Blastocyst implantation failure relates to impaired translational machinery gene expression

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Abstract

Oocyte quality is a well-established determinant of embryonic fate. However, the molecular participants and biological markers that affect and may predict adequate embryonic development are largely elusive. Our aim was to identify the components of the oocyte molecular machinery that take part in the production of a healthy embryo. For this purpose, we used an animal model, generated by us previously, the oocytes of which do not express Cx43 (Cx43del/del). In these mice, oogenesis appears normal, fertilisation does occur, early embryonic development is successful but implantation fails. We used a magnetic resonance imaging analysis combined with histological examination to characterise the embryonic developmental incompetence. Reciprocal embryo transfer confirmed that the blastocyst evolved from the Cx43del/del oocyte is responsible for the implantation disorder. In order to unveil the genes, the impaired expression of which brings about the development of defective embryos, we carried out a genomic screening of both the oocytes and the resulting blastocysts. This microarray analysis revealed a low expression of Egr1, Rpl21 and Eif4a1 in Cx43del/del oocytes and downregulation of Rpl15 and Eif4g2 in the resulting blastocysts. We propose that global deficiencies in genes related to the expression of ribosomal proteins and translation initiation factors in apparently normal oocytes bring about accumulation of defects, which significantly compromise their developmental capacity. The blastocysts resulting from such oocytes, which grow within a confined space until implantation, may be unable to generate enough biological mass to allow their expansion. This information could be implicated in diagnosis and treatment of infertility, particularly to IVF.


Introduction

It is well established that oocyte quality has a major impact on the fate of pregnancy (Krisher 2004). However, the molecular participants that determine the properties of an oocyte remain largely unknown and biological markers that may predict its chances to develop into a healthy embryo are practically unavailable. Moreover, even when oogenesis along with folliculogenesis seems to be completed successfully, there are apparently some, hitherto unidentified, specific processes occurring within the oocyte that are required for acquisition of developmental competence. These processes, collectively defined as cytoplasmic maturation (Eppig 1996, De Sousa et al. 1998), may be essential for the successful development of the embryo before and after activation of the zygotic genome. Developmental incompetence is frequently associated with aneuploidy (Baird et al. 2005). Additive causes of oocyte developmental incompetence include inappropriate oocyte metabolism (Lane & Gardner 2000), disturbed ion transport and faulty mitochondrial function (Krisher 2004, Dumollard et al. 2007).

Beyond intraoocyte factors, developmental competence is greatly influenced by the ability of the ovary to supply the oocyte with nutrients facilitating its growth (Eppig 1996). Cell-to-cell communication in the ovarian follicle is established by gap junctions during fetal life (embryonic day 11.5 (Perez-Armendariz et al. 2003)) and persists throughout the later stages of follicular growth (Mitchell & Burghardt 1986). These channels also facilitate the supply of cAMP (Dekel et al. 1981) as well as cGMP (Norris et al. 2009, Vaccari et al. 2009), maintaining the oocyte in meiotic arrest. A gap junction channel consists of two connexons, each comprising six connexin (CX) proteins (Unger et al. 1999) that are
Docked in the plasma membrane of closely apposed cells (Sosinsky & Nicholson 2005). Several Cxs have been detected in the ovarian follicles of different species, among which the indispensability of connexin 37 (Cx37, encoded by the gene Gja4) and connexin 43 (Cx43, encoded by the gene Gja1) has been demonstrated (Gittens & Kidder 2005, Gershon et al. 2008a). In a model of Cx37 knockout (KO) mouse, both germ cell development and ovarian folliculogenesis were arrested at an early stage (Simon et al. 1997). In order to circumvent postnatal lethality in mice that lack Cx43 (Reaume et al. 1995), ovariess removed from Cx43 KO mice prenatally, were allowed to further develop either in vitro, in organ culture, or in vivo, under the kidney capsule of WT mice. Under both experimental conditions, folliculogenesis in Cx43-deficient ovaries did not proceed beyond the primary follicle stage, and oocyte growth was retarded. Furthermore, oocytes recovered from these grafts failed to resume meiosis and could not be fertilised (Juneja et al. 1997, Ackert et al. 2001).

In an attempt to direct the depletion of Gja1 to the oocyte, we used previously the cre-loxP strategy (Gershon et al. 2008b). In this study, we crossed females that carry a Cx43 coding region, flanked by loxP recognition sites, with males expressing the Cre recombinase under the control of Zp3 promoter. Oocytes of the resultant Zp3Cre;Gja1lox/lox female mice did not express Cx43 and were referred to as Cx43del/del. Although a decrease in Cx43 was also observed in the cumulus/granulose cells of some of the follicles as well, the Zp3Cre;Gja1lox/lox mice ovulated mature fertilisable oocytes. However, their mating with WT males resulted in a reduced rate of parturition and a substantial decrease in litter size that was apparently attributed to implantation failure of the blastocysts.

The subfertility of Zp3Cre;Gja1lox/lox females may represent an impaired quality of the Cx43del/del oocytes, suggesting that those processes within the oocytes that are essential for acquisition of developmental competence may require the expression of Cx43. However, the failure of such processes to occur can also be secondary to the reduced expression of Cx43 in the cumulus/granulose cells that result in inadequate cell-to-cell communication. These processes may include mRNA transcription, protein translation and post-translational modifications. Yet, the oocytes that reside in this follicular Cx43-defective environment developed into blastocysts, which are unable to implant effectively. The exact mechanism that underlies this implantation failure was unresolved. Nevertheless, this animal model represents a particular example of oocytes that seem to undergo normal oogenesis according to standard morphological and functional parameters, but are developmentally incompetent. In the present study, we employed the Zp3Cre;Gja1lox/lox mouse model generated by us previously. We hypothesised that an impaired gene expression might be responsible for the development of the defective embryos. In an attempt to unveil these genes, we carried out a genomic screening of both the oocytes and the resulting blastocysts. We herein provide evidence that oocyte developmental incompetence is associated with global defects in ribosomal proteins, translation initiation factors and other genes associated with cellular biosynthetic and metabolic processes. These genes are apparently dispensable for normal oogenesis, fertilisation and early embryonic development, but may affect the ability of the blastocysts to progress beyond this embryonic stage.

Materials and methods

Animals

Transgenic, C57BL/6-Tg(Zp3-cre)3Mrt/J male mice expressing the Cre recombinase, under the control of Zp3 promoter (de Vries et al. 2000), were purchased from Jackson Laboratories (Bar Harbor, ME, USA). The Cx43lox/lox mice (Theis et al. 2001) were kindly provided by Klaus Willecke, University of Bonn, Germany. The Zp3Cre;Gja1lox/lox females were previously generated in our laboratory (Gershon et al. 2008b). Mice were maintained on a 12 h light:12 h darkness cycle. All animal experiments were approved by the Weizmann Institutional Animal Care and Use Committee.

Animal treatment

Sexually immature 23-day-old female mice received 5 IU of pregnant mare’s serum gonadotropin (PMSG Chrono-gest Intervet, Boxmeer, The Netherlands) for stimulation of follicle development. Ovulation was induced by injecting 5 IU of human chorionic gonadotropin (hCG, Chrono-gest Intervet) 48 h after PMSG administration. The animals were killed by cervical dislocation 24 h later and the ovulated oocytes arrested at the second metaphase (MII) were collected from the oviductal ampulla. To achieve pregnancy, 25-day-old, PMSG/hCG-treated female mice were housed overnight with males and examined the next morning for the presence of a vaginal plug. This day of pregnancy is defined as embryonic day 0.5 (E0.5). Pseudopregnancy was achieved by mating the PMSG/hCG-treated females with vasectomised males of proven sterility.

Genotype analysis

Genomic DNA from mouse tail was extracted using the Direct PCR Kit (Viagen, Los Angeles, CA, USA) according to the manufacturer protocol. The PCR conditions for genotyping the Cx43-locus transgene in the Zp3Cre;Gja1lox/lox mice were described previously (Gershon et al. 2008b). The PCR conditions for genotyping the Cre recombinase transgenic in Zp3-Cre mice were described previously (Lan et al. 2004).

In vivo contrast-enhanced magnetic resonance imaging studies

Contrast-enhanced magnetic resonance imaging (MRI) experiments were carried out on a horizontal 4.7 T Bruker Biospec spectrometer (Bruker, Karlsruhe, Germany) as previously...
described (Plaks et al. 2006). In brief, at the pregnancy days indicated (E4.5, E5.5 and E9.5), the females were anesthetised by an i.p. injection of 75 mg/kg ketamine (keta); Fort Dodge Laboratories, Fort Dodge, IA, USA) combined with 3 mg/kg xylazine (2% Xylen; VMD, Arendonk, Belgium). A series of variable-flip-angle precontrast T1-weighted 3D gradient-echo (3D-GE) images were acquired, after which, a bolus of BSA-based macromolecular contrast material, biotin-BSA-Gd-DTPA (3D-GE) images were acquired, after which, a bolus of BSA-based macromolecular contrast material, biotin-BSA-Gd-DTPA (biotin3-BSA-Gd-DTPA33; about 82 kDa), was injected through a tail vein catheter (18 mg/mouse in 0.2 ml PBS).

For dynamic postcontrast imaging, T1-weighted 3D-GE images were acquired from the time of biotin-BSA-Gd-DTPA administration and up to 15 min. At the end of the MRI session, Evans blue (Sigma; 1% w/v in saline, 100 μl) was intravenously injected via the tail vein and allowed to circulate for 10 min to enable ex vivo detection of implantation sites.

**Histology**

Uteri were fixed in Carnoy’s solution (BDH Chemicals, Radnor, PA, USA) for 24 h and paraffin embedded. Cross sections of 5 μm were mounted on slides. The sections were then stained by haematoxylin and eosin (H&E) or processed for immuno-fluorescence analysis as described later.

Quantification of decidualisation was performed on sections with the widest decidual diameter using the (ImageJ software, http://imagej.nih.gov/ij/). Staining intensity was measured in absolute counts. The average intensity was calculated by the ratio of the signal to the area of the region of interest.

**Immunohistochemistry**

Immunohistochemistry was carried out as described previously (Israely et al. 2003, Plaks et al. 2006). Briefly, uterine samples with implantation sites were fixed in Carnoy’s solution, sectioned serially at 4 μm thickness, and stained by H&E or processed for immuno-fluorescence analysis as described later.

RT analysis

Total RNA was extracted from oocytes and blastocysts using Trizol reagent according to manufacturer protocol (Sigma). RNAs at the implantation sites were extracted using the EZ RNAII Kit,

### Table 1 PCR primers list.

<table>
<thead>
<tr>
<th>Gene</th>
<th>Forward primer</th>
<th>Reverse primer</th>
<th>Tm (°C)</th>
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<td>GGAAGTCTGCTCTG3CAT</td>
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</tr>
<tr>
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<td>CCGTCAGGCTTATGGTTAC</td>
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<tr>
<td>β-actin</td>
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Table 2 Real-time PCR primers list.

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<th>Reverse primer</th>
<th>Tm (°C)</th>
</tr>
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<td>Eif4A1</td>
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<td>GCTATCCACATCTGCTCCCA</td>
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<td>TGGAGATGCAATTCTGTTG</td>
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<td>CTTGGAGATGCTGGCGCTTC</td>
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<tr>
<td>Eif4G</td>
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<tr>
<td>B2M</td>
<td>CCCCATTGAACATGGCATTGTA</td>
<td>TTATGTCAGGGCGATTTTC</td>
<td>55</td>
</tr>
</tbody>
</table>
according to manufacturer protocol (Biological Industries, Kibbutz Beit Haemek, Israel). RT was carried out by mixing 1 μg RNA with 4 μl of MMLV-RT 5× reaction buffer (Promega), 10 mM dNTP, 0.5 μg oligo (dT)12-18 (Promega), 40 units of RNasin (Promega), 200 units of Moloney murine leukemia virus reverse transcriptase (M-MLV Reverse transcriptase, Promega) and 3 μl DDW. This mixture was incubated at 37 °C for 2 h.

**PCR**

The cDNAs generated by the protocol mentioned earlier were used for PCR amplification, with primer sets for Cre-Zp3, Cx43, Gjb2 and β-actin (Table 1) in a 25 μl reaction volume with 10 mM Tris–HCl (pH 9.0), 50 mM KCl, 0.1% Triton X-100 (Promega), 2.5 mM MgCl2, 400 μM each d-NTP and 0.625 units of Taq DNA Polymerase (Promega). The PCR was carried out by initial denaturation at 94 °C for 3 min, then 20–35 cycles at 94 °C for 1 min followed by 55 °C for 1 min, 72 °C for 1 min, and a final incubation at 72 °C for 7 min. The number of cycles used ensured that the reaction could be quantified within the log phase of the amplification reaction.

The reaction mix (24 μl) was run on a 1.5% agarose gel stained with ethidium bromide and quantified using UV imaging (Gel Doc 1000, Bio-Rad) and Molecular Analyst software (Bio-Rad). Each sample was analysed in triplicates. Band density of Cx43 and Gjb2 was quantified using the ImageJ software.

**Embryo collection and transfer**

For the recovery of eight-cell embryos, superovulated females mated with males and examined for vaginal plugs the following morning (0.5 days post-coitum, d.p.c), were killed on 2.5 d.p.c. The blastocysts, developed in vitro after 24 h of incubation, were transferred to the uteri of 2.5 d.p.c pseudopregnant females (8–10 blastocysts per uterine horn). At the end of pregnancy, the number of neonates was monitored.

**Isolation and hybridisation of RNA for microarray analysis**

For isolation of RNA from oocytes, blastocysts and implantations site, the PerfectPure RNA Cultured Cell Kit (5 Prime, Hamburg, Germany) including DNase 1 digestion and depleted of rRNA was used. Two different pools of samples from each experimental group were processed as recommended by the manufacturer.

**Figure 1** Characteristics of the implantation disorder of embryos originating from Zp3Cre;Gja1lox/lox oocytes. Dynamic contrast-enhanced Magnetic resonance imaging DCE-(MRI) of pregnant female mice on E5.5. Representative MRI images show fewer implantation sites (indicated by arrows) in Zp3Cre;Gja1lox/lox (b) compared with WT (a) mice. Arrowheads in figures (c and d) indicate implantation sites. The number of implantation sites correlates well with that detected ex vivo (inserts) ov, ovaries (n=3 females of each genotype). Representative images of histological longitudinal sections of implantation sites recovered from pregnant WT (c and d, n=4) and Zp3Cre;Gja1lox/lox (e and f, n=5) mice on E5.5. Note that in Zp3Cre;Gja1lox/lox females decidualisation is weak (e). Arrowhead in figure 1e indicate weak decidualisation and embryo resorptions are observed (f). Arrowhead in figures 1f indicate resorption site, dec, decidua; res, resorption. Quantification of decidualisation in Zp3Cre;Gja1lox/lox compared with WT mice (g). Asterisk in figure 1g indicate significant difference between WT and Zp3Cre; Gja1lox/lox (P<0.05). Histological longitudinal section of implantation sites of E4.5 WT (h) and Zp3Cre;Gja1lox/lox (j and k, n=4) mice. Arrowhead in figures 1c, d, h, i, j, k indicate embryo. Note that the Zp3Cre;Gja1lox/lox embryo has a delayed implantation phenotype, as no implantation chamber has formed, decidualisation is weak and embryo is in the blastocyst stage (j). dec, decidua; ue, uterine epithelium. Size bars for c, e, h, j=500 μm, size bar for d, f, i, k=100 μm.
Quantitative PCR

All real-time PCR analyses were carried out on a Rotor-Gene 3000 (Corbett Research, Sydney, NSW, Australia), using the Absolute QPCR Master Mix (ABgene, Surrey, UK) with SYBR Green. Reaction protocols had the following format: 15 min at 95 °C for enzyme activation, followed by 40 cycles of 15 s at 95 °C, 30 s at 60 °C and 15 s at 72 °C, at the end of fluorescence was measured with the Rotor-Gene. SYBR Green I assays also included a melt curve at the end of the cycling protocol, with continuous fluorescence measurement from 65 to 99 °C. All reactions contained the same amount of cDNA, 10 µl Absolute QPCR Master Mix, primers for the indicated genes (Table 2) and UltraPure PCR-grade water (Fisher Biotec, Subiaco, WA, Australia) to a final volume of 20 µl.

Each real-time PCR analysis included a no-template control as well as five or six serial fourfold dilutions, in duplicate, of a cDNA pool containing all experimental samples of the respective tissue. The prenormalised DNA quantity of each gene in every sample was estimated relative to this dilution series. This dilution series also served to assess the reaction performance (E and r²). The threshold cycle (Ct) was set so as to obtain the highest reaction efficiency and correlation coefficient.

Statistical analysis

Each experiment was carried out at least three times, with samples pooled from at least three to four mice. Data points are presented as mean ± S.E.M. Statistical significance was evaluated using Student’s two-tailed unpaired t-test (Microsoft Excel).

Results

Characteristics of the implantation disorder of embryos originating from Cx43del/del oocytes

Our previous study (Gershon et al. 2008b) showed that Zp3Cre;Gja1lox/lox females mated with WT males, produce a reduced number of embryos which traces back to a failure at the stage of embryo implantation. In the present study, using conventional ex-vivo examination, after i.v. injection of Evans blue, complemented by macro-molecular dynamic contrast-enhanced magnetic resonance imaging (DCE-MRI; Plaks et al. 2006), we wished to further map this subfertility to a particular stage of implantation. For this purpose, we employed a macromolecular MR-contrast material that selectively extravagates from areas of high permeability, allowing non-invasive detection of implantation sites, which was followed by a detailed histological examination.

Our previous report showed a significant reduction in the number of implantation sites in Zp3Cre;Gja1lox/lox females compared with WT (Gershon et al. 2008b). We extended this study demonstrating herein that an average of six implantation sites is detected by dynamic contrast-enhanced magnetic resonance imaging (DCE-MRI; Plaks et al. 2006) in a E5.5 Zp3Cre;Gja1lox/lox pregnant mice compared with 11 in the WT (Fig. 1a and b, n = 3). The data generated by MRI correlate well with that obtained by ex vivo analysis of the same mouse after i.v. injection of Evans blue (Fig. 1a and b, inserts).
Upon examination of uterine histological sections, a heterogeneous phenotype was found as follows. At E5.5, the WT decidua was expanded (Fig. 1c and d, n = 12) while in the Zp3Cre;Gja1lox/lox decidualisation was 70% weaker (this phenotype was observed across implantations sites in four out of four females, Fig. 1e, f and g). Moreover, resorptions were observed in the Zp3Cre;Gja1lox/lox (this phenotype was observed across implantations sites in five females, Fig. 1f). In addition, in the E4.5 WT mice, the embryos reached the egg cylinder stage and the stromal tissue proliferated and differentiated into the decidua (Fig. 1h and i, this phenotype was observed across implantations sites in four out of four females). On the other hand, implantation sites of Zp3Cre;Gja1lox/lox females, examined at E4.5, exhibited weak decidualisation, no implantation chamber and embryos that were still in their blastocyst stage (this phenotype was observed across implantations sites in four females, Fig. 1j and k). On E9.5 (Fig. 2), the reduction in the number of Zp3Cre;Gja1lox/lox implantation sites vs WT was maintained. In both WT (Fig. 2a and b) and Zp3Cre;Gja1lox/lox (Fig. 2c and d), existing implantation sites looked normal (Fig. 2e), although histological sections revealed that some of the embryos in the Zp3Cre;Gja1lox/lox were going through resorption (Fig. 1f, i and g). In Zp3Cre;Gja1lox/lox females, the embryos that appears normal probably proceeded till birth as no defects were observed in Zp3Cre;Gja1lox/+ neonates (three pups in each group were visually examined and two pups in each group, male and female, had their vital organs examined for possible pathologies in histological sections, data not shown).

**Decidual proliferation is intact but decidual differentiation is impaired in Zp3Cre;Gja1lox/lox implantation sites**

As can be seen using immunostaining with Ki67, proliferation of stromal tissue (as it converts into the decidua) was not significantly different between WT (Fig. 3a, b and e) and Zp3Cre;Gja1lox/lox implantation sites (Fig. 3c, d and e). The expression of specific Cxs in the endometrium is one of the earliest physiological changes derived from

![Figure 3](image_url)

*Figure 3* Decidual differentiation is impaired in Zp3Cre;Gja1lox/lox implantation sites. Representative images of immunostaining of Ki67 (brown) show no difference in proliferation of stromal tissue (as it converts to the decidua) between implantation sites of E4.5 WT (a and b, a total of three mice with an average of 11 implantation sites per female) vs Zp3Cre;Gja1lox/lox mice (c and d, a total of three mice with six implantation sites per female). Quantification of proliferation in Zp3Cre;Gja1lox/lox compared with WT mice (e). Representative images of confocal microscopy of E4.5 implantation sites sections show a substantial decrease in Cx43 expression (green) in the decidua and in Gjb2 (red) expression in the uterine epithelium of Zp3Cre;Gja1lox/lox (f) compared with WT females (g). Nuclei are stained with TO-PRO-3 (blue). e, embryo; ue, uterine epithelium; dec, decidua. Size bars for a, c = 200 µm, for b, d = 50 µm and for e, g = 150 µm. RT-PCR analysis of Cx43, Gjb2 Zp3-Cre recombinase and β-actin (h and i) in implantation sites of WT and KO samples (recovered from Zp3Cre;Gja1lox/lox mice). The results of one representative out of a total of three independent experiments (each including a pool of implantation sites from three mice) with similar results are presented.
foeto–maternal interactions (Winterhager et al. 1993). Therefore, the expression of Cx43 in the decidua and that of Cx26 in the uterine epithelium was examined (Fig. 3f and g). The expression of Cx43 mRNA in the decidua was reduced by 50% in Zp3Cre;Gja1lox/lox compared with WT females (Fig. 3h and i). There was also a 30% reduction in Cx26 expression in Zp3Cre;Gja1lox/lox females compared with WT (Fig. 3h and i). Note that Cx43 reduction was not due to a non-specific expression of Cre recombinase in the implantation sites (Fig. 3h, first two lanes).

Defects in the embryo rather than in the mother are responsible for the implantation disorder in the Zp3Cre;Gja1lox/lox females

To further substantiate the crucial factor that causes implantation failure, reciprocal embryo transfer experiments were carried out: Zp3Cre;Gja1lox/lox+ embryos were transferred to WT females and vice versa. These experiments revealed that Zp3Cre;Gja1lox/lox females bearing WT embryos gave birth to normal litters as compared with the poor birth rate obtained in the reciprocal experiment (n = 5 females for each experimental group in three independent experiments, Table 3).

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<tr>
<th>Females</th>
<th>Pups</th>
<th>Average (pups/female)</th>
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<tbody>
<tr>
<td>No.</td>
<td>Genotype</td>
<td>No.</td>
</tr>
<tr>
<td>5</td>
<td>WT</td>
<td>1</td>
</tr>
<tr>
<td>5</td>
<td>Zp3Cre;Gja1lox/lox</td>
<td>27</td>
</tr>
</tbody>
</table>

Three independent experiments.

Gene expression analysis of the Zp3Cre;Gja1lox/lox model suggests that the implantation failure of the resulting blastocysts is associated with impaired ribosomal and translational machinery

In order to identify the components of the oocyte molecular machinery that take part in the production of a healthy embryo, we screened the transcriptome in the Zp3Cre;Gja1lox/lox model (KO) vs the control (WT). The experimental design included sampling of RNA of ovulated oocytes at MII (n = 120 per replicate), early blastocysts (washed from the uterus just before implantation, n = 37 per replicate) and E5.5 implantation sites (consisting of the implanted embryos surrounded by maternal uterine tissue, n = 4–5 per replicate from three mice per biological replicate) (Fig. 4a). The data was analysed to find differentially expressed genes by comparing the WT and KO samples in each tissue (oocytes, blastocysts, and implantation sites). A general view at the data set using principal component analysis (PCA) shows the differences between the various samples analysed. This analysis revealed that the largest difference between our KO model and WT seems to be in the blastocysts samples (Fig. 4b). After identifying the differentially expressed genes, we used DAVID web tool (Huang da et al. 2009) for enrichment analysis. The differentially expressed genes in each tissue were divided into either upregulated (KO>WT) or down-regulated (KO<WT) genes, and then analysed for enrichment of biological processes and pathways (Fig. 5). Importantly, we noticed the involvement of translation-related events (e.g. ribosomes) as well as metabolic-related processes in the MII oocytes and blastocysts. Since the implantation sites represent mostly maternal tissue, which was shown not to be the detrimental factor in the implantation disorder of the Zp3Cre;Gja1lox/lox blastocysts, the number of differentially expressed genes was smaller between KO and WT in these samples and enrichment analysis shows no significance.

A significant down regulation of transcripts related to translation, such as ribosomal proteins and eukaryotic translation initiation factors (EIFS), was found mainly in the Cx43 del/del (KO) MII oocytes as well as in the resulting blastocysts. This was accompanied by a significant global reduction in the gene expression of the Cx43 del/del (KO) MII oocytes and the resulting blastocysts, indicating a major impairment of the translational machinery.

Real-time quantitative PCR was carried out to validate specific candidates of the differentially expressed genes. This analysis revealed that Egr1, Rpl21 and Eif4a1 were significantly downregulated in the Cx43 del/del MII oocytes (Fig. 6a, Egr1 P = 0.0047, Rpl21 P = 7.5 × 10⁻4, Eif4a1 P = 0.0464).
Eif4a1 \( P = 0.0024 \) and that Rpl15 and Eif4g2 were significantly downregulated in Zp3Cre;Gja1lox/lox blastocysts (Fig. 6b, Rpl15 \( P = 0.048 \), Eif4g2 \( P = 0.042 \)). The differences in expression levels shown by the PCR confirmed those found in the array analysis.

We also decided to trace back the findings concerning impaired translation to the point of Cx43 deletion by the Zp3-Cre, i.e. day 3 postnatal. We therefore compared ovaries from neonates on postnatal days 2–3, 5 and 15 with ovaries of 25-day-old female mice after hormonal stimulations and postovulation, as well as to the ovulated MII oocytes. First, we verified that Cx43 is not expressed along all the developmental stages tested (Fig. 6c). Next, we examined the expression levels of Rps6, a major ribosomal protein. We found that a significant reduction in translational and metabolic machineries.

Eif4a1 was observed in Zp3Cre;Gja1lox/lox females. However, this reduction was not observed in WT females. The differences in expression levels of Rps6 were significant, as determined by the PCR. The expression levels of Rps6 were significantly lower in Zp3Cre;Gja1lox/lox females than in WT females. We also observed that the expression levels of Rps6 were significantly lower in Zp3Cre;Gja1lox/lox blastocysts than in WT blastocysts. Therefore, the expression levels of Rps6 in Zp3Cre;Gja1lox/lox blastocysts were significantly lower than in WT blastocysts.

We present herein a particular example of oocytes that undergo normal oogenesis according to standard morphological and functional parameters but give rise to defective blastocysts. We demonstrate, for the first time, that failure of blastocysts that originate from such oocytes to implant is apparently due to a critical shutdown in the translational and metabolic machineries.

Unlike the oocytes of the systemic Cx43 KO mice, which never expressed Cx43, the deletion of Cx43 in our model occurs postnatally, around day 3, at the age at which the Zp3 gene is expressed and Cre recombinase is activated (Chaddha et al. 2004). Therefore, the oocytes and the ovarian follicle cells in our model do express Cx43 throughout the prenatal life, as well as during the first 3 postnatal days, an age at which folliculogenesis proceeds to the primary stage (Epifano et al. 1995) (Schematic Fig. 7; red boxes mark stages of oocyte and embryonic development at which Cx43 is present). Nevertheless, embryos originating from such oocytes exhibited implantation disorders. Our present findings combined with previous reports of the phenotype of systemic Cx43 KO (Juneja et al. 1999, Ackert et al. 2001) reveal that the time
at which Cx43 depletion takes place plays a crucial role in the acquisition of developmental competence by the oocyte. The fact that the systemic Cx43 KO mice suffer a severe impairment of follicle development and retarded oocyte growth, whereas folliculogenesis and oogenesis in the Zp3Cre;Gja1lox/lox mice appear normal, is apparently attributable to the relatively delayed time point of Cx43 depletion in our model. Furthermore, this may be the reason that, unlike the oocytes recovered from the ovaries of the systemic Cx43 KO, oocytes in our model resume meiosis, can be fertilised and successfully undergo early embryonic development. Nevertheless, this late depletion in follicular Cx43 still leads to subfertility, which in our case is manifested by the development of blastocysts that appear morphologically normal but exhibits retarded implantation abilities. On the contrary, a Cx43 KO embryo is a result of Cx43 heterozygous mating. Oocytes from such mating will lose the single copy of Cx43 only after the first polar body extrusion, which occurs much later than in the Cx43 KO oocytes recovered from the fetal ovaries of the systemic Cx43 KO and also later than in the Zp3Cre;Gja1lox/lox model presented here. The outcome of the oocyte from a heterozygous Cx43 mating, even though fertilised by a sperm already missing the single Cx43 copy, is still far better, as evidenced by the fact that the resulting foetus proceeds throughout pregnancy and dies from cardiac malfunction at birth (Reaume et al. 1995). Table 4 summarises these differences between the various models. This table shows that the time at which Cx43 depletion takes place plays a crucial role in the acquisition of developmental competence by the oocyte.

Most importantly, we show herein that the apparently normal Cx43del/del MII oocytes, as well as the resulting blastocysts exhibit global perturbations in the profile of transcripts regulating protein synthesis. Transcripts and proteins of the oocyte may be involved in cellular processes critical for successful development of the embryo before and after activation of the zygotic genome. For example, blastocyst formation in the mouse is dependent on oocyte transcripts and proteins (De Sousa et al. 1998), generated during the growth phase, that function after fertilisation to support and regulate pre-implantation embryonic development. In fact, in vitro matured human and bovine oocytes have been shown to have reduced protein content compared with in vivo matured oocytes (Trounson et al. 2001), suggesting that proteins play a critical role in the acquisition of developmental competence (Baird et al. 2005).
Enrichment analysis of the differentially expressed genes in our present study indicated a strong perturbation in the translation/ribosomal machinery. One of the main genes examined in the oocytes that was found to be significantly reduced in the Zp3Cre;Gja1lox/lox vs WT was early growth response 1 (Egr1). This gene was already shown to be critical to female fertility. Knocking out Egr1 gene in mice resulted in female infertility, although in this case it was due to LH deficiency in the pituitary (Lee et al. 1996). This gene was also shown to be induced in rat ovaries in response to an ovariolytic dose of hCG (Espey et al. 2000) and to regulate the expression of the rat LH receptor gene (Yoshino et al. 2002). Moreover, granulosa cells Egr1 mRNA was previously identified to be associated with bovine oocyte developmental competence (Robert et al. 2001). These data suggest that the impaired acquisition of developmental competence observed in our study could possibly be attributed to Cx43 depletion-modulated Egr1 expression.

A significant reduction in numerous ribosomal proteins was exhibited in both oocytes and blastocysts. It was previously shown that ribosomal proteins have a substantial impact on the control of global gene expression and subsequent mouse embryonic development and that mutations in a single ribosomal protein may have detrimental effects (Kondrashov et al. 2011). Focusing on representative differentially downregulated candidates, we verified the expression of ribosomal protein L (Rpl) 21 in the Cx43del/del (KO) MI oocytes and Rpl15 in the resulting blastocysts. Rpl21 mRNA is expressed during Xenopus embryogenesis and functions as a translational regulator (Loreni et al. 1992). Rpl15 is expressed during bovine meiotic maturation and embryogenesis. The mRNA of Rpl15 decreases during bovine oocytes meiotic maturation and increases in the morula and blastocyst stages of bovine embryogenesis (Bettegowda et al. 2006). This gene is upregulated in bovine follicular cystic ovaries and is probably responsible for the delayed regression with persistent follicle growth (Choe et al. 2010). We further suggest that Cx43 depletion modulate also ribosomal proteins expression affecting acquisition of developmental competence by the oocyte as well.

Along with the findings mentioned earlier, elf4 translation initiation factors were also differentially expressed in both Cx43 KO oocytes and in the resulting blastocysts. Elf4 are effectors of mRNA recruitment to ribosomes and regulators of translation (Gingras et al. 1999). Elf4a1, which has an RNA helicase activity, and Elf4g2, which performs a ribosome/mRNA bridging function (Gingras et al. 1999), are representative for these regulators in oocytes and blastocysts, respectively. Both Elf4a1 and Elf4g were found to be associated with the translation machinery in embryo divisions after fertilisation. Each of them is co-localised with the RNA-binding protein SAM68 in the zygote cytoplasm during translation inhibition (Paronetto et al. 2008) and plays roles in cell divisions (Hutchins et al. 2004). This data suggest that the reduced expression of the elf4 family members in the Cx43-depleted oocytes and the resulting blastocysts might disturb cell division, providing at least a partial explanation for the impaired fertility in Zp3Cre;Gja1lox/lox females.

The impaired developmental capacity of the Cx43del/del oocytes can possibly represent the lack of Cx43 within the oocyte, as well as inadequate transfer of nutrients from the follicular somatic cells also partially depleted from Cx43. Actually, Cx43 has been shown as a major contributor to gap junctions in human cumulus cells and its expression level was positively correlated with intercellular conductance, embryo quality and pregnancy rate (Wang et al. 2009). Regulation of nutrient metabolism in the oocyte may be critical to create an environment supportive of nuclear and cytoplasmic maturation (Gardner et al. 2000). Glucose metabolism is essential in the control of meiosis in mouse oocytes (Downs 1995). Exposure of oocytes to elevated glucose concentrations during the
maturation period may cause deleterious effects in the resulting embryo. High glucose levels during mouse preimplantation embryo development caused metabolic anomalies, resulting in diminished ATP stores, increased oxygen radicals, and altered gene expression, leading to apoptosis and malformations in the resulting foetus (Leunda-Casi et al. 2001). We also examined the expression of genes related to translation as well as to (glucose) metabolism during early ovarian and oocyte development (from days 2–3 postnatal, the time at which Cx43 is first depleted), such as ribosomal protein S6 (Rps6). A critical role of Rps6 in mouse embryo development is long established (Meyuhas 2008). Recent studies have been beginning to disclose a critical role of Rps6 in a signalling network involved in the regulation of cell size (Meyuhas & Dreazen 2009). Although many links and effectors are still unknown, central components of this network include the mammalian target of rapamycin and its downstream effectors, the ribosomal protein S6 kinase (S6K) and the translational repressor EIF4e-binding protein (Magnuson et al. 2012). A knockout in mouse carrying mutations at all phosphorylation sites in the primary S6K substrate, Rps6, has provided insights into the physiological role of this protein phosphorylation. In addition to its role in glucose homeostasis in the whole mouse, phosphorylation of Rps6 was shown to be essential for regulating the size of at least some cell types (Ruvinsky & Meyuhas 2006). Rps6 phosphorylation is a determinant of cell size and glucose homeostasis. Embryo fibroblasts from mice lacking phosphorylated Rsp6 are significantly smaller than controls and display an increased rate of protein synthesis and accelerated cell division (Ruvinsky et al. 2005).

In summary, based on the current data showing a low expression of ribosomal proteins and translation initiation factors such as Egr1, Rpl21 and Eif4a1 in Cx43 depleted mouse oocytes and Rpl15 and Eif4g2 in the resulting blastocysts, we argue that the mouse oocyte accumulates defects during the growing phase, which significantly compromise its developmental capacity. These implications take into account the differentially expressed genes related to the translational machinery and metabolism. It seems that the blastocysts resulting from such oocytes, which grow within a confined space until implantation, are unable to generate enough biological mass to allow its expansion. Nevertheless, the possibility that Cx43 depletion in the oocyte might also lead to an inadequate transfer of nutrients from the follicular somatic cells into the oocytes cannot be ruled out. This in turn could affect acquisition of developmental competence and the subsequent impaired embryo development.

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


