

Original Article

Recombinant adenovirus (AdEasy system) mediated exogenous expression of long non-coding RNA H19 (lncRNA H19) biphasic regulating osteogenic differentiation of mesenchymal stem cells (MSCs)

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Abstract: Background: We previously constructed AdEasy system for rapid generation of recombinant adenovirus expressing coding genes. However, it is unclear if AdEasy system could be used for exogenous expression of long noncoding RNAs (lncRNAs). Here we investigated how to overexpress lncRNA H19 with AdEasy system and identified the effect of overexpression H19 on mesenchymal stem cells (MSCs) osteogenic differentiation. Methods: H19 fragment 1 and H19 fragment 2 were amplified from mouse genomic DNA separately and then connected for full-length H19. H19 was firstly subcloned to homemade pMOK plasmid, then H19 was cut off from pMOK-H19 and subcloned to recombinant adenovirus plasmid. After homologous recombination in AdEasy cells (BJ5183 cell), packing in mammalian packaging cell line and amplification in 293pTP cells, high titer AdH19 was obtained. Immortalized mouse adipose-derived progenitors (iMADs) were infected by AdH19 with different infection rate, the expression of H19, H19 related microRNAs (miRs) and osteogenic differentiation markers were determined by TqPCR. Alkaline phosphatase (ALP) activities and matrix mineralization were determined by ALP assays and Alizarin red S staining respectively. Results: AdEasy system was suitable for rapid generation and production of H19, AdH19 can effectively overexpress H19 and serve as functional lncRNA in mesenchymal stem cells (MSCs). Higher dosage of AdH19 inhibited osteogenic differentiation of MSCs, however, lower dosage of AdH19 promoted osteogenic differentiation of MSCs. Conclusions: We firstly reported the method for the generation of functional lncRNA with AdEasy system, and identified the biphasic effect of H19 on MSCs osteogenic differentiation.

Keywords: lncRNA H19, AdEasy system, mesenchymal stem cells (MSCs), osteogenic differentiation

Introduction

With the development of whole genome and transcriptome sequencing technologies, non-coding RNAs (ncRNAs), especially long non-coding RNAs (lncRNAs) were recognized as regulatory RNAs [1-5]. Recently, lncRNAs were reported to regulate the target gene expression in the initiation of transcription, during the transcription, post-transcription and post-transcription modification etc. [4, 6]. However, be different from coding genes, lncRNA coding no protein, it is difficult for the investigators to mimic the expression or identify the function of lncRNAs [5, 7, 8]. Therefore, it is necessary to construct a vector which can simulate the expression of lncRNA exogenously.

Recombinant adenoviruses are replication-defective adenoviral vectors, and have been widely used as gene transfer vehicles in many areas [9-11]. We previously optimized and constructed the AdEasy system which simplifies the production and generation of recombinant adenoviruses, at the same time, AdEasy system hold the advantage of high titer, easy for preparation, can transduce a wide variety of cells or tissues [9, 11, 12]. What is more, recently, we optimized the procedures of adenovirus generation from the aspects of packing, amplification etc. [13, 14] However, it is not clear whether AdEasy system can effectively express lncRNA as a ncRNA vehicle.

lncRNA H19 (H19) was firstly isolated and reported in 1980s by 4 different laboratories,

which is one of most widely and deeply studied lncRNAs so far [15-22]. As imprinted genes, H19-Igf2 locus was define as the paradigm for the study of genomic imprinting [23, 24]. Recently, H19 was reported play an essential role in the osteogenic differentiation process [25-27]. Huang [27] et al found that H19 promotes osteoblast differentiation via TGF- β 1/Smad3/HDAC signaling pathway by deriving miR-675. Liang [26] et al identified that H19 acting as ceRNA to promote osteogenic differentiation by targeting Wnt signaling pathway. In our previous study [28], we found the biphasic expression of H19 in BMP9 induced osteogenic differentiation of MSCs, which indicated the biphasic effect of H19 in regulating osteogenic differentiation of MSCs. However, it is not clear whether H19 regulate osteogenic differentiation of MSCs in a dosage dependent manner.

In the present study, we successfully constructed the recombinant adenovirus expression H19 with AdEasy system, and identified AdH19 mediated exogenous expression of H19 could act as functional lncRNA. What is more, by using different dosage of AdH19 we identified the biphasic effect of H19 on osteogenic differentiation of MSCs, which is helpful for further exploring the regulatory function of H19 in osteogenic differentiation of MSCs.

Materials and methods

Cell culture and chemicals

Human embryo kidney 293 cell line (HEK 293) was purchased from American Type Culture Collection (ATCC, Manassas, VA), 293pTP cells were derived from HEK 293 cell which express high level of human Ad5 pTP gene as described previously [13]. RAPA (rapid adenovirus production and amplification) cell line was derived for 293T cell which express high level of EA1 and pTP genes as previously characterized [14]. The mouse embryonic fibroblasts (MEFs) and immortalized mouse adipose-derived (iMAD) cells are mouse mesenchymal stem cells as reported respectively [29, 30]. Cells were maintained in complete Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% fetal bovine serum (FBS, Gemini Bio-Products, West Sacramento, CA), 100 U/ml penicillin, and 100 mg/ml streptomycin, maintained at 37°C in a humidified 5% carbon dioxide (CO₂) atmo-

sphere [29-32]. Restriction enzymes and ligation buffers were supplied by New England Biolabs (Ipswich, MA). Unless indicated otherwise, all chemicals were purchased from Sigma-Aldrich (St. Louis, MO) or Thermo-Fisher Scientific (Waltham, MA).

Genomic DNA extraction

The MEF cells were cultured in 100 mm dishes, at 80% confluence, cells were spun down and collected in 1.5 ml tube, then washed with PBS twice. DNA extraction buffer (244.5 μ l ddH₂O, 10N NaOH 5 μ l, 0.5M EDTA (PH 8.0) 0.5 μ l) was used to lysis the cells. MEFs were resuspended with DNA extraction buffer, and then keep in vibrating metal bath for 20 minutes. When the mixture was cool down at room temperature, PC8 (phenol/chloroform, pH 8.0) was used to purification the DNA, after precipitation, the DNA pipet was dissolved in ddH₂O. At the same time whole genomic DNA was checked in PAGE (Polyacrylamide Gel Electrophoresis) gel.

The amplification of whole H19 fragment

According to the mouse lncRNA H19 (NR_130973.1), whole H19 fragment primers were designed as: Fwd: 5'-atcatcgatGGGTGTGGGA-GGGGGGTGGGGGTGGGGGTGGGGGGTATC-GGGGAAACTG-3', Rev: 5'-acgacgcgtAATGACT-GTAACTGTATTTATTGATG-3'. Two fragment primers were respectively designed as: Fragment 1: Fwd: 5'-atcatcgatGGGTGTGGGAGGGGGGTGGG-GGGTGGGGGTGGGGGGTATCGGGGAAACTG-3', Rev: 5'-gagaaatgaagacatgagttaattg-3', Fragment 2: Fwd: 5'-gggtaagtgtctgtcccgtcgtggtcacc-3', Rev: 5'-acgacgcgtAATGACTGTAACTG-TATTTATTGATG-3'. Cleavage sites were contained in primers. An overlap was included for two fragments design. A touchdown cycling program was as follows: 94°C for 2 minutes for 1 cycle; 92°C for 20 seconds, 65°C for 30 seconds, and 72°C for 13 cycles decreasing 1°C per cycle; and then at 92°C for 20 seconds, 60°C for 30 seconds, and 72°C for 20 seconds for 20-25 cycles, depending on the abundance of a given gene. PCR products were resolved on 1.5% agarose gels.

Construction and generation of recombinant adenoviral vector

The full-length H19 was firstly subcloned to homemade pMOK plasmid (MluI and BglII),

which contains diversity restriction endonuclease sites. The length of pMOK was around 3000 base pair, which was approximate to the full-length of H19. The full-length of H19 was cut off from pMOK-H19 between XbaI and SalI restriction endonuclease sites, and then subcloned into an adenoviral shuttle vector pAdtrace-Tox, resulting in pAdtrace-H19, as previously characterized [11, 31-34]. Bacteria screening, plasmid screening and DNA sequencing were carried out to confirm the veracity of the clone. After linearized with restriction enzyme EcoRV, pAdtrace-H19 was transfected into AdEasier cells (BJ5183 cell), generating recombinant adenovirus pAd5-H19. After linearized with restriction enzyme PacI, recombinant adenovirus pAd5-H19 was transfected into RAPA cells and generating recombinant adenoviruses AdH19. AdH19 was amplified in 293pTP cells, and high titer AdH19 was collected as previously described [11], the packing and amplification process was shown in [Supplementary Figure 1](#).

Semi-quantitative PCR

H19 screening primers were designed by using the Primer3 program. H19 fragment 1 screening primers were as follows: Fwd: 5'-GCAGTGCAGGGTGTACACAGAAGG-3', Rev: 5'-CAATTA-CTCATGTCTTCATTCTC-3'. H19 fragment 2 screening primers are as follows: Fwd: 5'-CATCTTCATGGCCAACTCTGCCTG-3', Rev: 5'-CA-TCAATAAATACAGTTACAGTCATT-3'. A touchdown cycling program was as follows: 94°C for 2 minutes for 1 cycle; 92°C for 20 seconds, 65°C for 30 seconds, and 72°C for 10 cycles decreasing 1°C per cycle; and then at 92°C for 20 seconds, 57°C for 30 seconds, and 72°C for 20 seconds for 15-20 cycles, depending on the abundance of a given gene. PCR products were resolved on 1.5% agarose gels.

RNA isolation and touchdown quantitative real-time PCR (TqPCR)

The immortalized multipotent adipose-derived (iMAD) mesenchymal stem cells (MSCs) were seeded in 60 mm dishes, at 40 to 50% confluence, cells were infected with AdH19, AdRFP was used as control. Cells were harvested at desired time points for subsequent analysis. Total RNA was isolated with TRIZOL Reagent (Invitrogen, Carlsbad, CA) according to the manufacturer's instructions. Reverse transcription reactions were performed using hexamer and

M-MuLV Reverse Transcriptase (New England Biolabs, Ipswich, MA). PCR primers were designed by using the Primer3 Plus program [35]. The resultant cDNA products were diluted 10- to 100-fold and used as PCR templates. The quantitative PCR analysis was performed using our optimized TqPCR protocol [28, 36]. Briefly, qPCR reactions were set up with SYBR Green (Bimake, Houston, TX) master mix according to the manufacturer's instructions. The cycling program was modified by incorporating 4 cycles of touchdown steps prior to the regular cycling program as previously described [36]. The dissolve curve did not determine any nonspecific amplification. All sample values were normalized to GAPDH expression by using the $2^{-\Delta\Delta Ct}$ method. The TqPCR primer sequences are listed in [Table 1](#).

Alkaline phosphatase (ALP) assay

The ALP activities were assessed using the modified Great Escape SEAP chemiluminescence assay (BD Clontech) and/or histochemical staining, as described previously [31, 32, 37, 38]. For ALP histochemical staining, the cells were induced for osteogenic differentiation using osteogenic medium (containing ascorbic acid (50 mg/ml) and β -glycerophosphate (10 mM)). At the scheduled time, cells were fixed with 0.05% glutaraldehyde at room temperature for 10 min. After washing with distilled water, cells were stained subjected to histochemical staining with a mixture of 0.1 mg/mL of naphthol AS-MX phosphate and 0.6 mg/mL of Fast Blue BB salt. Histochemical staining was recorded using bright light microscopy.

For the chemiluminescence assay, the cells were lysed by the Cell Culture Lysis Buffer (Promega, Madison, WI). Then 5 μ l Cell Lysis Buffer, 5 μ l substrate (BD Clontech) and 15 μ l Lupo Buffer were mixed well under a light-proof condition, and incubated at room temperature for 20 minutes before measuring chemiluminescence signals. Each assay condition was performed in triplicate, and the results were repeated in at least 3 independent experiments. The ALP activity was normalized by total cellular protein concentrations among the samples.

Matrix mineralization assay (alizarin red S staining)

The iMAD cells were seeded in 24-well plates and cultured in the presence of ascorbic acid

Table 1. List of TqPCR primers

| Gene | qPCR Primer Sequences | |
|-------------------|-----------------------|-----------------------|
| | Forward | Reverse |
| mouse GAPDH | GCCTCGTCCCGTAGACAAAA | TCCCCATTCTCGGCCTTGAC |
| mouse Runx2 | CCGGTCTCCTTCCAGGAT | GGGAAGTGTGTGGCTTC |
| mouse BSP | AGGGAAGTACCAGTGTGG | ACTCAACGGTGTGCTTTTT |
| mouse OCN | CCAAGCAGGAGGGCAATA | TCGTACAAGCAGGGTCA |
| mouse OPN | CCTCCCGGTGAAAGTGAC | CTGTGGCGCAAGGAGATT |
| mmu-H19-Fragment1 | CAGAGTCCGTGGCCAAGG | CGCCTTCAGTACTGGCA |
| mmu-H19-Fragment2 | GCTGGGAAGGGTTCGACC | TGTGCCATTCTGTGCGA |
| mmu-miR-675 | ATTCCCATGAGGCACTGCGG | ATGTTCTGTCTGTCATGCCA |
| mmu-miR-106b | CCTGCTGGGACTAAAGTGCT | TACCCACAGTGC GG TAGC |
| mmu-miR-125a | CCCTTTAACCTGTGAGGACGT | GGCTCCCAAGAACCTCACC |
| mmu-miR-449b | AGACTCGGGTAGGCAGTGT | GTGGCAGGGTAGCTGTGG |
| mmu-miR-17 | CAAAGTGCTTACAGTGCAGGT | GTGCCCTACTGCAGTAGA |
| mmu-miR-449a | TGTGATGGCTTGGCAGTGT | TTAGCTGGTGGCGCTCAC |
| mmu-miR-34a | TGGCAGTGTCTTAGCTGGT | CAATGTGCAGCACTTCTAGGG |
| mmu-miR-107 | TCAGTCTCTTACAGTGTGCG | AGCCCTGTACAATGCTGCT |
| mmu-miR-27b | AGGTGCAGAGCTTAGCTGA | GCCACTGTGAACAAAGCGG |
| mmu-miR-199b | CGGGAGCGGAGAGGGCCAGA | TACAAGGATGATGAGCCGAG |
| mmu-miR-132 | ACCGACGCCTGGCCCGGGCA | GCAGCGATACCTCGAGGGCG |
| mmu-miR-93 | CCCCTCTTGACCTTAGTCA | CACATCAGAGGTTGTGTCC |
| mmu-miR-129-1 | CACAGCTGTCTCCTTTGGAT | AGACCAAGCCTCCCGTAGAT |
| mmu-miR-let-7d | GACCAGCAAGAATAAAATGG | AACGTATGCTGGTATAATAA |

(50 mg/ml) and β -glycerophosphate (10 mM). On day 15 after infection, cells were treated with 4% paraformaldehyde for 30 minutes. After washing with PBS, cells were incubated with 2% alizarin red S for 30 minutes, followed by extensive washing with distilled water [31, 37-39]. The staining of calcium mineral deposits was recorded using bright light microscopy.

Clustering analysis

The clustering analysis was carried out with the using of Multiple Experiment Viewer (MeV) software. H19 related microRNAs (miRNAs) were detected by TqPCR. Relative normalized expression of the miRNAs were subjected to MeV software.

Statistical analysis

All quantitative experiments were performed in triplicate and/or repeated 3 times. Data were expressed as mean \pm standard deviation (SD). The one-way analysis of variance or paired t-test were used to analyze statistical significance. A value of $P < 0.05$ was considered statistically significant.

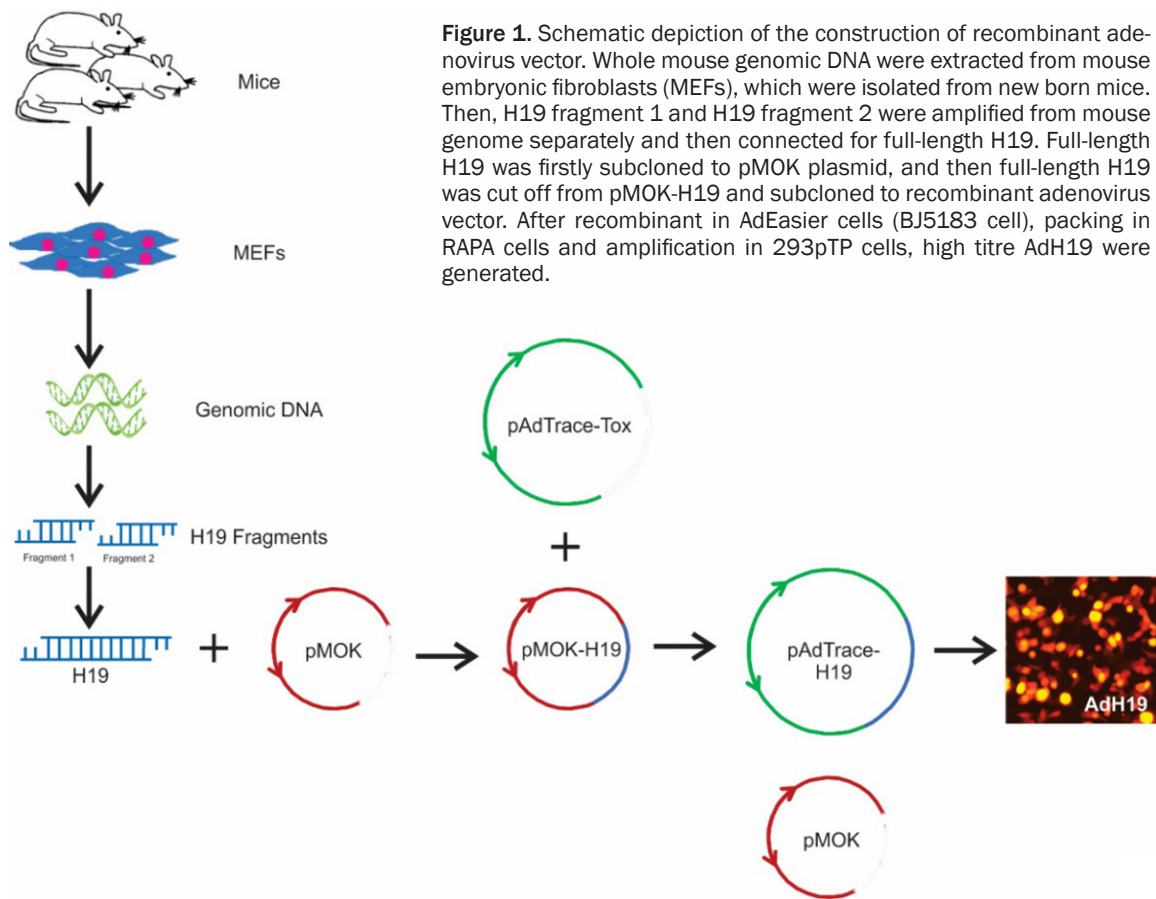
Results

Schematic depiction of the generation of AdH19

The process of construction of pAdtrace-H19 was shown in **Figure 1**. Briefly, whole mouse genomic DNA was extracted from MEF cells. H19 fragment 1 and fragment 2 were amplified by touchdown PCR respectively, and then H19 fragment 1 and fragment 2 were digested by restriction endonuclease and ligated by ligation buffer stepwisely, which result in full-length H19. Full-length H19 was firstly cloned into homemade plasmid pMOK which possessing a similar base pair with H19. Then, full-length H19 was cut off from pMOK-H19 and subcloned to pAdTrace-Tox plasmid, which generating pAdtrace-H19. After recombinant in AdEasier cells (BJ5183 cell), packing in RAPA cells and amplification in 293pTP cells, high titre AdH19 were generated.

AdH19 effectively overexpress H19 and miR-675 in MSCs

The iMAD cells were cultured and infected by recombinant adenoviruses expression H19 and



RFP respectively. As shown in **Figure 2A**, the red fluorescence indicated the effective infection at day 2. The H19 expressions in AdH19 group were upregulated significantly at 2 days and 5 days after transduction compared with AdRFP group using Tq-PCR analysis (**Figure 2B**). At the same time, we determined the expressions of microRNA-675 (miR-675), which is encoded by H19, and found that H19 could be effectively upregulated by AdH19 at day 2 and day 5 respectively. These results suggest AdH19 can effectively mediate the overexpression of H19 and H19 coded miR-675.

AdH19 function as competitive ceRNA

One of the most important function of lncRNA is acting as ceRNA. H19 was reported working as functional lncRNA by several authors. Here, we investigated whether AdH19 influence the expressions of miR-675, miR-125a, miR-199b, miR-132, miR-27b, miR-34a, miR-449a, miR-449b, miR93, miR-106b, miR-107, miR129-1, miR-17 and miR-let-7d. iMAD cells were infected with AdH19, AdRFP was used as control,

total RNAs were isolated 2 days after infection. The expressions of miRs were detected by Tq-PCR. In accordance with the previous reports [24, 40-51], miR-675, miR125a, miR-199b were upregulated by AdH19, and miR-132, miR-27b, miR-34a, miR-449a, miR-449b, miR-93, miR-106b, miR-107, miR-129-1, miR-17 and miR-let-7d were downregulated by AdH19 at different levels (**Figure 3**). These results indicate that except working as pre-miR of miR-675, AdH19 can also working as ceRNA to competitively combine with some miRs.

H19 and osteogenic differentiation markers expression during the osteogenic differentiation of MSCs

In consideration the regulatory function of H19 in the process of osteogenic differentiation, we firstly explored the expression of H19 and osteogenic differentiation markers expression level in different time point. With the stimulation of osteogenic medium, we found that H19 expression level increased gradually from day 1 to day 3, and reach the peak level at day 3, then

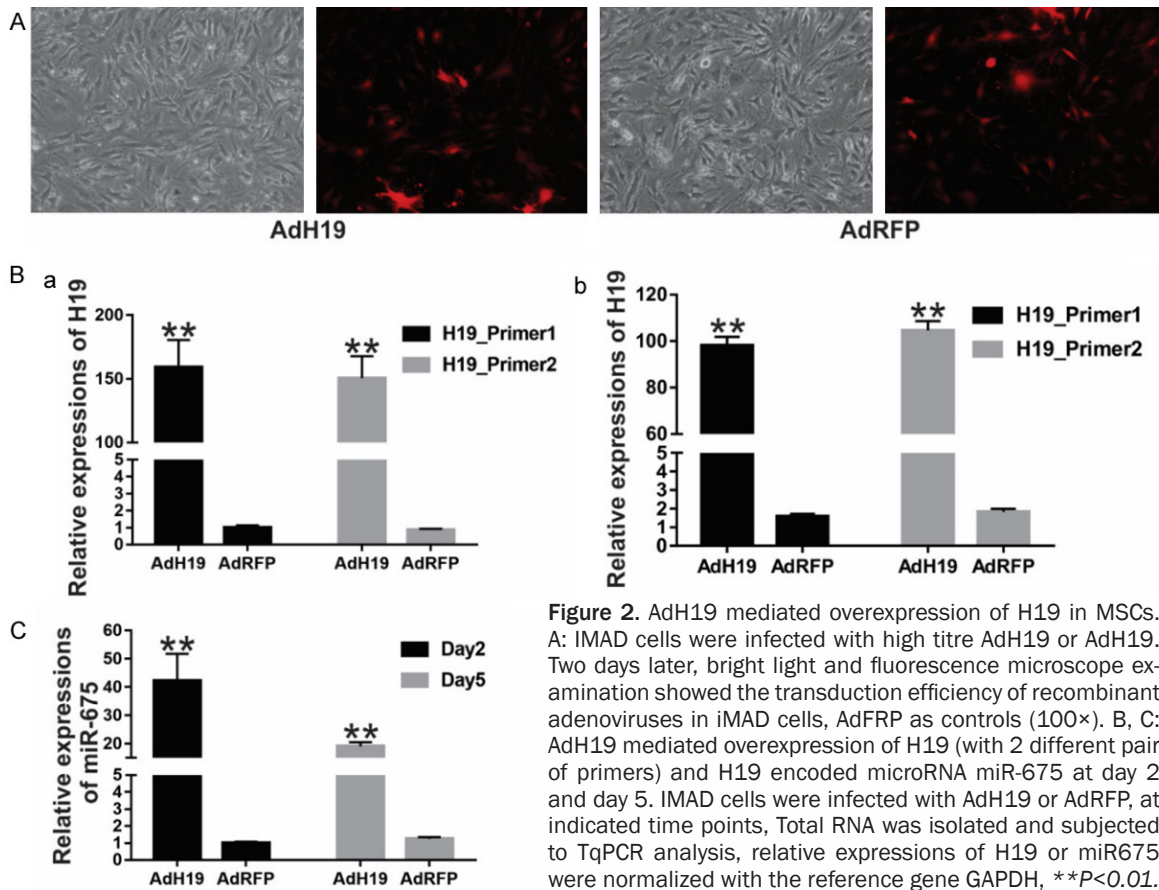


Figure 2. AdH19 mediated overexpression of H19 in MSCs. A: iMAD cells were infected with high titre AdH19 or AdRFP. Two days later, bright light and fluorescence microscope examination showed the transduction efficiency of recombinant adenoviruses in iMAD cells, AdRFP as controls (100×). B, C: AdH19 mediated overexpression of H19 (with 2 different pair of primers) and H19 encoded microRNA miR-675 at day 2 and day 5. iMAD cells were infected with AdH19 or AdRFP, at indicated time points, Total RNA was isolated and subjected to TqPCR analysis, relative expressions of H19 or miR675 were normalized with the reference gene GAPDH, ** $P < 0.01$.

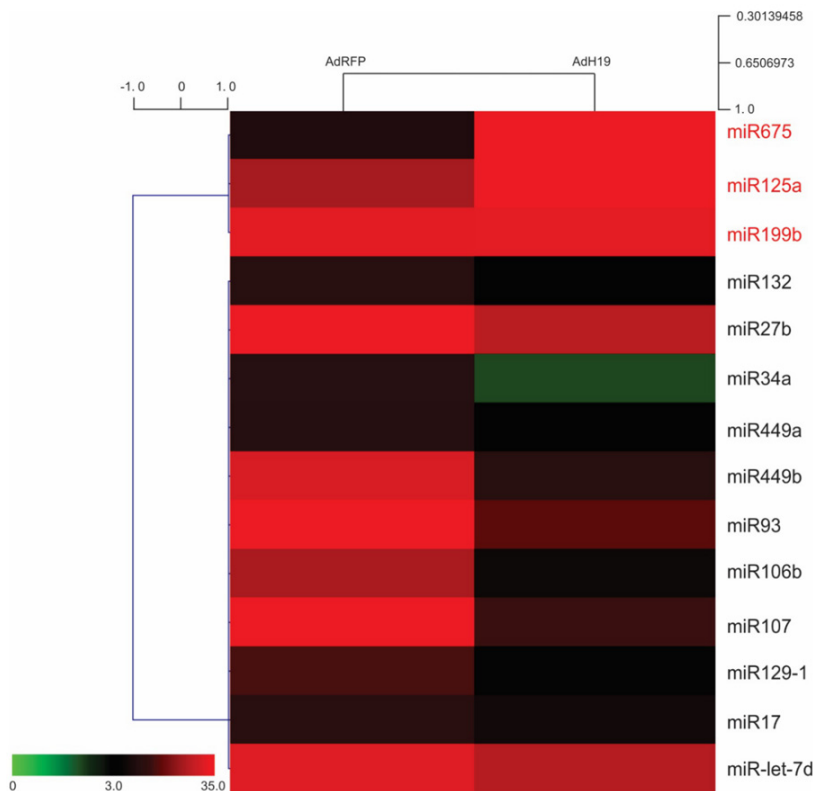


Figure 3. Functional identification of AdH19 mediated overexpression of H19. Subconfluent iMADs were infected with AdH19 or AdRFP for 2 days, total RNA was isolated from the infected iMADs and subjected to TqPCR analysis of the selected 14 miRNAs which may be associated with H19. The relative normalized expression of these miRNAs was subjected to clustering analysis, 3 miRs are upregulated and 11 miRs are downregulated.

the expression of H19 decreased gradually and maintained in a relatively high level at day 7 and day 9 (**Figure 4A**). Meanwhile, the expression of early osteogenic differentiation marker Runx2 increased from day 3 to day 5 and back to the basal

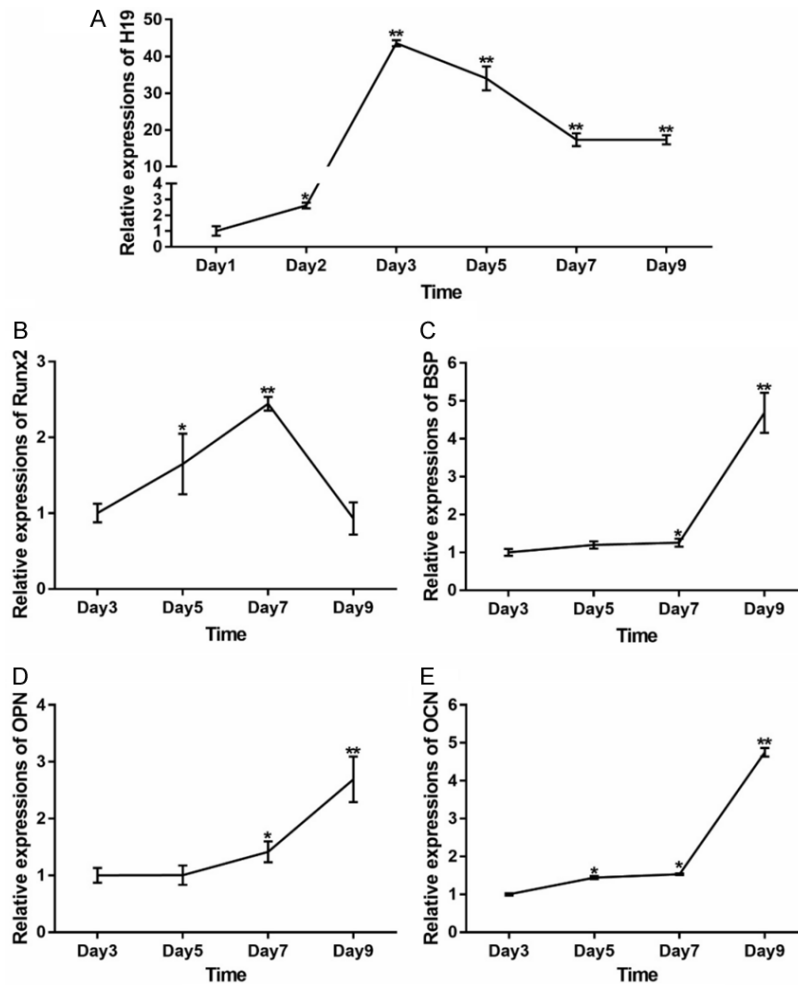


Figure 4. Expression levels of H19 and osteogenic differentiation markers during osteogenic differentiation of MSCs. IMAD cells were cultured in osteogenic medium, at the indicated time points, total RNA was isolated and subjected to TqPCR analysis. (A) Expression level of H19 (A) and osteogenic differentiation markers (B-E) at different time point. All samples were normalized with the reference gene GAPDH. Each assay condition was done in triplicate. Relative expression was calculated by dividing the relative expression values (i.e., gene/GAPDH). ** $P < 0.01$, * $P < 0.05$, Runx2, runt-related transcription factor 2; BSP, bone sialoprotein; OPN, osteopontin; OCN, osteocalcin.

level at day 7 (**Figure 4B**), late osteogenic differentiation markers increased gradually from day 3 to day 9 (**Figure 4C-E**). These results suggest that a low or medium level of H19 is necessary for osteogenic differentiation of MSCs.

AdH19 mediated overexpression of H19 in MSCs is in a dosage dependent manner

IMAD cells were infected with AdH19 or AdRFP in three dosage (low, medium, high), as shown in **Figure 5A**, the infection rate of low dosage was about 20%, 40% for medium dosage and

80% for high dosage. Total RNA was isolated at day 2 and was subjected to reverse transcription and qPCR analysis, the expression level of H19 were positively correlated with the infection rate, as for high dosage, the expression level of H19 was around 285 times higher than control group (**Figure 5B**). These data suggest that adenovirus mediated overexpression of H19 in MSCs is in a dosage dependent manner.

AdH19 biphasic regulating osteogenic differentiation of MSCs

We further explored the effect of different expression level of H19 on osteogenic differentiation of MSCs. IMAD cells were incubated in osteogenic medium and infected with AdH19 or AdRFP in low, medium or high dosage. Total RNA was isolated at the indicated time points and was subjected to reverse transcription and qPCR analysis. As shown in **Figure 6**, the expression of Runx2 at day 7, OPN and OCN at day 9 were upregulated in low dosage of AdH19, and downregu-

lated in medium or high dosage of AdH19 compared with control group.

Then we analyzed the effect of different dosage of AdH19 on early osteogenic differentiation of MSCs. We found that low dosage of AdH19 dramatically upregulated ALP activities both qualitatively and quantitatively, however high dosage of AdH19 significantly downregulated ALP activities both qualitatively and quantitatively (**Figure 7A, 7B**). Similarly, late osteogenic differentiation marker matrix mineralization was determined at day 15. As exhibited in

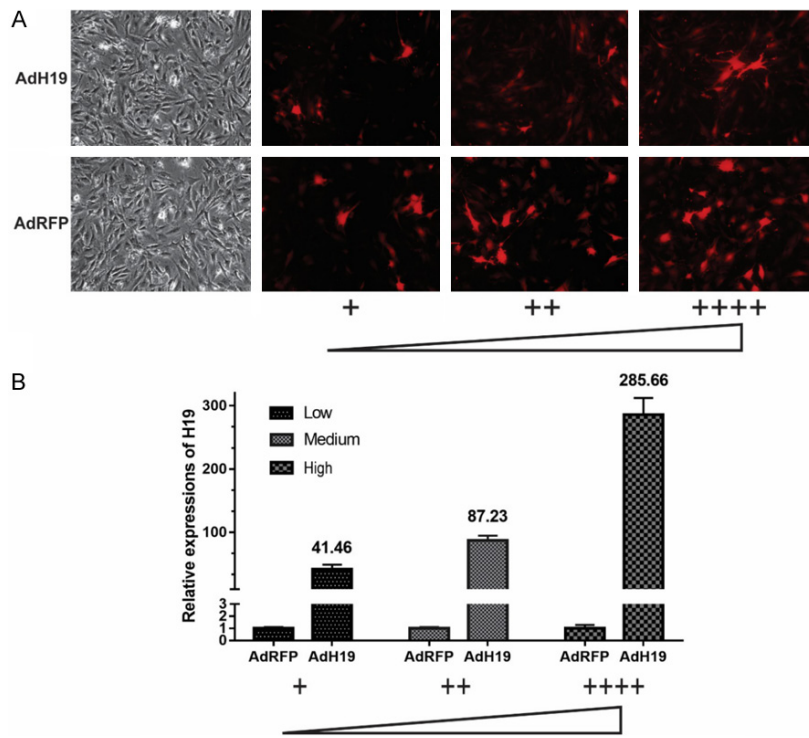


Figure 5. AdH19 mediated overexpression of H19 in MSCs is in a dosage dependent manner. A: Bright light and fluorescence microscope examination showed the transduction efficiency of recombinant adenoviruses in iMAD cells two days after infection, AdRFP as controls (100×). The infection rate of low dosage was about 20%, 40% for medium dosage and 80% for high dosage. B: Expression levels of H19 in different infection rate at day 2. All samples were normalized with the reference gene GAPDH. Each assay condition was done in triplicate, ** $P < 0.01$.

Figure 7C, low dosage of AdH19 promoted matrix mineralization of MSCs, however, medium and high dosage of AdH19 inhibited matrix mineralization of MSCs. These data indicated that low dosage of AdH19 promoted osteogenic differentiation of MSCs, and high dosage of AdH19 inhibited osteogenic differentiation of MSCs, namely, AdH19 biphasic regulating osteogenic differentiation of MSCs.

Discussion

Current evidence shows that only about 1.2% the mammalian genome codes for amino acids in proteins, however, vast majority of the genome is transcribed, which is well beyond the boundaries of known genes [3, 52]. Therefore many investigators pay attention to identify the function of ncRNA, especially lncRNA [53-55]. Owing to lncRNA coding no protein, regulating multiple stages during both transcription and translation [5, 6, 53], it is essential to mimic the overexpression of lncRNA exoge-

nously. Here, in order to explore an effective method to overexpression lncRNA exogenously, we choose H19 as an example, which is one of the best known lncRNA and hold the potential to regulate several processes during cancer developing, cell proliferation etc. [16, 27, 56-58], and confirmed that AdEasy system could overexpression H19 in a stable, replicable, simple and convenient manner.

Full-length H19 was generated by two separate fragments containing specific enzyme sites, which were amplified from mouse genomic DNA respectively. We firstly subcloned full-length H19 into homemade plasmid pMOK, which hold a variety of restriction endonuclease sites, and then subcloned full-length H19 into recombinant adenovirus vector, that was because we

could not subclone full-length H19 into recombinant adenovirus vector directly or subclone H19 fragment 1 and H19 fragment 2 into recombinant adenovirus vector stepwisely. These results indicate the importance of diversity of restriction endonuclease sites in vectors.

Recombinant adenoviruses are replication-defective adenoviral vectors which are used for gene therapy, vaccine therapy and basic biology [9, 10, 59]. During the past decades, we constructed AdEasy system for rapid generation and production of recombinant adenovirus vectors, at the same time, we optimized the procedures of adenovirus generation from the aspects of packing, amplification [11, 13, 14, 34]. In the present study, we identified that H19 could be subcloned into our AdEasy system, and generating adenovirus overexpression H19 with the using of our optimized pTP293 cells and rapid adenovirus production and amplification (RAPA) cells [13, 14], which indicate the optimized procedures of AdEasy system are

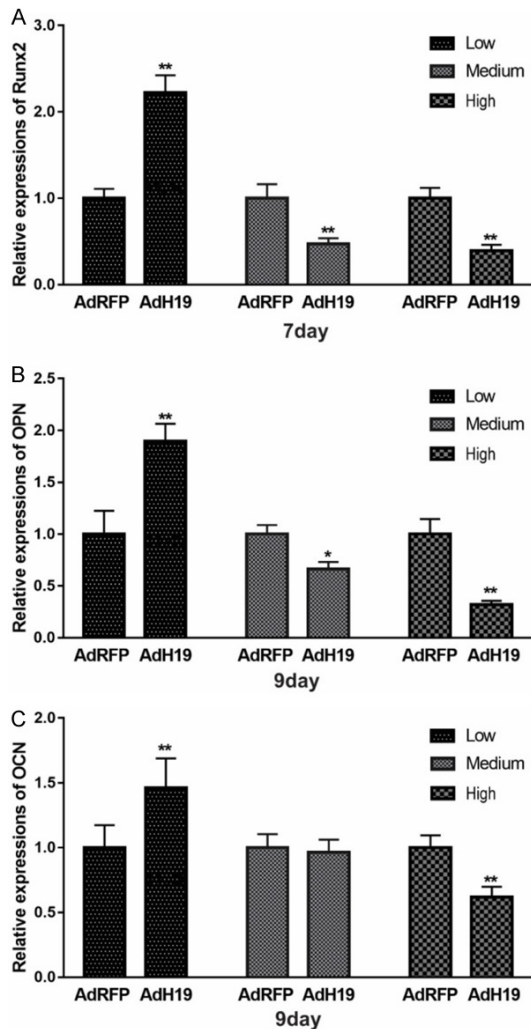


Figure 6. AdH19 mediated overexpression of H19 biphasic regulating osteogenic differentiation markers expression during osteogenic differentiation of MSCs. IMAD cells were cultured in osteogenic medium, at the indicated time points, total RNA was isolated and subjected to TqPCR analysis. A: Expression level of Runx2 at day 7. B: Expression level of OPN at day 9. C: Expression level of OCN at day 9. Each assay condition was done in triplicate. ** $P < 0.01$, Runx2, runt-related transcription factor 2; OPN, osteopontin; OCN, osteocalcin.

applicable for exogenous generation lncRNA. In other words, this is the first time to report that lncRNA could be overexpressed exogenously with AdEasy system, which is helpful for next identify the function of lncRNAs.

H19 has been identified nearly four decades ago, the diverse of H19 functions, including regulating embryonal development and growth [23], acting as oncogene [60, 61] or tumor sup-

pressor [16, 17], working as modular scaffold of histone modification complexes [22] etc. have been reported during the past years. However, one of H19's most important function is acting with microRNAs. While function as nocoding RNA, H19 also encoding miR-675 [46, 62, 63]. Huang [27] et al reported that H19-miR-675 axis regulated osteoblast differentiation through TGF- β signaling pathway. Dudek [64] et al found that H19-miR-675 regulated type-II collagen expression. Steck [65] et al found that H19-miR-675 was associated with the anabolism and catabolism of osteoarthritis cartilage. Here, we found that adenovirus mediated overexpression of H19 up-regulated miR-675 dramatically, which indicates adenovirus mediated overexpression of H19 is functional.

Meanwhile, H19 was found to act as ceRNA or molecular sponge [7, 24, 51, 66, 67]. In the present study, we also explored whether adenovirus mediated overexpression of H19 acting as ceRNA. Among the 14 miRs which we selected may associated with H19 [24, 40-51], we found that 3 miRs (miR-675, miR-125, miR-199b) were upregulated by overexpression of H19, and 11 miRs (miR-132, miR-27b, miR-34a, miR-449a, miR-449b, miR-93, miR-106b, miR-107, miR-129-1, miR-17 and miR-let-7d) were downregulated by overexpression of H19. Be consistent with the previous reports, H19 was found to be act as ceRNA or molecular sponge of miR-107 [21, 43], miR-let-7 [24, 44, 45], miR-93 [68], miR-106b [69], miR-17 [51]. These results suggest that adenovirus mediated overexpression of H19 could work as functional ceRNA or molecular sponge.

Recently, H19 regulating osteogenic differentiation of MSCs were reported [25-27]. We found that the expression level of H19 in MSCs is relatively higher than other genes [28], at the same time, H19 is upregulated during the early stage, and sustained in a relatively high level during the late stage of osteogenic differentiation of MSCs. So, we asking if higher expression level of H19 could promote osteogenic differentiation. Here, with the advantage of semi-quantitative feature of adenovirus, we identified that adenovirus mediated low overexpression level of H19 could promote osteogenic differentiation of MSCs, nevertheless, high expression level of H19 inhibited osteogenic differenti-

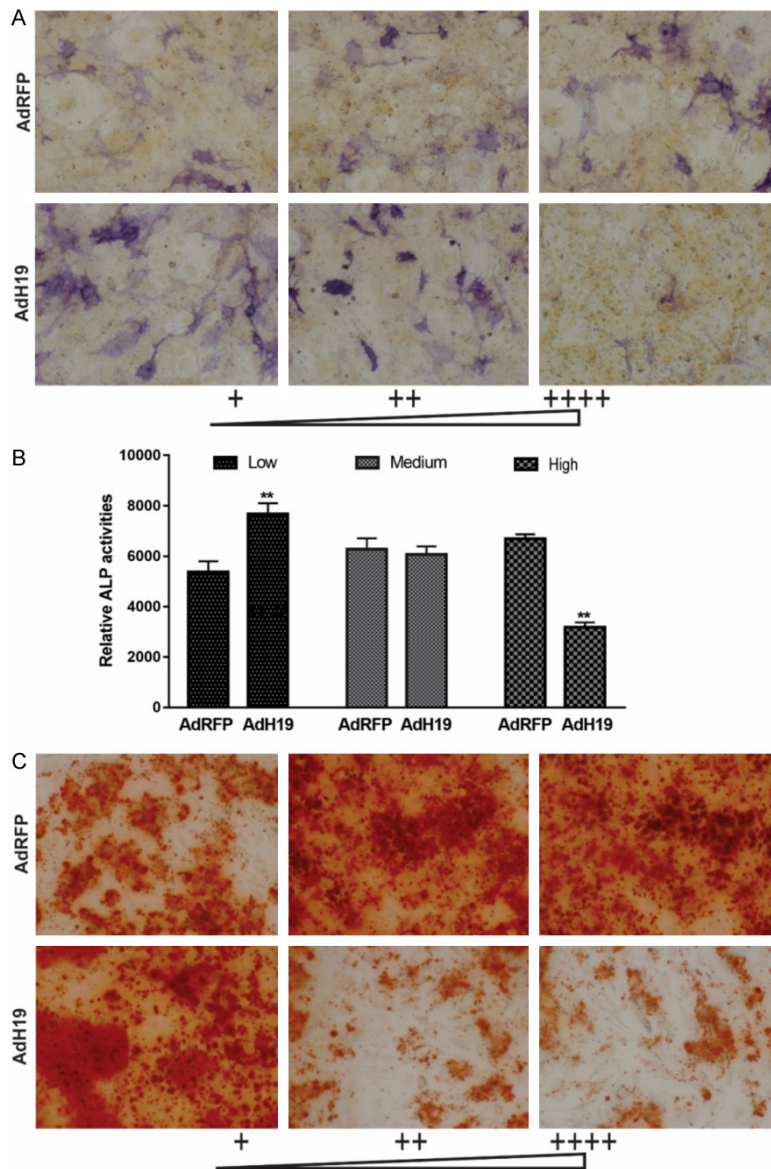


Figure 7. AdH19 mediated overexpression of H19 biphasic regulating early and late osteogenic differentiation of MSCs. (A, B) AdH19 mediated overexpression of H19 biphasic regulating ALP activity in MSCs. Subconfluent iMAD cells were infected with AdH19 or AdRFP with different dosage. At day 7 after infection, the infected cells were subjected to ALP activity assays by either histochemical staining (100×) (A) or quantitative bioluminescence assay (B). Each assay conditions were done in triplicate. Representative staining is shown, ** $P < 0.01$. (C) AdH19 mediated overexpression of H19 biphasic regulating matrix mineralization of MSCs. Subconfluent iMAD cells were infected with AdH19 or AdRFP with different dosage. At day 15 after infection, the infected cells were subjected to Alizarin Red S staining. Each assay condition was done in triplicate. Representative microscopic images are shown (100×).

on of MSCs. In summary, we found the biphasic effect of H19 in regulating osteogenic differentiation of MSCs, which suggest the flexibility of lncRNA in regulating physical or pathological processes.

Conclusion

We firstly reported AdEasy system mediated overexpression of H19 could act as functional lncRNA, and further identified the biphasic effect of H19 in regulating osteogenic differentiation of MSCs. These results are helpful for further identify the function and regulatory mechanisms of H19 in osteogenic differentiation of MSCs.

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interpretation of data; in writing of the report; and in the decision to submit the paper for publication.

Disclosure of conflict of interest

None.

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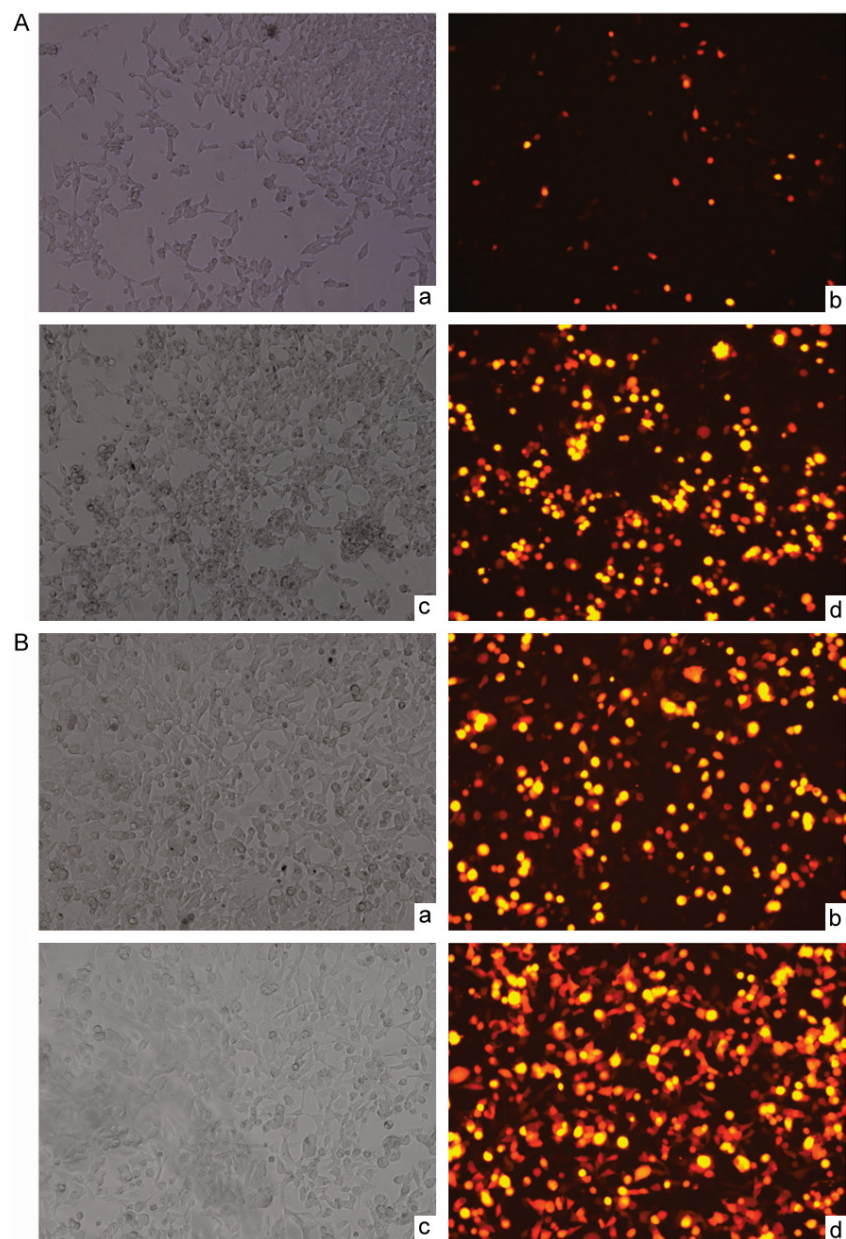
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Supplementary Figure 1. The packing and amplification of AdH19 in HEK 293 cells. (A) The packing of AdH19 in RAPA cell lines. Recombinant adenovirus pAd5-H19 was transfected into RAPA cells and generating recombinant adenoviruses AdH19, the fluorescence indicates the packing of AdH19 in cells at day 2 (a, b) and day 5 (c, d). When more than 50% cells showed cytopathogenic effect (CPE), the adenovirus was collected and addressed for first generation amplification. (B) The amplification of AdH19. AdH19 was collected and used to amplify in pTP 293 cells, the fluorescence indicates the infection of cells at day 2 (a, b) and day 5 (c, d). When more than 50% cells showed cytopathogenic effect (CPE), the adenovirus was collected and addressed for the infection of target cells.