Suppression of the transcription factor MSX1 gene delays bovine preimplantation embryo development in vitro

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D Tesfaye and A Regassa contributed equally to this work

Abstract

This study was conducted to investigate the effect of suppressing transcription factor gene MSX1 on the development of in vitro produced bovine oocytes and embryos, and identify its potential target genes regulated by this gene. Injection of long double-stranded RNA (LdsRNA) and small interfering RNA (siRNA) at germinal vesicle stage oocyte reduced MSX1 mRNA expression by 73 and 37% respectively at metaphase II stage compared with non-injected controls. Similarly, injection of the same anti-sense oligomers at zygote stage reduced MSX1 mRNA expression by 52 and 33% at 8-cell stage compared with non-injected controls. Protein expression was also reduced in LdsRNA- and siRNA-injected groups compared with non-injected controls at both stages. Blastocysts rates were 33, 28, 20 and 18% in non-injected control, scrambled RNA (scRNA), LdsRNA- and siRNA-injected groups respectively. Cleavage rates were also significantly reduced in Smartpool siRNA (SpsiRNA)-injected group (53.76%) compared with scRNA-injected group (57.76%) and non-injected control group (61%). Large-scale gene expression analysis showed that 135 genes were differentially regulated in SpsiRNA-injected group compared with non-injected controls, of which 54 and 81 were down- and up-regulated respectively due to suppression of MSX1.

Additionally, sequence homology mapping and gene enrichment analysis with known human pathway information identified several functional modules that were affected due to suppression of MSX1. In conclusion, suppression of MSX1 affects oocyte maturation, embryo cleavage rate and the expression of several genes, suggesting its potential role in the development of bovine preimplantation embryos.


Introduction

The MSX family genes are one of the most highly conserved homeobox-containing genes that are identified in several animal species. The three mammalian members, MSX1, MSX2 and MSX3, share 98% homology in their protein domain (Davidson & Hill 1991, Davidson 1995). They play important roles in inductive tissue interactions during vertebrate organogenesis, and their differential expression mediates patterning, morphogenesis and tissue formation (Chen et al. 1996, Bendall & Abate-Shen 2000). They encode closely related homeoproteins that function as transcriptional repressors through interacting with the components of the core transcription complex as well as other homeoproteins (Catron et al. 1996), and promote apoptosis in developing limbs and cephalic neural crest (Song et al. 1992, Graham et al. 1993, 1994, 1996, Davidson 1995, Marazzi et al. 1997, Gomes & Kessler 2001).

Although it is expressed in diverse tissues, MSX1 gene expression is mainly associated with multi-potent progenitor cell (Bendall & Abate-Shen 2000). It is strongly expressed in a region of highly proliferative, multi-potent cells that give rise to chondrogenic and osteogenic derivatives of the limb but absent in regions where cells stopped to proliferate and begun to undergo differentiation (Bendall & Abate-Shen 2000). MSX1 is also expressed at high levels in adult mouse uterine epithelium and decreases during pregnancy following embryonic implantation to regulate various aspects of uterine epithelial morphology and maintain the adult uterus in a morphogenetically and developmentally responsive state (Pavlova et al. 1994). It is detected at lower level in endometrium and placentomes particularly after 60 days of gestation in cows (Ishiwata et al. 2003).

In our recent study, we found higher expression of MSX1 in bovine oocytes that were derived from subordinate follicles of the dominance phase of the
first follicular wave compared with oocytes derived from the growth phase (Ghanem et al. 2007). We also found relatively higher abundance of MSX1 transcript in embryo biopsies derived from blastocysts that resulted in no pregnancy compared with blastocysts that resulted in successful calf delivery after transfer to recipients (El-Sayed et al. 2006). On the other hand, higher expression of MSX1 was reported in developmentally competent bovine oocytes (Donnison & Pfeffer 2004) and blastocysts (Lazzari et al. 2006). This shows the lack of clear relationship between the expression of MSX1 and developmental potential of bovine oocytes and embryos. Therefore, we aimed to investigate the role of MSX1 in the development of preimplantation bovine embryos especially in regulating the expression of developmentally important genes by suppressing its transcript during bovine oocyte maturation and cleavage stage embryo development.

Results

Expression profiling of MSX1 in bovine preimplantation embryos

To get an insight into its preimplantation expression profile, we analysed MSX1 expression across different stages of bovine preimplantation embryo development. The analysis showed that it is highly expressed at germinal vesicle (GV) stage oocyte followed by a moderate expression at metaphase II (MII) stage oocyte. Its expression level starts to decline sharply from zygote up to 8-cell stage and diminishes starting from morula stage onwards (Fig. 1).

Experiment 1: suppression of MSX1 during bovine oocyte maturation

In this experiment, MSX1 long double-stranded RNA (LdsRNA), small interfering RNA (siRNA) and scrambled RNA (scRNA) were microinjected at GV stage oocytes after partial removal of cumulus cells. Expression analysis of the target mRNA in MII oocytes 28 h post microinjection showed that injection of MSX1 LdsRNA and siRNA at GV stage oocyte reduced the mRNA expression levels by 73 and 37% respectively at MII stage compared with non-injected controls (Fig. 2).

In order to confirm the sequence-specific suppression of LdsRNA and siRNA, the mRNA expression level of a closely related transcript, bovine MSX2, was quantified using the same samples that were used to quantify MSX1 mRNA. The expression data showed that there was no reduction in the level of MSX2 mRNA in either case (Fig. 2).

The protein expression analysis indicated subsequent reduction in the expression of the target MSX1 protein at MII oocyte stage (Fig. 3) compared with non-injected controls.

About 27, 25 and 26% of oocytes from scRNA, LdsRNA and siRNA treatment groups respectively did not survive the physical injuries due to microinjection procedure as determined 2–3 h post injection. However, these differences are not statistically significant. Although statistically not significant, the percentage of oocytes that reached MII stage was higher in non-injected controls (81.87%) and scRNA-injected (79.47%) groups compared with those injected with LdsRNA (73.75%) and siRNA (75%; Table 1).

Experiment 2: suppression of MSX1 retards the development of cleavage stage embryos

In this experiment, microinjection of scRNA, LdsRNA and siRNA was performed at zygote stage, and the effects were assessed at different preimplantation developmental stages. As in experiment 1, about 21, 23 and 24% of the zygotes from scRNA, LdsRNA and siRNA treatment groups respectively did not survive the physical injuries during microinjections. However, these differences are not significant. Microinjection of LdsRNA and siRNA at zygote stage reduced the mRNA expression levels by 52 and 33% at the 8-cell stage.
compared with non-injected control (Fig. 4). As in experiment 1, to confirm the gene-specific suppression due to injection of LdsRNA and siRNA a closely related bovine transcript, MSX2 was quantified at 8-cell stage embryos, and no effect on the expression level of this transcript was observed at both developmental stages (Fig. 4).

In order to study the effects of suppressing MSX1 mRNA on protein expression, 2-, 4- and 8-cell stage embryos from all treatment groups were immunostained using rabbit anti-human polyclonal MSX1 primary antibody. As shown in Fig. 5, reduction in the protein expression as estimated from the intensity of florescence signal was observed in embryos that were treated with LdsRNA and siRNA compared with non-injected control and scRNA-injected groups.

Table 1 Percentage of oocytes (mean ± s.e.m.) that survived the physical injuries during microinjection and formed polar body after 24-h culture in different treatment groups. Numbers in the parentheses indicate the number of oocytes that survived mechanical injury during microinjection and formed polar bodies out of the total number of injected oocytes.

<table>
<thead>
<tr>
<th>Treatment</th>
<th>Number of oocytes</th>
<th>Survival rate</th>
<th>Extrusion of polar bodies</th>
</tr>
</thead>
<tbody>
<tr>
<td>Non-injected</td>
<td>298</td>
<td>100.00 ± 0.0 (298)</td>
<td>80.87 ± 1.91 (241)</td>
</tr>
<tr>
<td>scRNA injected</td>
<td>367</td>
<td>73.02 ± 2.52 (268)</td>
<td>79.47 ± 3.00 (213)</td>
</tr>
<tr>
<td>LdsRNA injected</td>
<td>376</td>
<td>75.00 ± 1.92 (282)</td>
<td>73.75 ± 2.13 (208)</td>
</tr>
<tr>
<td>siRNA injected</td>
<td>367</td>
<td>74.11 ± 8.18 (272)</td>
<td>75.00 ± 1.91 (204)</td>
</tr>
</tbody>
</table>

The proportions of 2-, 4- and 8-cell stage embryos were determined at 72 h post insemination (hpi) to estimate cleavage rates (Table 2). No significant differences were observed in the cleavage rates of zygotes until 4-cell stage but higher proportion of zygotes (P ≤ 0.05) from non-injected control group developed to 8-cell stage compared with those injected with LdsRNA and siRNA. Further observation of embryonic development beyond 8-cell stage until day 8 blastocyst stage showed that zygotes injected with LdsRNA and siRNA developed at a lower rate to the blastocysts stage compared with scRNA-injected group and non-injected controls (Table 3). While 61 and 56% of the 8-cell embryos from non-injected controls and scRNA-injected groups respectively reached blastocysts stage, 50 and 47% of embryos from LdsRNA- and siRNA-injected groups respectively reached the same stage.

**Experiment 3: suppression of MSX1 resulted in differential expression of developmentally important genes at the time of maternal to embryonic genome transition**

In this experiment, Smartpool siRNAs (SpriRNAs) consisting of four pools of siRNAs (Dharmacon, Inc., Chicago, IL, USA) were used to suppress MSX1 and investigate the effect on the development of preimplantation embryos and target genes. Three pools of zygotes were injected with SpriRNAs and scRNA, and relative MSX1 mRNA abundance and their cleavage rates were compared with non-injected control. Injection of SpriRNAs resulted in a 40% reduction in MSX1 transcript abundance as shown in Fig. 6. Similar to LdsRNA and siRNA, suppression of MSX1 due to injection of SpriRNAs reduced cleavage rates as significantly lower 53.76% of embryos from this group reached 8-cell stage compared with 61 and 57.76% of embryos from non-injected and scRNA-injected groups respectively (Table 4).

Following this, two groups including zygotes injected with SpriRNAs and non-injected controls were used to analyse differential gene expression due to suppression of MSX1. Eight-cell stage embryos from SpriRNA-injected groups were compared with non-injected
controls by hybridising with a bovine cDNA array. Each comparison was done using six independent hybridizations including dye-swap. Analysis of the array data revealed that 135 genes were differentially expressed in SpsiRNA-injected group compared with non-injected controls, of which 54 and 81 were down- and up-regulated respectively due to suppression of MSX1 (Supplementary Tables 1 and 2, see section on supplementary data given at the end of this article). The hierarchical clustering and heat map of those differentially regulated genes is indicated in Fig. 7. Gene ontology terms (molecular functions and biological processes) showing the proportion of differentially expressed genes due to suppression of MSX1 are presented in Figs 8 and 9.

Another three pools of (n=60) 8-cell embryos were used for total RNA isolation, cDNA synthesis and real-time qRT-PCR validation of the array data. The results of the analysis showing that real-time qRT-PCR validation of the array data has confirmed the expression pattern of four out of seven transcripts are in accordance with the microarray result. However, the fold change difference obtained by qRT-PCR validation is slightly lower than the array result (Fig. 10).

In order to identify functional modules related to MSX1 target genes, we carried out enrichment analysis using a comprehensive database resource (http://cpdb.molgen.mpg.de). In CPDB, twelve different pathways and interaction databases are integrated by identifier mapping (Kamburov et al. 2009). Using this integrated content, we generated gene sets (neighbourhood-based entity sets, NESTs) that are related via functional interactions. Enrichment of MSX1 target genes with respect to these gene sets was judged by P values computed from the hypergeometric distribution. A total of 135 bovine genes show significant changes with respect to the SpsiRNAs, of which 97 had a human homolog and 57 of these genes can be mapped to the known functional interactions. Figure 11 shows two NESTs enriched by MSX1 target genes.

Discussion
Despite previous studies in mouse models, the role of MSX1 in the development of bovine preimplantation embryo is poorly understood. Here, we showed that suppression of MSX1 transcript and protein impaired the development of bovine oocytes and embryos through.

Table 2 Percentage of zygotes (mean ± S.E.M.) that reached different developmental stages by 72 h post insemination. Zygotes were injected with long double-stranded RNA (LdsRNA), small interfering RNA (siRNA) and scrambled RNA (scRNA), and their development was compared with non-injected controls. Numbers in the parentheses indicate the number of zygotes that survived mechanical injury during microinjection, not cleaved, reached 2-, 4- and 8-cell stages out of the total number of injected zygotes.

<table>
<thead>
<tr>
<th>Treatment</th>
<th>Number of zygotes</th>
<th>Survival rate</th>
<th>Non-cleaved zygotes</th>
<th>2-Cell stage</th>
<th>4-Cell stage</th>
<th>8-Cell stage</th>
<th>Cleavage rate</th>
</tr>
</thead>
<tbody>
<tr>
<td>Non-injected</td>
<td>445</td>
<td>100.0 ± 0 (445)</td>
<td>20.16 ± 2.63 (89)</td>
<td>10.69 ± 1.91 (47)</td>
<td>13.88 ± 1.51 (62)</td>
<td>54.44 ± 4.36a (247)</td>
<td>79.01 ± 2.59</td>
</tr>
<tr>
<td>scRNA injected</td>
<td>652</td>
<td>79.14 ± 4.74 (513)</td>
<td>21.24 ± 1.62 (109)</td>
<td>13.25 ± 2.69 (66)</td>
<td>15.78 ± 1.53 (81)</td>
<td>49.70 ± 2.80ab (255)</td>
<td>78.73 ± 2.35</td>
</tr>
<tr>
<td>LdsRNA injected</td>
<td>636</td>
<td>76.51 ± 5.38 (485)</td>
<td>29.66 ± 4.38 (137)</td>
<td>13.02 ± 1.53 (64)</td>
<td>18.25 ± 2.18 (90)</td>
<td>39.05 ± 2.59c (194)</td>
<td>70.32 ± 2.1</td>
</tr>
<tr>
<td>siRNA injected</td>
<td>619</td>
<td>76.03 ± 4.67 (470)</td>
<td>33.20 ± 3.86 (153)</td>
<td>14.57 ± 2.42 (68)</td>
<td>11.23 ± 3.20 (54)</td>
<td>40.96 ± 3.45 (195)</td>
<td>66.78 ± 3.02</td>
</tr>
</tbody>
</table>

Means with a column followed by different superscripts are significantly different (P≤0.05).

Means with in a column followed by different superscripts are significantly different (P≤0.05).

Table 3 Percentage of zygotes (mean ± S.E.M.) that reached 8-cell stage at 72 hpi and blastocyst stage at 8 days post insemination. Zygotes were injected with long double-stranded RNA (LdsRNA), small interfering RNA (siRNA) and scrambled RNA (scRNA), and their development was compared with non-injected controls. Numbers in the parentheses indicate the number of zygotes that reached 8-cell and blastocyst stages out of the total number of injected zygotes.

<table>
<thead>
<tr>
<th>Treatment</th>
<th>Number of zygotes</th>
<th>Proportion of 8 cells</th>
<th>Blastocysts rate</th>
<th>Blastocysts to 8 cells ratio</th>
</tr>
</thead>
<tbody>
<tr>
<td>Non-injected</td>
<td>222</td>
<td>54.50 ± 4.12 (121)</td>
<td>33.35 ± 2.64 (74)</td>
<td>0.61</td>
</tr>
<tr>
<td>scRNA injected</td>
<td>282</td>
<td>49.64 ± 2.64 (140)</td>
<td>27.93 ± 1.74 (71)</td>
<td>0.56</td>
</tr>
<tr>
<td>LdsRNA injected</td>
<td>274</td>
<td>39.41 ± 2.53 (108)</td>
<td>19.65 ± 3.49 (49)</td>
<td>0.50</td>
</tr>
<tr>
<td>siRNA injected</td>
<td>253</td>
<td>38.87 ± 3.23 (98)</td>
<td>18.27 ± 2.96 (47)</td>
<td>0.47</td>
</tr>
</tbody>
</table>

The efficacy of suppressing the targeted transcripts in mammalian oocytes and embryos appears to determine the extent of change in developmental phenotype. Suppression of developmentally important gene delays cellular growth (El-bashir et al. 2001). Accordingly, suppression of MSX1 reduced the number of zygotes that developed to 8-cell and blastocyst stages, and this can be explained by the dependence of early preimplantation bovine embryos on maternally derived and accumulated transcripts and proteins until the onset of major embryonic genome activation (Telford et al. 1990, Memili et al. 1998, Memili & First 1999, 2000). Thus, the significant difference among zygotes from the controls and LdsRNA- and siRNA-injected groups in developing to 8-cell stage and the small differences among the groups regarding early cleavage rates might be explained by the beneficial effects of maternally accumulated transcripts and proteins during oocyte maturation and their persistent activity until the onset of major embryonic genome activation (Davidson 1986, Eyestone & First 1986, Frei et al. 1989, Kopency et al. 1989) and to the temporal variation in mRNA and protein turn over rates (Li et al. 2004). We propose that the accumulated MSX1 transcript and protein are used by the embryos in the LdsRNA- and siRNA-injected groups to undergo normal early cleavage but their cleavage is reduced due to further depletion of the respective transcript and protein at latter stages. Phenotypic data, particularly those related to development to 8-cell and blastocyst stages, suggest that MSX1 expression is required for the development of preimplantation bovine embryos particularly during maternal to embryonic genome transition.

Injections of MSX1 LdsRNA and siRNA at GV stage oocyte and zygote stages resulted in the sequence-specific degradation of the target message at MI oocyte and 8-cell stages. Relatively higher suppression was recorded for LdsRNA at MI oocyte compared with the 8-cell stage (Figs 2 and 4). This difference might be associated with the observed differences in the abundance of MSX1 transcript (Fig. 1) at these stages as the abundance of the target transcript greatly affects RNAi-mediated suppression efficiency (Hu et al. 2004, Tesfaye et al. 2007). Similarly, there were differences in suppression efficiencies between LdsRNA and siRNA at the same stage, and this might be due to the difference in the inherent suppression efficiencies of the two RNAs which in turn depends on variation in the corresponding RNA sequences (Holen et al. 2002). Reduction in the protein expression of the groups injected with LdsRNA and siRNA compared with the controls could also be due to the RNAi effect that leads to degradation of the endogenous complementary mRNA or blockage of ribosomal movement along the native mRNA to halt...
Table 4 Percentage of zygotes (mean ± S.E.M.) that reached different developmental stages at 72 hpi. Numbers in the parenthesis indicate the number of zygotes that survived mechanical injury during microinjection, not cleaved, reached 2-, 4- and 8-cell stages out of the total number of injected zygotes.

<table>
<thead>
<tr>
<th>Treatment</th>
<th>Number of zygotes</th>
<th>Survival rate</th>
<th>Non-cleaved zygotes</th>
<th>2-Cell stage</th>
<th>4-Cell stage</th>
<th>8-Cell stage</th>
<th>Cleavage rate</th>
</tr>
</thead>
<tbody>
<tr>
<td>Non-injected</td>
<td>479</td>
<td>100.0 ± 0</td>
<td>(479)</td>
<td>18.14 ± 1.36 (89)</td>
<td>7.40 ± 2.23 (37)</td>
<td>12.20 ± 1.16 (61)</td>
<td>61.04 ± 2.11 (292)</td>
</tr>
<tr>
<td>scRNA injected</td>
<td>497</td>
<td>85.33 ± 5.65 (427)</td>
<td>21.66 ± 1.37 (92)</td>
<td>7.45 ± 1.16 (33)</td>
<td>13.11 ± 0.84 (56)</td>
<td>57.76 ± 0.96 (246)</td>
<td>78.63 ± 1.47</td>
</tr>
<tr>
<td>SpsiRNA injected</td>
<td>653</td>
<td>83.03 ± 2.94 (540)</td>
<td>24.58 ± 2.31 (113)</td>
<td>5.62 ± 1.46 (32)</td>
<td>15.78 ± 2.03 (86)</td>
<td>53.76 ± 2.38 (287)</td>
<td>75.42 ± 2.31</td>
</tr>
</tbody>
</table>

Means with in a column followed by different superscripts are significantly different (P<0.05).

Translation and eventually blocks protein synthesis via introduction of dsRNAs into the cell (Fire et al. 1998).

Transcription factors are proteins involved in the regulation of gene expression through binding to the promoter elements upstream of genes and either facilitate or inhibit their transcription. As a transcription factor, the protein of MSX1 orchestrates gene expression and regulates cell growth, proliferation, differentiation, cell-to-cell communication and the apoptotic pathway during pattern formation in vertebrate embryogenesis (Song et al. 1992, Graham et al. 1993, 1994, Davidson 1995, Chen et al. 1996, Marazzi et al. 1997, Bendall & Abate-Shen 2000, Gomes & Kessler 2001). In support of this notion, a number of developmentally important genes were down-regulated due to suppression of MSX1. These include bone morphogenetic protein 15 (BMP15), various forms of zinc finger proteins (ZNF43, ZNF65 and ZNF91), rino kinase 3 (RIOK3), general transcription factor IIa, 1-like (ALF), aurora kinase A (AURKA), pituitary tumour transforming gene 1 (PTTG1), Bos taurus elongation factor 1a (EEF1A1) and others.

A maternal transcript, BMP15, along with growth and differentiation factor 9, regulates follicular development in rodents, sheep and humans (Elvin et al. 2000, McNatty et al. 2003, Di Pasquale et al. 2004, Shimasaki et al. 2004) and ovulation rate in sheep (Davis et al. 1991, Galloway et al. 2000, Hanrahan et al. 2004, Juengel et al. 2004). It has been detected at higher level in bovine oocytes that were derived from the dominance phase of follicular development where MSX1 has been found to be up-regulated (Ghanem et al. 2007) suggesting that the two genes are operating in the same signalling pathway and involve in the development of bovine preimplantation embryos.

Under expression of transcripts such as ZNF proteins, RIOK3, ALF and AURKA due to suppression of MSX1 might evidence that these genes are the downstream effectors of MSX1 effects as both of them are involved in the biology of oocytes. For instance, ZNF proteins are involved in a DNA-dependent regulation of transcription, and RIOK3 plays a role in the process of chromosome segregation and amino acid phosphorylation. Both chromosome segregation and protein phosphorylation are among the processes that are critically required during oocyte maturation. ALF encodes a germ cell-specific counterpart of the large (α/β) subunit of general transcription factor, and is involved in Xenopus oocyte maturation (Han et al. 2003). AURKA has been suggested to be involved in the maturation of bovine oocytes (Vigneron et al. 2004).

Figure 7 Heat map and list of some differentially regulated genes at 8-cell stage embryos due to suppression of MSX1. The red and green blocks represent the up- and down-regulated genes respectively.
PTTG1 has the same expression pattern as MSX1 (El-Sayed et al. 2006, Ghanem et al. 2007), and its involvement in apoptosis and zygotic genome activation (Hamid & Kakar 2004) might indicate its association with MSX1 during embryonic patterning. EEF1A1 encodes a ubiquitous protein which is involved in the elongation step of protein synthesis and catalyzes the binding of aminoacyl-tRNA to the ribosome (Merrick 1992). In many organisms, it belongs to a multigene family, in which genes are expressed in a developmental or tissue-specific manner.

On the other hand, suppression of MSX1 has increased the expression of various transcripts including meiosis-specific nuclear structural protein 1 (MNS1), β-galactoside-binding lectin (LGALS3), interferon τ 1 (IFNT), ribosomal protein L23 (RPL23), placental 8 (PLAC8) and others. IFNT encodes a signalling protein secreted by the bovine conceptus during preimplantation period and is responsible for the recognition of pregnancy via preventing the pulsatile release of luteolytic PGF_{2\alpha} (Ezashi & Roberts 2004, Robinson et al. 2006). It is also important for the proliferation and distribution of peripheral blood lymphocyte subsets during one-way mixed lymphocyte reaction in cows and heifers (Gierek et al. 2006). According to Dai et al. (2004), RPL23 stimulates p53-dependent transcription and G_{1} cell cycle arrest through binding to the murine double minute (MDM2) and inhibiting the MDM2-mediated p53 degradation process. It also plays an important role in the ribosomal biogenesis-p53 pathway.

Functional characterization in cultured cell has indicated that MNS1 is a detergent and high salt-resistant skeletal protein, which is involved in the organization of the nuclear or pronuclear architecture, and is specifically expressed at the pachytene stage during spermatogenesis (Furukawa et al. 1994). LGALS3 is widely expressed in epithelial tissues, and has been implicated in a variety of cellular processes including adhesion and polarization. More specifically, it is required for optimal long-term cell adhesion to both collagen I and laminin 11 (Friedrichs et al. 2007).

The consensus pathway database enrichment analysis showed that genes differentially regulated due to suppression of bovine MSX1 to be enriched with two functional modules, namely checkpoint with forkhead and ring finger domains (CHFR), which interacts with Aurora A. The other module which is enriched with the MSX1 target genes (nucleolar protein 12 and Aurora A) is superoxide dismutase 2 (Fig. 9).

This study has generated some important data regarding the role of MSX1 in bovine preimplantation embryo development. However, it has also few limitations. The difficulty to follow up the development of microinjected embryos during foetal development beyond blastocysts stage limits the application of such study to the in vivo system due to the transient RNAi-based suppression effect. Secondly, although several
genes were found to be differentially regulated due to suppression of MSX1, we believe that these might not be the only MSX1-dependent transcripts as the bovine cDNA array that was used in this study contains a limited number of clones. Moreover, because the bovine genome is not completely annotated, the predicted pathways in the present study might be incomplete due to missing genes and a number of differentially expressed genes are uncharacterised, their molecular functions are poorly understood and their association with MSX1 could not be established.

It is true that cellular response to mechanical injury could result in the misexpression of certain genes, and we believe that scRNA or nuclease-free water injected zygotes should have been included as negative controls in this microarray experiment, so that the reported differential gene expression can be attributed only to RNAi-mediated suppression of MSX1. However, the expected RNAi effect due to injection of the anti-sense oligomers cannot be completely ruled out as blastocyst rates in zygotes injected with scRNA were significantly different from those in zygotes injected with LdsRNA and siRNA. Interestingly, even though statistically non-significant (due to a narrow margin of the P value), zygotic development to 8-cells in the scRNA-injected group was higher than that in SpisiRNA-injected groups, necessitating the need to consider the supposed biological implication.

The qRT-PCR showed that the mRNA expression of some of the differentially expressed genes was reduced compared with the non-injected controls but such differences appeared to be statistically non-significant. Although this is the case, the observed reduction in the mRNA expression level of these genes is believed to have significant biological effects as validated by protein expression data and the effect on oocyte maturation and cleavage rate due to suppression of MSX1. Additionally, the current gene expression data alone cannot be conclusive that the differentially expressed genes are targeted by MSX1. Therefore, there is a need for further
manipulation of the key gene products in order to identify proteins/pathways that are involved in this phenomenon. In conclusion, suppression of MSX1 affects oocyte maturation, embryo cleavage rate and potentially the expression of several genes, suggesting that it has a role in the development of bovine oocytes and preimplantation embryos.

Materials and Methods

Experimental design

This study was conducted using four treatment groups in experiments 1 and 2 and two treatment groups in experiment 3.

In experiment 1, microinjection of 341 bp LdsRNA, 19 bp siRNA and 19 bp scRNA was done at GV oocyte stage and developmental stage, and mRNA and protein expression data were collected at MI oocyte.

In experiment 2, microinjection of the same anti-sense oligomers was done at zygote stage. Development to 2-, 4- and 8-cells was assessed at 72 hpi, and that to blastocysts was assessed at 7 days post insemination. The mRNA expression level was determined at 8-cell stage, and protein expression was investigated at 2-, 4- and 8-cell stages.

In experiment 3, in order to investigate the cleavage rate of embryos and identify genes affected due to suppression of bovine MSX1, 10 μg/μl custom SpisRNAs consisting of four different siRNAs (Dharmacon, Inc.) were used to microinject the zygotes, and large-scale gene expression analysis was performed at 8-cell stage using a BlueChip bovine cDNA array.

Table 5 Details of primers that were used for qRT-PCR quantification and long double-stranded RNA (LdsRNA) synthesis.

<table>
<thead>
<tr>
<th>Gene name</th>
<th>Accession number</th>
<th>Primer sequences</th>
<th>Annealing temperature (°C)</th>
<th>Product size (bp)</th>
</tr>
</thead>
<tbody>
<tr>
<td>MSX1a</td>
<td>NM_174798</td>
<td>F: 5'-AGGGATCCATCACGTCCGCCGCGCT-3’&lt;br&gt;R: 5'-TCTGCTCCTCTGCTGCAAGATTC-3’</td>
<td>58</td>
<td>150</td>
</tr>
<tr>
<td>MSX1b</td>
<td>NM_174798</td>
<td>F: 5'-AGGAACAGTACCTGTCATCGG-3’&lt;br&gt;R: 5'-GGCCTTCTATGTCAGGTGTA-3’</td>
<td>56</td>
<td>341</td>
</tr>
<tr>
<td>MSX1c</td>
<td>NM_174798</td>
<td>F: 5'-GTAATACTGACTCTATAGG&lt;br&gt;AGAAGCAGTACCTGTCATCGG-3’&lt;br&gt;R: 5'-GTAATACGACTCTATAGG&lt;br&gt;GCCCTTCTATGTCAGGTGTA-3’&lt;br&gt;GCCCTTCTATGTCAGGTGTA-3’</td>
<td>57</td>
<td>191</td>
</tr>
<tr>
<td>MSX2</td>
<td>XM_592489</td>
<td>F: 5'-TCCTCTTTCATCCACACTCTTTC-3’&lt;br&gt;R: 5'-ACATCCATCTCCGCGGAC-3’</td>
<td>57</td>
<td>178</td>
</tr>
<tr>
<td>BMP15</td>
<td>AY304484</td>
<td>F: 5'-CTGAGACGAGTACCTGCAAGAC-3’&lt;br&gt;R: 5'-CTGCAACGAGCTGCGG-3’&lt;br&gt;AAGGACGAGCTGCGG-3’</td>
<td>60</td>
<td>396</td>
</tr>
<tr>
<td>PTTG1</td>
<td>NM_004219</td>
<td>F: 5'-GAAGGACGACGAGCTGCGG-3’&lt;br&gt;R: 5'-GTCAACGAAACAGTGGTGGA-3’&lt;br&gt;LdsRNA-3’</td>
<td>55</td>
<td>204</td>
</tr>
<tr>
<td>GAPDH</td>
<td>BC102589</td>
<td>F: 5'-ACCCGAGAGCTGTCAGTTGG-3’&lt;br&gt;R: 5'-AGCAGCCCCAAGCCT-3’&lt;br&gt;AAGCAGCCCCAAGCCT-3’</td>
<td>60</td>
<td>247</td>
</tr>
<tr>
<td>ALF</td>
<td>NM_006872</td>
<td>F: 5'-CTCTCTCTTGTGATGATTGCA-3’&lt;br&gt;R: 5'-CTCTCTCTTGTGATGATTGCA-3’&lt;br&gt;AAGCAGCCCCAAGCCT-3’</td>
<td>53</td>
<td>215</td>
</tr>
<tr>
<td>RIOK3</td>
<td>NM_003831</td>
<td>F: 5'-CTCAGCGTGAGTCCTCCGAG-3’&lt;br&gt;R: 5'-TCACTCTCCTCCAAGTGGCAG-3’&lt;br&gt;R: 5'-CTCAGCGTGAGTCCTCCGAG-3’</td>
<td>56</td>
<td>185</td>
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<tr>
<td>ZNF85</td>
<td>BC047646</td>
<td>F: 5'-GGGATCAATATCTCGGCTG-3’&lt;br&gt;R: 5'-TTCCTCTCTCTCCGCTG-3’&lt;br&gt;R: 5'-TTCCTCTCTCTCCGCTG-3’</td>
<td>54</td>
<td>105</td>
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<tr>
<td>PTGS2</td>
<td>AF031698</td>
<td>F: 5'-GGAATATCTCACCTCAGAC-3’&lt;br&gt;R: 5'-GTCATTGACCCGG-3’&lt;br&gt;R: 5'-GTCATTGACCCGG-3’&lt;br&gt;AAGCAGCCCCAAGCCT-3’</td>
<td>56</td>
<td>221</td>
</tr>
</tbody>
</table>

MSX1a, primers that were used for real-time quantification of MSX1 mRNA; MSX1b, primers that were used for synthesis of LdsRNA; MSX1c, primers that were used for double-stranded DNA amplification.

Synthesis of long double-stranded RNA

Pairs of primers (Table 5) were designed according to the bovine cDNA sequence found in gene bank using primer express software v 2.0 (Applied Bio Systems, Foster City, CA, USA) to amplify a fragment of bovine MSX1. Primer-generated PCR amplicon that corresponds to the coding sequence of MSX1 was identified, and the product was confirmed by sequencing. The first round of PCR was performed using thermocycler program at 95 °C for 5 min followed by 40 cycles of denaturing at 95 °C for 30 s and annealed at 56 °C for 30 s. Extension was done at 72 °C for 1 min, and a 10-min elongation step at 72 °C was performed after the last cycle. The same procedure was repeated for the second round of PCR using T7 promoter (GTAATACGACTCTATAGGG) attached to the 5’ end of each primer to generate two different templates for in vitro transcription of sense and anti-sense RNA strands. The DNA template coupled with T7 promoter was in vitro transcribed using RiboMaxTM large-scale RNA production systems (Promega), in which sense and anti-sense strands were transcribed from cDNA template in different reactions (Amdam et al. 2003). After in vitro transcription, the cDNA template was removed by digesting in RNase-free DNase at 37 °C for 15 min. Subsequently, sense and anti-sense RNA strands were annealed by incubating the reaction at 37 °C for 4 h to synthesise the LdsRNA (Wianny & Zernicka 2000). Following phenol/chloroform extraction, the RNA was precipitated with 0.1 ml of 3 M sodium acetate (pH 5.2) and 2.5 ml of 100% ethanol and was centrifuged at 800 g for 30 min, and the resulting pellet was washed with 70% ethanol. Finally, the LdsRNA pellet was resuspended in 10 μl nuclease-free water and concentration was measured. The LdsRNA was eluted in nuclease-free water.
to obtain a final concentration of 25 ng/µl and was stored at
−80 °C. The size and purity of the LdsRNA were evaluated on a
2% agarose gel electrophoresis.

**Oocyte recovery, in vitro maturation and IVF**

Bovine ovaries were collected from local slaughterhouse and
transported to the laboratory within 2–3 h in a thermo flask
containing 0.9% physiological saline solution (NaCl) at 39 °C.
Subsequently, cumulus–oocyte complexes (COCs) were aspi-
rated from follicles with a diameter of 2–8 mm using 5-ml
syringe attached to 18-gauge needle. COCs with evenly
granulated cytoplasm and multiple layer of cumulus cell
were picked using a glass pipette and washed three times in
drops of modified parker’s medium supplemented with 12%
oestrous cow serum (OCS). COCs were cultured in groups
of 50 in 400-µl maturation medium under mineral oil (Sigma)
in four-well dishes (Nunc, Roskilde, Denmark) for 22 h at 39 °C in
an incubator with humidified atmosphere containing 5% CO₂.
Based on the number of oocytes, 2–4 straws of semen collected
from known breeding bull were thawed, and motile sperma-
tozae were obtained by swim-up procedure (Parish et al. 1998).
After maturation, COCs were transferred into a four-well dish
containing 400 µl of fertilization medium (Fert-TALP) supple-
mented with 2 µg/ml heparin and 0.2 mM pyruvate (Sigma),
and 25 µl/men penicillin and hygromycin B was added to each
well to initiate sperm motility and was covered with mineral oil (Sigma). Finally, IVF was performed
using 1 × 10⁶ sperm cells for a group of 50 oocytes and
co-incubated for 20 h.

**In vitro culture of embryos**

Following IVF, presumed zygotes were gently vortexed to
separate them from the surrounding cumulus cells and dead spermatids. Cumulus-free zygotes were washed three times
and cultured in CR-1 aa culture medium (Rosenkrans & First
1994) supplemented with 10% OCS, 10 µM/ml BME (essential amino acids) and 10 µM/ml MEM (non-essential amino acids) for 8 days at 39 °C in an incubator with humidified atmosphere
containing 5% CO₂.

**Microinjection of oocytes and zygotes**

In addition to LdsRNA, 10 µg/µl siRNA S'GGG CCG AGU
UCU CCA GUU CUU-3' S'GAA CUG GAG AAC UCG GCG
CUU-3' and scRNA S'GGG CCU GUU CGU UCU CUA CGA CUU-3'
S'GUC GUA CGA GAA CCG GGU CUU-3' (Eurofins MWG
Operon, Ebersberg, Germany) were used for microinjection.
COCs with compact and multiple layers of cumulus cells and
evenly granulated cytoplasm were selected for microinjection
(Leibfried & First 1979) prior to partial removal of the surrounding cumulus cells to avoid difficulties during micro-
injections. Oocytes were held in Hepes-buffered Medium 199
supplemented with 0.1% BSA, 0.2 mM pyruvate and 50 µg/ml
gentamicin sulphate (Sigma) in a humidified atmosphere
containing 5% CO₂ at 39 °C. Prior to injection, oocytes were
incubated for 20 min in Hepes-buffered Medium 199 supple-
mented with 8 µg/ml cytochalasin B (Paradis et al. 2005). In four
experimental sessions, a total of 1408 GV stage oocytes were
randomly allocated to the four groups, namely non-injected
controls (n=298), scRNA injected (n=367), LdsRNA injected
(n=376) and siRNA injected (n=367). Zygotes were
injected 20 h after fertilization. Microinjection was performed
on an inverted microscope (Nikon TS-100) with a magnification
of 200X by aspirating the RNAs into a 0.5-µm diameter
injection capillary (Femtotjet II; Eppendorf, Hamburg,
Germany). Injection volume of ~7 pl was estimated from the
displacement of the meniscus of mineral oil in the capillary.
After microinjections, oocytes from all groups were washed
three times in CR-1aa medium, and set back into culture and
checked for survival 1 h after injection.

In experiment 2, a total of 2352 zygotes were randomly
allocated to four groups, namely non-injected controls
(n=445), scRNA injected (n=652), LdsRNA injected
(n=636) and siRNA injected (n=619). In experiment 3,
in order to assess the effect of SpsiRNAs on the development of
preimplantation embryos, additional pools of zygotes were
injected with SpsiRNAs (n=479), and scRNA (n=497) and
their cleavage rate were compared with non-injected control
(n=653). After assessing the effect of SpsiRNAs on the
development of embryos, a total of 600 zygotes were
microinjected (in three different microinjection sessions) using
10 µg/µl custom SpsiRNAs for global gene expression analysis.
After injection, all groups of zygotes were washed three times in
CR-1aa medium, and set back into culture medium (Rosenkrans & First
1994) supplemented with 10% OCS, 10 µM/ml BME (essential amino acids) and 10 µM/ml MEM (non-essential amino acids) for 8 days in experiment 2 and 72 hpi in experiment 3 at
39 °C in an incubator with humidified atmosphere containing
5% CO₂. The zygotes were checked for survival 2 h after
injection, and cleavage rates were assessed at 72 hpi.

**Collection of oocytes and embryos**

In order to study the effects of the injected anti-sense oligomers
on the relative abundance of the target mRNA and protein,
oocytes and embryos were collected at specific time point after
microinjection. In experiment 1, following phenotypic data
collection, matured oocytes were frozen for mRNA and protein
expression analysis 28 h post microinjection. In experiment 2,
zygotes were cultured until 8-cell (72 hpi) and day 8 blastocyst
(7 days post insemination) stages to assess developmental
phenotypes, mRNA and protein expression. Cumulus-free
zygotes were washed twice and cultured in CR-1aa culture
medium supplemented with 10% OCS, 10 µM/ml BME (essential
amino acids) and 10 µM/ml MEM (non-essential amino acids)
for 8 days in experiment 2 and 72 hpi in experiment 3 at
39 °C in an incubator with humidified atmosphere containing
5% CO₂. The zygotes were checked for survival 2 h after
injection, and cleavage rates were assessed at 72 hpi.

**RNA isolation and RT**

Three pools of biological replicates each containing ~30 ML
zygotes and 24 8-cell stage embryos from each treatment
group were used for mRNA isolation. mRNA was isolated using oligo
Quantification of mRNA levels using qRT-PCR

The ABI prism 7000 apparatus (Applied Biosystems) was used to perform the quantitative analysis using SYBR Green incorporation for dsDNA-specific fluorescent detection dye. For this, both MSX1 and MSX2 genes were quantified using sequence-specific primers. Standard curves were fitted for both target and internal control gene, GAPDH, using serial dilutions of plasmid DNA containing $10^{1}$ to $10^{4}$ molecules and were run in separate wells. During each reaction, samples from the same cDNA were run in duplicate to control the reproducibility of the results. Final quantitative analysis was done using the relative standard curve method, and the results were reported as mean percentage values using the non-injected control group as calibrator, for which the mRNA expression levels were reported as mean percentage values using the non-injected control group as calibrator, for which the mRNA expression levels were assigned 1 or 100%.

Statistical analysis

The normalised mRNA expression and developmental data were analysed by ANOVA, and the mean values were compared for statistical significance using Tukey test (SPSS Inc., Chicago, IL, USA). Differences were considered statistically significant at $P \leq 0.05$.

Immunofluorescence staining

MII oocytes were obtained after 22 h in vitro maturation of GV stage oocytes and zygotes, 2-, 4- and 8-cells were collected at 20, 32, 48 and 72 hpi respectively for immunofluorescence staining. Ten individual MII oocytes, zygotes, 2-, 4- and 8-cell stage embryos from each treatment group were washed three times in PBS and fixed in 4% (w/v) paraformaldehyde overnight at 4°C. The fixed specimens were permeabilised during 2.5-h incubation in 0.5% (v/v) Triton-X100 (Sigma) in PBS. In order to inhibit non-specific binding of the antibodies, samples were subsequently blocked in 3% (w/v) BSA in PBS for 1 h. The oocytes and embryos were then incubated for 1 h at 39°C with 1:100 dilution of rabbit anti-human polyclonal MSX1 primary antibody (Lifespan Biosciences, Inc., Seattle, WA, USA).

Oocytes and embryos were washed three times in PBS and further incubated for 1 h with 100× diluted FITC-conjugated anti-rabbit IgG secondary antibody (Sigma). Negative controls were processed in the same manner by omitting the use of primary antibody. In order to visualise the nucleus of the cell, oocytes and embryos were finally incubated in 0.5 mg/ml propidium iodide (Sigma). After the final wash in PBS, oocytes and embryos were mounted on glass slides and visualised on a confocal laser scanning microscope (CLSM LSM-510; Carl-Zeiss, Jena, Germany).

Large-scale gene expression analysis

RNA amplification

In order to identify the differentially expressed genes due to suppression of MSX1, large-scale gene expression analysis was done using a BlueChip bovine cDNA array (Sirard et al. 2005). First- and second-strand cDNAs were synthesised as described in our previous study (El-Sayed et al. 2006). Ten amplification cycles were used during second-strand cDNA synthesis to increase the representativeness of the original RNA population after in vitro transcription. The synthesised cDNA was then purified and used for in vitro transcription using AmpliScribe T7 transcription kit (Epicentre Technologies, Oldendorf, Germany) according to the manufacturer's instructions. Then, the amplified RNA (aRNA) was purified using RNeasy Mini kit (Qiagen) and eluted in 30 µl RNase-free water, from which 8 µl were taken to estimate the yield and purity of aRNA through gel electrophoresis and spectrophotometric analysis at A260/280 using Ultrospec 2100 pro u.v./Visible Spectrophotometer (Amersham Bioscience).

Aminoallyl labelling and dye coupling

Minimum Information About Microarray Experiments guidelines were followed in the experimental design. Two independent labelling reactions were carried out per aRNA sample pertinent to each biological replicate for dye-swap hybridizations. Accordingly, 3 µg of aRNA from each pool of 8-cell embryos were used as a template in RT reactions incorporating amino-modified dUTPs into the cDNA using the CyScribe Post-Labeling Kit (Amersham Biosciences) as described previously (El-Sayed et al. 2006). The cDNA samples from each treatment groups were differentially labelled indirectly using N-hydroxysuccinate-derived Cy3 and Cy5 dyes and incubated for 1.5 h at room temperature in darkness. At the end of incubation, non-reactive dyes were quenched by adding 15 µl of 4 M hydroxylamine solution (Sigma) and incubated for 15 min at room temperature in darkness. To avoid variation due to dye coupling, aRNA samples from the same treatment group were labelled reversibly with either Cy3 or Cy5 for dye-swap hybridizations.

Probe hybridization, scanning and data analysis

Pre-hybridization of the slides was performed by placing the array slides into a corning GAPS II slide container as described in El-Sayed et al. (2006). Hybridization and post-hybridization
procedures and washes were carried out as previously described elsewhere (Hegde et al. 2000) with slight modifications as indicated in our previous report (Ghanem et al. 2007). The slides were scanned using Axon GenePix 4000B scanner (Axon Instruments, Foster City, CA, USA). The GenePix Pro 4.0 software (Axon Instruments) was used to capture the images, find spots, integrate robot-spotting files and finally create reports of spot intensity data. LOWESS normalization of microarray data was performed using GProcessor 2.0a software (http://bioinformatics.med.yale.edu/group). The normalised data were used to calculate the intensity ratios of all replicates and to obtain one value per clone. Ratios were finally transformed to log2 and submitted to significance analysis for microarray (SAM). The resulting data were analysed using SAM software (http://www-stat.stanford.edu/~tibs/SAM). The true differential expression of genes was validated at false discovery rate <5% and P value <0.05, and a clone with a fold change value ≥1.5 in the microinjection treatment groups compared with the controls was considered differentially expressed.

Custom Chip bovine cDNA array (Sirard et al. 2005) with ~2000 clones representing known genes and expressed sequence tags was used in this study. The glass slide contains 4928 spots divided into two sub-arrays. Each sub-array is composed of 2304 randomly selected clones obtained from four different subtraction suppressive hybridizations (SSHs) made using bovine embryos and tissues (First SSH: GV oocytes subtracted from somatic tissues, second SSH: GV oocytes subtracted from day 8 blastocysts, third SSH: day 8 blastocysts subtracted from GV oocytes and fourth SSH: day 8 blastocysts subtracted from somatic tissues). All the clones were spotted in each sub-array using four replicates per slide. Eleven more samples namely empty (32 spots), alien1 (8 spots), alien2 (8 spots), GFP (4 spots), GFP1 (4 spots), GFP1/2 (4 spots), GFP1/4 (4 spots), GFP1/8 (4 spots), GFP 1/16 (4 spots) and H2O/DMSO (50 spots) were spotted to be used as negative controls for determination of hybridization background during the statistical analysis. Housekeeping genes including tubulin (8 spots), ubiquitin (8 spots), b-actin (6 spots) and actin (8 spots) were also added as positive controls.

Identification of functional modules

Enrichment analysis of MSX1 target genes with respect to functional modules was performed with the Consensus Pathway Database which integrates the content of twelve different pathways and interaction databases that carry information of various heterogeneous levels of information such as signalling, protein–protein interactions and metabolic reactions (http://cpdb.molgen.mpg.de). Interactions were mapped to each other by identifier mapping (Kamburov et al. 2009). Functional modules were identified by creating gene sets (NESTs) from the integrated interaction graph. Significance of enrichment with respect to set of NESTs was judged with p-values derived from the hypergeometric distribution.

Supplementary data

This is linked to the online version of the paper at http://dx.doi.org/10.1530/REP-09-0312.

Declaration of interest

The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

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References


