Seasonal effects on gene expression, cleavage timing, and developmental competence of bovine preimplantation embryos

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Abstract

We examined the association between season and expression of genes involved in early embryonic development with an emphasis on cleavage rate and timing of the first embryonic cleavage. In Exp. 1, oocytes were aspirated during the cold (Dec–Apr) and hot (May–Nov) seasons. Matured oocytes were chemically activated and cultured in vitro. The developmental peak to the two- and four-cell stages occurred earlier, with a higher proportion of first-cleaved embryos, during the cold season relative to the hot season (P<0.01). In Exp. 2, a time-lapse system was employed to characterize the delayed cleavage noted for the hot season. Cleavage to the two-cell stage occurred in two distinct waves: early cleavage occurred between 18 and 25 h post activation, and late cleavage occurred between 27 and 40 h post activation. In Exp. 3, oocytes were aspirated during the cold and hot seasons, matured in vitro, fertilized, and cultured for 8 days. In each season, early- and late-cleaved two-cell stage embryos were collected. Total RNA was isolated, and semi-quantitative and real-time PCRs were carried out with primers for GDF9, POU5F1, and GAPDH using 18S rRNA as the reference gene. In both seasons, the expression of all examined genes was higher (P<0.05) in early- versus late-cleaved embryos. POU5F1 expression was higher (P<0.05) in early-cleaved embryos developed in the cold season versus the hot season counterparts. The findings suggest a deleterious seasonal effect on oocyte developmental competence with delayed cleavage and variation in gene expression.

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Introduction

Reduced reproductive performance of lactating cows during the summer has been well documented and mostly attributed to the sensitivity of the ovarian tissues to elevated temperature (Wolfenson et al. 2000, Roth et al. 2008). Hyperthermia can directly disrupt follicular function (Roth et al. 2000) as expressed by altered follicular development, depressed dominance, and impaired follicular steroidogenesis and gonadotropin secretion (Wolfenson et al. 2000). Alternatively, perturbation in the physiology of the follicle-enclosed oocyte can potentially lead to its reduced competence for fertilization and subsequent development.

Mammalian oocytes are arrested in the prophase stage of the first meiotic division, and acquire their meiotic competence and fertilization potential in a stepwise manner (Masui 2001). As a result, they are potentially exposed to various environmental stressors during follicular development. Oocytes harvested from cows during the summer exhibit reduced embryonic developmental competence following IVF (Rocha et al. 1998, Al-Katanani et al. 2002) or chemical activation (Zeron et al. 2001). A seasonal study, performed from late summer to early winter, indicated that a period of two to three estrous cycles is required for recovery from heat damage and appearance of competent oocytes (Roth et al. 2001). Similarly, induction of maternal hyperthermia in mice carried over through three pregnancy cycles (Aroyo et al. 2007), suggesting that not only the individual ovulated oocyte, but also the ovarian pool of oocytes can be damaged during heat exposure. Nevertheless, the mechanism underlying the disruption in oocyte developmental competence is not entirely clear, and therefore, the changes that occur at the molecular and cellular levels in the oocytes in response to heat stress need to be investigated further.

Changes in gene expression are an integral part of the cellular response to heat shock. While the genes encoding heat shock proteins (HSPs) have been best studied, it has recently become apparent that thermal stress also affects a substantial number of genes which are not directly associated with HSPs (Sonna et al. 2002). Therefore, the current study examines the association between seasons and the expression of genes playing an essential role during oogenesis, folliculogenesis, or early embryonic development. Among these genes is growth differentiation factor 9 (GDF9), a germ-cell marker and...
member of the large transforming growth factor β superfamily (TGFβ; McPherron & Lee 1993). GDF9 plays a pivotal role in folliculogenesis since homozygous knockout female mice are sterile due to blockage of follicles at the primary stage (Dong et al. 1996). It also regulates cumulus cell function in the preovulatory period (Gui & Joyce 2005), and therefore, it might be involved in oocyte maturation. Another examined gene is POU5F1 (also known as OCT4), a member of the POU family of transcriptional activators which contain the DNA-binding POU domain (Ryan & Rosenfeld 1997). The POU5F1 gene is essential for the maintenance of totipotency/pluripotency in embryonic stem cells and primordial germ cells: a progressive loss of POU5F1 has been associated with loss of pluripotency (Okamoto et al. 1990, Yeom et al. 1996). The current study examines the association between elevated temperature and expression of genes involved in oocyte maturation early in embryonic development, with an emphasis on cleavage timing of the two first embryonic developmental deviations.

Results

Experiment 1: seasonal effects on cleavage timing and developmental competence of bovine oocytes following chemical activation

Oocytes were collected during the cold (n = 2218) and hot (n = 3198) seasons. The number of follicles (3–8 mm in diameter) per ovary collected during the cold season was higher than that collected in the hot season (29.0 ± 1.0 vs 24.0 ± 1.0 respectively; P < 0.03). The average number of oocytes aspirated in the cold season was higher than that aspirated in the hot season (8.5 ± 0.5 vs 6.0 ± 0.5 respectively; P < 0.01). The proportion of parthenotes that cleaved to the two- to four-cell stage was higher in the cold season than in the hot season (72 ± 0.9 vs 46 ± 0.8% respectively; P < 0.01). The developmental peak of the two-cell stage embryo was higher (39 vs 21%; P < 0.01) and occurred earlier (22–27 vs 40 h post activation; Fig. 1A) in the cold versus hot season respectively. Similarly, the developmental peak of the four-cell stage was higher (33 vs 21%; P < 0.01) and occurred earlier (46–52 vs 52–70 h post activation; Fig. 1B) in the cold versus hot season respectively.

Experiment 2: using time-lapse system to evaluate the accurate cleavage timing

This experiment was performed during two consecutive hot seasons using a time-lapse system. In the first year, 137 bovine oocytes, in two replicates, were examined (Fig. 2A). In the second year, 171 oocytes, in four replicates, were examined (Fig. 2B). Time-lapse examination of the first embryonic division revealed that during the hot season, embryos cleave in two distinct waves. The first cleavage wave occurred between 18 and 25 h post activation, and the second cleavage wave occurred between 26 and 42 h post activation.
Experiment 3: seasonal variation in gene expression in two-cell stage embryos

The percentage of embryos developed to the blastocyst stage was higher in the cold season than in the hot season (23.0 ± 2.3 vs 9.0 ± 3.5% respectively; *P* < 0.05). The percentage of embryos that cleaved to the two- to four-cell stage (42 h post fertilization) did not differ between seasons (80.0 ± 4.5 vs 73.3 ± 3.2% respectively; Fig. 3). However, the proportion of two-cell stage embryos recorded in the hot season was twofold higher than that of the four-cell stage embryos, suggesting a delay in the second embryonic division (Fig. 4). In addition, the proportion of embryos developed to the four-cell stage (42 h post fertilization) was higher in the cold season than in the hot season (Fig. 4).

Seasonal effect on gene expression in two-cell stage embryos

Examination of gene expression in both early (27 h post fertilization) and late (42 h post fertilization) first-cleaved embryos (i.e. two-cell stage embryos) revealed higher expression of GDF9 and POU5F1 in the early- versus late-cleaved embryos in both the cold and hot seasons (Figs 5A and B and 6A and B). With respect to GAPDH, while semi-quantitative PCR did not reveal any differences in its expression between early- and late-cleaved embryos (Figs 5A and 6A), real-time PCR, which is a more sensitive method, demonstrated a significant difference (Figs 5B and 6B). Therefore, GAPDH was not used as a reference gene for PCR analysis. Instead, the 18S rRNA gene was used as an internal reference since it was expressed at similar levels in both early- and late-cleaved embryos, in both seasons. A comparison of gene expression in early-cleaved embryos revealed higher expression of POU5F1 in the cold versus hot season, without any effect on GDF9 or GAPDH expressions (Fig. 7). No seasonal variations in gene expression were noted for late-cleaved embryos (data not shown).

Discussion

Season-induced disruption in the developmental competence of bovine oocytes appears to involve more than one mechanism. The current study indicates that the adverse effect of summer thermal stress on embryonic development is associated with seasonal variation in the expression of genes involved in oocyte maturation and early embryonic development. These alterations were also associated with delayed cleavage of the two first cell stages.

Figure 3 Seasonal effects on oocyte developmental competence. The proportion of oocytes cleaved to the two- to four-cell stage, 42 h post fertilization, and the proportion of embryos that developed to the blastocyst stage 8 days post fertilization are presented. Data are presented as means ± S.E.M.; a,b different superscripts indicate seasonal effect within embryonic stages, *P* < 0.05.

Figure 4 Seasonal variation in embryonic-stage distribution. The proportion of oocytes that were fertilized and cleaved to two- and four-cell stages at 42 h post fertilization is presented. Data are presented as means ± S.E.M.; a,b different superscripts indicate seasonal effect between and within embryonic stages, *P* < 0.05.

Figure 5 Transcript levels of GDF9, POU5F1, and GAPDH in both early- (27 h post fertilization (PF)) and late-cleaved (42 h PF) embryos to the two-cell stage in the cold season. Data from semi-quantitative PCR (A) and real-time PCR (B) are presented as means ± S.E.M.; a,b different superscripts indicate cleavage timing effect within genes, *P* < 0.05.

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embryonic deviations and decreased embryonic development to the two- and four-cell stage followed by a reduced proportion of embryos developing to the blastocyst stage.

**Early cleavage and cleavage timing**

Findings of the present study indicated delayed cleavage timing for both bovine parthenotes (Exp. 1) and in vitro derived embryos (Exp. 3) which developed from oocytes collected during the hot season. In the cold season, the developmental peak to the two-cell stage was higher and occurred about 13 h earlier than that in the hot season. A similar delay was found for the second deviation to the four-cell stage, as expressed by the twofold higher proportion of two-cell stage embryos versus four-cell stage embryos at 42 h post fertilization. Early stages of embryonic development are key parameters in predicting which embryos will have high developmental competence. Early cleavage and the time of the first mitotic division are considered to be indicative of embryo quality, in particular of whether the embryo is transferable (Hasler et al. 1995, Shoukir et al. 1997, Sakkas et al. 1998) or competent to survive cryopreservation (Hasler et al. 1995, Van Montfoort et al. 2004). Indeed, the timing of the first divisions (Shoukir et al. 1997, Sakkas et al. 1998) and of the formation of an eight-cell embryo (Edwards et al. 1984) or blastocyst (Shoukir et al. 1998, Schwarzler et al. 2004) are used as valuable means of narrowing the number of embryos selected for transfer or cryopreservation. It has been reported that embryo evaluation based on sequential assessment, which takes several development stages into account, appears to be superior to the selection of the best embryos at a specific time point (Gardner & Sakkas 2003, Neuber et al. 2003). Therefore, the delayed cleavage timing noted in the current study throughout the hot season might suggest a seasonal reduction in oocyte developmental competence.

A recent study in which the time-lapse system EmbryoGuard was used to determine the accurate cleavage timing of mouse embryos suggested that the time of the first embryonic cleavage to the two-cell stage, rather than further embryonic divisions, predicts developmental competence of embryos (Arav et al. 2008). The time-lapse system facilitates continuous noninvasive monitoring of embryos while maintaining them under optimal culture conditions in the incubator. Use of this system in the current study made it possible to collect accurate data on cleavage timing of the entire embryo population without examining embryos at subjectively selected time points, as performed in Exp. 1. In vitro studies have shown a clear relationship between early cleavage and developmental competence of bovine embryos (Lonergan et al. 1999). It has also been demonstrated that early-cleaved embryos have significantly higher cell numbers and better embryo morphology (van Soom et al. 1997, Rieger et al. 1999). Use of the EmbryoGuard system enabled us to accurately define the time at which bovine oocytes are cleaved. Cleavage to the two-cell stage was found to occur in two distinct waves: early cleavage occurred between 18 and 25 h post activation and late cleavage occurred between 26 and 42 h post activation. Although the experiment was performed only during the hot season, the
information was highly valuable in collecting early- and late-cleaved embryos to examine seasonal effects on gene expression (Exp. 3).

Our results provided evidence of higher gene expression (GAPDH, GDF9, and POU5F1) in early-versus late-cleaved embryos, in both cold and hot seasons, suggesting a differential pattern of maternal gene expression which is tightly associated with cleavage timing. GAPDH is one of the most common ‘housekeeping’ genes, widely used to normalize gene data in various procedures, including quantitative and real-time PCR. Nevertheless, it has recently been reported that the transcription levels of GAPDH vary among cell types (Barber et al. 2005), developmental stages (Robert et al. 2002), and experimental conditions (Ito et al. 1996, Zhong & Simons 1999), emphasizing the need to validate housekeeping genes for each examination. In the current study, two genes were considered for use as the internal control gene, GAPDH, and 18S rRNA. Our findings indicated that whereas the expression of 18S rRNA was stable, that of GAPDH differed between early- and late-cleaved embryos, with a lower level in the latter. This was true for both hot and cold seasons. Similarly, Mamo et al. (2007) showed higher expression of GAPDH in early- versus late-cleaved in vivo derived mouse embryos. However, Dode et al. (2006) reported constant expression of GAPDH in early- and late-cleaved bovine embryos. GAPDH plays a key role in energy metabolism. It is one of the enzymes that catalyze reactions in the glycolytic pathway, in particular converting glyceraldehyde-3-phosphate to 1,3-diphosphoglycerate (Sirover 1999). GAPDH also plays a role in cellular functions which are not related to glycolysis. These include membrane fusion (Robbins et al. 1995, Hesser et al. 1998), DNA repair (Baxi & Vishwanatha 1995), nuclear RNA export (Zhang & Snyder 1992, Singh & Green 1993), cytoskeletal organization (Launay et al. 1989, Walsh et al. 1989), phosphotransferase activity (Kawamoto & Caswell 1986, Engel et al. 1998), and apoptosis (Ishitani & Chuang 1996, Ishitani et al. 1997, Tajima et al. 1999). Therefore, reduced GAPDH expression or, alternatively, alterations in one or more of these GAPDH activities might underlie the reduced developmental competence of late-cleaved embryos. This, might explain, at least in part, the reduced developmental competence of bovine oocytes during the hot season.

Reduced expression of GDF9 was also noted for late-cleaved two-cell stage embryos in both hot and cold seasons. Studies of mutant mice (Dong et al. 1996, Carabatsos et al. 1998) and GDF9-modified sheep (Hanahan et al. 2004) have indicated that GDF9 plays an important role in the stimulation of early follicular growth. Female mice lacking a functional GDF9 gene were infertile and characterized by arrested follicular growth at the primary stage (Dong et al. 1996). In fact, GDF9 transcript is highly expressed in immature oocytes while they are enclosed in antral follicles, but decreases throughout early embryonic development, with only trace levels at the eight-cell stage (Penmetier et al. 2004). Therefore, it is suggested that seasonally induced alterations in GDF9 expression are involved in the reduced developmental competence noted for oocytes collected in the hot season. GDF9 is involved in the regulation of both oocyte and granulosa cell function at a very early stage of follicular development in rats (Vitt et al. 2000). In cattle and sheep, GDF9 mRNA is expressed in the primordial and subsequent stages of developing follicles (Bodensteiner et al. 1999). GDF9 has also been defined as a mitogenic factor since it stimulates proliferation of theca cells derived from small follicles of bovine (Spicer et al. 2008). Thus, it is possible that the seasonally induced alteration in GDF9 expression in the ovarian pool of follicles and/or their enclosed oocytes, as observed here, underlies the immediate and carry-over effect of summer thermal stress on follicular function and oocyte developmental competence recently reported for bovine (Roth et al. 2008). Likewise, maturation of mouse oocytes with exogenous GDF9 improves further embryonic development and fetal viability (Yeoo et al. 2007). While not examined here, impairment in the cooperative functioning of TGFB superfamily proteins, bone morphogenetic protein 15, with GDF9 to maintain cumulus–oocyte complexes (COCs) integrity cannot be ruled out (Su et al. 2004).

Interestingly, while the expressions of GAPDH and GDF9 did not differ among the subpopulation of early-cleaved embryos, those that developed during the hot season expressed lower levels of POU5F1. POU5F1 is known to activate or repress the transcription of various target genes, such as FGF4, ZP42 (REX-1), SPPI (OPN), UTF1, hCG, and IFNT, during early embryonic development (Curatola & Basilo 1990, Liu & Roberts 1996, Liu et al. 1997, Ben-Shushan et al. 1998, Botquin et al. 1998, Nishimoto et al. 1999, Ezashi et al. 2001). Up- or downregulation of POU5F1 can induce changes in developmental programs (Niwa et al. 2000). In mice, ablation of POU5F1 causes early embryonic lethality, since blastomeres are differentiated to trophectoderm rather than to inner cell mass (ICM; Nichols et al. 1998), indicating involvement of POU5F1 in the establishment of pluripotency. POU5F1 also plays a role in maintaining mammalian germline viability since primordial germ cells lacking POU5F1 expression have been shown to undergo apoptosis instead of differentiation (Kehler et al. 2004). A critical amount of POU5F1 protein is required to sustain embryonic stem cells: increasing its expression by less than twofold causes differentiation into primitive endoderm and mesoderm. Reparation of POU5F1 induces loss of pluripotency and dedifferentiation to trophectoderm (Niwa et al. 2000). In in vitro derived bovine embryos, POU5F1 transcription is expressed throughout the early developmental stages of pre-implantation embryos with high expression in immature
oocytes up to the four-cell stage, followed by down-regulation from the eight-cell stage to the morula, and relatively higher transcript at the blastocyst stage (Nganvongpanit et al. 2006). In contrast to mice (Palmieri et al. 1994, Kircof et al. 2000) and humans (Hansis et al. 2000), in bovine and porcine embryos, POU5F1 is not restricted to the ICM: it is present in both the ICM and the trophectoderm (Kircof et al. 2000). Taken together, low expression of POU5F1 in early-cleaved embryos supports the assumption that these embryos are of inferior quality. Furthermore, seasonal alteration in POU5F1 in early-cleaved embryos might explain, in part, the decrease in blastocyst development observed in the hot season (current study) and the concomitant reduced reproductive performance of dairy cows (Al-Katanani et al. 2002). In addition, POU5F1 plays a role as an anti-apoptotic factor (Guo et al. 2007), and therefore, a reduction in POU5F1 expression might impair the balance between pro- and anti-apoptotic factors, which in turn might lead to increased apoptotic cells upon heat stress, as previously reported for bovine oocytes and pre-implantation embryos (Roth & Hansen 2004a, 2004b).

In summary, delayed embryo cleavage was prominent during the hot season, indicating that during the summer, a high proportion of oocytes are of low developmental competence. Development and growth of embryos depend upon maternal mRNA and proteins stored in the oocyte. Thus, it is reasonable to assume that heat-induced alteration in the ovarian pool of oocytes affects the expression pattern of genes involved in early embryonic development, which in turn leads to a high proportion of late-cleaved embryos and reduced blastocyst formation.

Materials and Methods

All chemicals, unless otherwise specified, were purchased from Sigma–Aldrich. FSH and the ovine pituitary extract Ovagen were purchased from ICP Bio (Auckland, New Zealand). TriZol reagent, superscript II, Dynabeads mRNA DIRECT kit and nonessential amino acids (NEAAs) were purchased from Invitrogen. RNasin oligo(dT)_12–18, moloney murine leukemia virus (M-MLV) RT, dNTPs, and RQ1 RNase-free DNase were purchased from Promega. 5× TBE buffer (53 g of Tris base, 27.5 g of boric acid, and 20 ml of 0.5 M EDTA (pH 8.0) and diethylpyrocarbonate (DEPC)-treated water were purchased from Biological Industries (Beit-Haemek, Israel). DynNAmo qPCR kit was purchased from Zotal (Espoo, Finland). Double distilled water was purchased from Merck, and the culture media HEPES-Tyrode’s lactate (TL), SP-TL, and IVF-TL were prepared in our laboratory: HEPES-TL was supplemented with 0.3% (w/v) BSA, 0.2 mM sodium pyruvate, and 0.75 mg/ml gentamicin (HEPES-TALP); SP-TL was supplemented with 0.6% BSA, 1 mM sodium pyruvate, and 0.2 mg/ml gentamicin (SP-TALP); IVF-TL was supplemented with 0.6% essential fatty acid-free BSA, 0.2 mM sodium pyruvate, 0.05 mg/ml gentamicin, and 0.01 mg/ml heparin (IVF-TALP; Parrish et al. 1986). Oocyte maturation medium (OMM) was made up of TCM-199 with Earle’s salts supplemented with 10% (v/v) heat-inactivated FCS (Bio-Lab), 0.2 mM sodium pyruvate, 50 μg/μl gentamicin, 1.32 μg/ml ovine FSH, and 2 μg/ml estradiol; potassium simplex optimized medium (KSOM) contained 95 mM NaCl, 2.5 mM KCl, 0.35 mM KH₂PO₄, 0.2 mM MgSO₄-7H₂O, 0.8% (v/v) sodium lactate, 0.2 mM sodium pyruvate, 0.2 mM dl-glucose, 25 mM NaHCO₃, 1 mM l-glutamine, 0.01 mM EDTA and 0.01 mM phenol red supplemented with 1.7 mM CaCl₂, 2H₂O, 0.1 mg/ml polynylin alcohol, 10 μl/ml essential amino acids and 5 μl/ml NEAAs, 100 U/ml penicillin-G and 0.1 mg/ml streptomycin.

In vitro production of embryos

Oocyte recovery and in vitro maturation

Bovine oocytes were obtained from a local abattoir from multiparous Holstein cows during the hot and cold seasons, and transported to the laboratory in physiological saline solution (0.9% (w/v) NaCl at 37 °C) with 50 μg/ml penicillin–streptomycin. The oocytes were transferred to the laboratory within 60–90 min, washed with fresh saline, cut through the center, and placed over a transillumination stand, so that follicles could be easily visualized (Arav 2001). COCs were aspirated from 3- to 8-mm follicles with an 18-gauge needle attached to a 10-ml syringe. COCs with at least three layers of cumulus surrounding a homogeneous cytoplasm were selected for further processing. After selection, COCs were washed three times in HEPES-TALP, and groups of ten oocytes were transferred into 50-μl droplets of OMM overlaid with mineral oil. The droplets containing COCs were incubated in humidified air with 5% CO₂ for 22 h at 38.5 °C.

Chemical activation of oocytes

Activation was performed (Exp. 1 and Exp. 2) as previously described by Zeron et al. (2001). Matured oocytes were denuded from the cumulus cells and placed for 5 min in 2.47 μM ionomycin dissolved in TCM-199 supplemented with 25 mM HEPES, 10% (v/v) heat-inactivated FCS, 0.2 mM sodium pyruvate, and 5 μg/ml gentamicin. Oocytes were then transferred to 2.45 μM 6-dimethylaminopurine dissolved in TCM-199 for 4.5 h to prevent extrusion of the second polar body, thereby creating a diploid parthenogenetic embryo. Oocytes were washed three times in IVF cleavage medium (Cook, Sydney, Australia) and transferred in groups of 10 into 50-μl droplets of OMM overlaid with mineral oil. Embryos were cultured at 38.5 °C, 5% CO₂, 5% O₂, and 95% humidity (ThermoForma Model 3110, Thermo Scientific, Marietta, OH, USA).

IVF

Matured COCs were washed three times in HEPES-TALP and transferred in groups of 30 oocytes to four-well plates containing 600 μl IVF-TALP and 25 μl of PHE (0.5 mM penicillamine, 0.25 mM hypotaurine, and 25 μM epinephrine in 0.9% (w/v) NaCl) per well and fertilized with ~1×10⁶ Percoll-purified spermatozoa from frozen–thawed semen. Spermatozoa were co-incubated with COCs for 18 h at 38.5 °C in a humidified atmosphere with 5% CO₂.
In vitro culture

After fertilization, putative zygotes were removed from the fertilization wells, denuded of cumulus cells by gentle vortexing in HEPES-TALP containing 1000 U/ml hyaluronidase, and randomly placed in groups of 10 in a 25-μl droplet of KSOM. All embryo droplets were overlaid with mineral oil and cultured for 8 days at 38.5 °C in an atmosphere of humidified air with 5% CO₂ and 5% O₂.

The EmbryoGuard system

The EmbryoGuard system (IMT Ltd, Ness Ziona, Israel) is a robotic device enabling real-time monitoring of embryo dynamics without disturbing culture conditions, i.e. temperature, air composition, and humidity. It comprises an inverted microscope, charge-coupled device cameras, and a light source. The optical system is placed on a mobile optical table that can move along the X and Y axes as well as the Z axis for focusing of all lenses. Embryos can be observed at three different magnifications: 4×, 200×, and 1000×. Automatic time-lapse photographs can be taken at specific preset intervals, and are saved in a database for subsequent analysis. The camera optics enable both automatic continuous time-lapse photography and real-time microscopic observation of individual embryos (Arav et al. 2008). In the current study, the unit was programmed to collect images at 60-min intervals. Culture dishes were placed in the tissue-culture incubator unit was programmed to collect images at 60-min intervals.

Gene quantification

Sample collection

Embryos were collected at specific cleavage times based on the EmbryoGuard data (Exp. 2): two-cell stage embryos collected at 27–28 h post fertilization were defined as early-cleaved embryos, while those collected at 42–43 h post fertilization were defined as late-cleaved embryos. For each group of embryos, four replicates were taken from different in vitro production runs, washed in PBS, snap frozen in liquid nitrogen, and stored at −80 °C until RNA extraction. Each sample for RNA extraction contained ten embryos at the two-cell stage.

Semi-quantitative RT-PCR

Total RNA was extracted from each sample by TRIzol reagent according to the manufacturer’s instructions (Invitrogen) with slight modifications. Briefly, 500 μl of TRIzol reagent with 1 μg glycogen as the carrier were added to each sample. After centrifugation with chloroform (100 μl), RNA was recovered (upper aqueous phase), precipitated with isopropanol, washed twice with ethanol, and dried for 5 min. After extraction, the RNA pellet was resuspended in 8 μl DEPC water and treated with DNase I according to the manufacturer’s instructions (Promega) to remove any DNA contamination. Isolated RNA was reverse-transcribed into cDNA in a total volume of 20 μl. The first step of the RT was incubation at 72 °C with 500 ng oligo(dT)12–18 for 10 min followed by incubation for 60 min with RT mix, containing M-MLV RT, 5× M-MLV-RT buffer, 200 μM dNTPs, 20 U of RNasin, and 3 μl of DEPC water. This mixture was incubated at 40 °C for 1 h.

The cDNAs were used for separate PCR amplification with primer sets (10 μM each) for GDF9, POU5F1, GAPDH, and 18S rRNA in a 25-μl reaction volume. The PCR program consisted of an initial denaturation step at 95 °C for 5 min followed by 35 cycles at 95 °C for 30 s, 55 °C for 30 s, 72 °C for 30 s, and a final extension at 72 °C for 10 min. Primer sequences, size of the amplified products, and GenBank accession numbers are provided in Table 1. The RT-PCR product (18 μl) with 3 μl of 6× loading buffer (0.25% (w/v) xylene cyanol and 25 mmol EDTA/l in 50% (w/v) glycerin) was loaded onto a 1.5% (w/v) agarose gel in TBE buffer containing 0.25% (w/v) xylene cyanol and 0.25% (w/v) bromide. After electrophoresis at 80 V for 60 min, the fragments were visualized on a 312-nm u.v. transilluminator. Scion-Image software (Frederick, MD, USA) was used to quantify the signal intensity of each band (data not shown).

Real-time PCR

Poly(A) RNA was isolated using Dynabeads mRNA DIRECT kit according to the manufacturer’s instructions (Invitrogen). In brief, embryos were lysed by adding 100 μl lysis-binding buffer. Prewashed oligo(dT)125 Dynabeads (20 μl) were added to each sample for reverse transcription. cDNA synthesis was performed using 200 ng oligo(dT)12–18 Dynabeads and 500 ng random primers according to the manufacturer’s instructions (Invitrogen). The cDNAs were used for separate PCR amplification with primer sets (10 μM each) for GDF9, POU5F1, GAPDH, and 18S rRNA in a 25-μl reaction volume. The PCR program consisted of an initial denaturation step at 95 °C for 5 min followed by 35 cycles at 95 °C for 30 s, 55 °C for 30 s, 72 °C for 30 s, and a final extension at 72 °C for 10 min. Primer sequences, size of the amplified products, and GenBank accession numbers are provided in Table 1. The RT-PCR product (18 μl) with 3 μl of 6× loading buffer (0.25% (w/v) xylene cyanol and 25 mmol EDTA/l in 50% (w/v) glycerin) was loaded onto a 1.5% (w/v) agarose gel in TBE buffer containing 0.2 μg/ml ethidium bromide. After electrophoresis at 80 V for 60 min, the fragments were visualized on a 312-nm u.v. transilluminator. Scion-Image software (Frederick, MD, USA) was used to quantify the signal intensity of each band (data not shown).

Table 1 Primers used in this study for semi-quantitative and real-time PCR.

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<tr>
<td>18S rRNA</td>
<td>Reverse</td>
<td>AF176811</td>
<td>TCAGGGGAAGTATTAAGTG</td>
<td></td>
</tr>
</tbody>
</table>

*Primers used for real-time PCR.*
tube and mixed for 5 min at room temperature to allow binding of poly(A) to the beads. The samples were put into a magnetic separator to remove the lysis buffer while retaining the Dynabeads. The Dynabeads were washed twice with 100 µl washing buffer A, twice with 100 µl washing buffer B, and once with 100 µl 10 mM Tris–HCl. After removal of Tris–HCl, 8 µl of sterile DEPC water were added, and the samples were immediately subjected to RT.

RT was performed in a total volume of 20 µl. The first step was incubation at 70 °C with 8 µl RNA sample, 1 µl oligo(dT)12–18 (500 µg/ml), 1 µl RNaseout, 1 µl dNTPs (10 mM each), and 1 µl (50 ng) random primer followed by 50-min incubation at 42 °C and 5 min at 70 °C with RT mix containing 4 µl 5× RT buffer, 200 U of superscript II RT, 2 µl 0.1 M dithiothreitol, and DEPC water. The samples were transferred to −20 °C until use.

Real-time PCR was conducted on an Mx3000p cycler (Stratagene, La Jolla, CA, USA) using SYBR green in a final volume of 20 µl containing 3 µl cDNA (equivalent to ten embryos at the two-cell stage) and 500 nM of each primer. The amplification program included preincubation for taq polymerase activation at 95 °C for 7 min followed by 40 amplification cycles of denaturation at 95 °C for 10 s and annealing–elongation at 60 °C for 15 s. All samples were run in duplicate in 96-well plates. A melting curve analysis was recorded at the end of the amplification to confirm that there is no contamination by primer dimers. For each gene, standard curves were established using six serial dilutions of a reference cDNA. Fluorescence was acquired to determine the threshold cycle during the log-linear phase of the reaction at which fluorescence rose above background. Genes were quantified and analyzed by MxPRO QPCR Software for Mx3000p and Mx3005p QPCR ver 3, and the ΔΔCt method was used to calculate relative concentration of each gene which was expressed relative to 18S rRNA.

**Experimental design**

A seasonal study was performed over three consecutive years. The first experiment was performed during the cold (Dec–Apr) and hot (May–Nov) seasons. Environmental data were obtained from the central meteorological station in Bet-Dagan, Israel. The maximum average air temperature and relative maximum humidity were 31.8 ± 1.4 °C and 84.3 ± 3.8% during the winter, and 16.8 ± 2.3 °C and 46.0 ± 15.0% during the summer.

Oocytes were aspirated from ovaries collected at the local abattoir, matured, activated, and in vitro cultured (Fig. 8). Early embryonic development with an emphasis on the rate of the two first deviations was recorded on 17, 22, 27, 40, 46, 52, 64, and 70 h post activation. The time of developmental pick was defined as the time in which the highest proportion of developing embryos at a given stage was recorded. The second experiment was conducted during the hot season. Accurate timing of parthenos division was observed and documented with the EmbryoGuard system at 1-h intervals, to characterize the pattern of first cleavage of bovine embryos, as previously described by Arav et al. (2008). The third experiment was performed during both the cold (Dec–Apr) and hot (Jun–Sep) seasons. Oocytes were aspirated from ovaries collected at the local abattoir, matured, fertilized, and in vitro cultured as described above. The proportion of oocytes cleaved to the two- and four-cell stages and further developed to the blastocyst stage was assessed at 27, 42–44 h, and 8 days post fertilization respectively. Early- and late-two-cell stage embryos were collected in each season (four experimental replicates, ten embryos each). Total RNA was isolated, and semi-quantitative PCR and real-time PCR were carried out with primers for GDF9, POU5F1, and GAPDH using 18S rRNA as the reference gene. The primers were derived from bovine sequences found in Genbank and designed using Primer Express software (Table 1).

**Statistical analysis**

Differences between treatments were subjected to one-way ANOVA (JMP-6; SAS Institute, Cary, NC, USA). χ2 test or Student’s t-test was used to compare data among the experimental groups. Data are presented as mean ± S.E.M. Relative gene expression was analyzed by one-way ANOVA followed by Tukey–Kramer test. Differences of P<0.05 were considered significant.

**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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