miRNA precursor negative control
20 (mock) or a pre-mir miRNA precursor for hsa-miR-148a (miR-148a). The data are
21 presented in a dot plot where every dot resembles the value of one donor. The mean
22 value of the samples is indicated by a line. Figure E: The first lane contains a protein
23 ladder, the following three standards of 0.005, 0.025, and 0.05 μ g type II collagen. *:
24 $p < 0.01$; ***: $p < 0.001$.

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