Bovine embryos produced in vitro differ substantially from embryos produced in vivo in the mRNA expression patterns of genes important for development. Several factors in the in vitro production systems have profound effects on embryonic mRNA expression patterns. The effects of the type of maturation on the expression pattern of genes important for development in blastocysts produced in vitro have not yet been investigated. The aim of the present study was to investigate the effects of various maturational protocols on the relative abundance of a panel of six marker genes, indicative of compaction and cavitation, metabolism, stress susceptibility and RNA processing, in bovine blastocysts produced in vitro. Four groups of blastocysts were analysed by a sensitive semi-quantitative RT–PCR assay. Blastocysts were produced in vitro from oocytes of different origin from: (1) 3–8 mm follicles; (2) preovulatory follicles before the LH surge; and (3) preovulatory follicles 24 h after the LH surge. The first two groups were matured in vitro, whereas the third group had undergone maturation in vivo. A fourth group comprised blastocysts developed entirely in vivo. Expression of glucose transporter 1 was significantly (P < 0.05) higher, and expression of desmocollin 2 and plakophilin tended to be higher (P < 0.1) for in vivo (group 4) compared with in vitro blastocysts (group 1), whereas no differences were found for heat shock protein 70.1, E-cadherin and poly(A) polymerase. Expression of the six transcripts did not differ among blastocysts produced in vitro from oocytes of groups 1, 2 and 3. Results indicate that alterations in the relative abundance of these transcripts in blastocysts produced in vitro cannot primarily be attributed to the origin of the oocyte, but are likely to have been induced by post-maturation or fertilization culture conditions.
with the quality of the resulting blastocyst (Brevini-Gandolfi et al., 1999). The amounts of mRNA encoding for Na–K-ATPase, Cu–Zn superoxide dismutase (SOD), basic fibroblast growth factor (bFGF), cyclin A and B in bovine oocytes are affected by the maturation medium (Watson et al., 2000). The intrinsic quality of the oocyte is a key factor in determining blastocyst yields (Sirard and Blondin, 1996; Rizos et al., 2002). These findings indicate that prematuration and maturation of the oocyte affect patterns of gene expression at the blastocyst stage.

Various differences have been described between embryos derived in vitro and in vivo (Holm and Callesen, 1998; Niemann and Wrenzyciki, 2000), including morphology (Van Soom and de Kruif, 1992; Van Soom et al., 1997a), number and allocation of cells (Van Soom et al., 1996; Viuff et al., 2001), frequency of apoptosis and mixoploidy (Viuff et al., 1999, 2001; Gjorret et al., 2001), tolerance to cryopreservation (Niemann, 1995; Enright et al., 2000), embryonic metabolism (Khurana and Niemann, 2000) and expression profile of specific mRNAs (Wrenzyciki et al., 1996, 2001a; Eckert and Niemann, 1998; Lequarre et al., 2001). The relative abundance of several gene transcripts thought to be critically involved in preimplantation development is affected by the choice of basic culture medium and the type of protein supplement (Wrenzycki et al., 1999, 2001a). The effects of different maturation protocols on the relative abundance of genes important in development in blastocysts derived in vitro have not yet been investigated.

The aim of the present study was to determine the effects of prematuration–maturation (in vitro versus in vivo) of the oocyte on the relative abundance of a panel of six ‘marker’ genes important in development: glucose transporter 1, desmocollin 2, E-cadherin, plakophilin, heat shock protein 70.1 and poly(A) polymerase. These genes were selected because they are indicative of various mechanisms in preimplantation bovine development in vitro. Plakophilin and desmocollin 2 are of embryonic origin, whereas the other genes are of maternal and embryonic origin. All six transcripts are sensitive markers for compaction and cavitation, metabolism, RNA processing and stress susceptibility, and thereby indicate the quality of blastocysts (Wrenzycki et al., 1999, 2001a). The effects of different oocyte origins on blastocyst gene expression were investigated by collecting and analysing four groups of blastocysts from: (i) oocytes lacking the preovulatory development (in vitro group); (ii) oocytes prematured in vivo and matured in vitro (pre-LH group); (iii) oocytes prematured and matured in vivo (post-LH group); and (iv) blastocysts developed entirely in vivo (in vivo group). Oocytes derived from these different sources were subjected to in vitro fertilization and cultured to blastocysts in vitro under identical conditions.

Materials and Methods

Experimental design

Four groups of blastocysts that differed with regard to either the origin of the oocyte or conditions of embryo development were collected. In the first (in vitro) group, oocytes from ovaries obtained from an abattoir were matured, fertilized and cultured in vitro up to the blastocyst stage. In the second and third groups, two groups of cows were synchronized and treated with FSH to stimulate a large population of follicles to undergo the normal events of prematuration. The oocytes were collected either before the LH surge (pre-LH group) or 24 h after the induced LH surge (post-LH group). The oocytes from the pre-LH group were prematured in vitro, and were then fertilized and cultured up to the blastocyst stage simultaneously with the oocytes from the post-LH group (Fig. 1). In the fourth (in vivo) group, blastocysts were collected from superovulated cows by flushing the uterus at day 7 after insemination. Oocytes and blastocysts were collected from Holstein Friesian cows. Oocytes were recovered from cows at a commercial abattoir for the in vitro group, whereas donor animals from the experimental herd of the Veterinary Faculty of Utrecht University were used for the other three groups.

Animals

For the pre-LH (n = 8) and post-LH (n = 9) groups, 17 clinically healthy, non-lactating Holstein Friesian cows were selected on the basis of progesterone concentrations in peripheral blood samples measured three times a week for at least 4 weeks before the experiment. The cows were fed 20 kg corn silage and 4 kg concentrate per day, and grass silage and water were supplied ad libitum. The cows were presynchronized using an ear implant for 9 days (3 mg norgestomet, Crestar; Intervet International BV, Boxmeer), together with 3 mg norgestomet and 5 mg oestradiol valerate i.m. (Intervet International BV). Two days before the implant was removed, progesterlandin (15 mg Prosolvil i.m.; Intervet International BV) was administered.

On day 8 of the synchronized cycle (oestrus = day 0), all follicles > 5 mm were removed by transvaginal ultrasound-guided aspiration to avoid the inhibitory effects of follicular dominance on the developmental capacity of oocytes from subordinate follicles (Bungartz and Niemann, 1994). On day 9 of the oestrous cycle, the cows received another ear implant (3 mg norgestomet, Crestar) for 5 days, but no further combined norgestomet and oestradiol valerate. From day 10 of the oestrous cycle onwards, the cows received o-FSH i.m. (Ovagen ICP, Auckland) twice a day in decreasing doses over 4 days (3.5 ml, 2.5 ml, 1.5 ml and 1.0 ml; in total 17 ml, equivalent to 299 iu NIH-FSH-S1). Prostaglandin (22.5 mg i.m.) was administered together with the fifth dose of FSH, and 55 h later the ear implants were removed (Fig. 1).

The day after the last FSH dose, transrectal ultrasound technology was used to collect oocytes from cows with more than eight follicles > 8 mm. For the pre-LH group, cows (n = 8) were ovarioctomized 2 h after removal of the implant. In the post-LH group, cows (n = 9) received GnRH (1.0 mg Fertagyl in 10 ml saline i.m.; Intervet International BV) at the time of removal of the implant and were
ovariectomized 26 h after receiving GnRH. Ovariectomy was performed by laparotomy through a flank incision under local anaesthetic, using lidocaine cum adrenaline (Alfasan, Woerden). Ovaries were collected in 0.9% (w/v) NaCl at 37°C and were immediately transported to the laboratory. Heparinized blood samples were collected from the jugular vein every day during the experimental cycle and every hour after removal of the second implant for 6 h or until ovariectomy. After immediate centrifugation at 1800 g for 10 min at 4°C, plasma was stored at –25°C.

The seven cows in the in vivo group were treated with 3000 iu eCG (Intergonan; Intervet, Tönisvorst) between day 9 and day 13 of the oestrous cycle, and with prostaglandin (Estrumate; Schering-Plough, Munich) 48 h later. At oestrus, the donors were inseminated twice at an interval of 12 h with semen of a bull with proven fertility. At day 7 after insemination, blastocysts were recovered by non-surgical flushing of the uterine horns with 300 ml PBS (Sigma, St Louis, MO) supplemented with 1% newborn calf serum (NBCS, No. 295957; Boehringer, Mannheim) using established procedures.

Only blastocysts of morphological grades I and II (Roberson and Nelson, 1998) were included in this study. The blastocysts were stored in a minimum volume of PBS with 0.1% (w/v) polyvinyl alcohol (PVA; Sigma) and stored at –80°C.

Radioimmunoassays for progesterone and LH

Concentrations of progesterone in plasma were estimated by a solid-phase 125I-radioimmunoassay (Coat-A-Count TKPG; Diagnostic Products Corporation, Los Angeles, CA) according to the instructions of the manufac-
turer as validated by Dieleman and Bevers (1987). The sensitivity was 0.15 nmol l–1, and the intra- and interassay coefficients of variation were 8 and < 11%, respectively.

Concentrations of LH in plasma were estimated by a validated homologous radioimmunoassay (Dieleman et al., 1983b). The sensitivity was 0.4 mg NIH-LH-B4 l–1. The intra- and interassay coefficients of variation were < 9%.

Collection of oocytes and in vitro maturation

In vitro group. Bovine ovaries were collected in a thermos flask at a local abattoir from Holstein Friesian cows of unknown reproductive status and were then transported to the laboratory. Cumulus–oocyte complexes (COCs) were aspirated from 3–8 mm follicles, but only those with a multi-layered compact cumulus investment were used for the experiments. An average of ten usable COCs was collected per ovary. Selected COCs were rinsed once with Hepes-buffered M199 supplemented with 10% fetal calf serum (FCS; Gibco BRL, Paisley) and once with maturation medium. Groups of 35 oocytes were randomly allocated to wells of four-well culture plates (Nunc A/S, Roskilde) containing 500 µl maturation medium (M199; Gibco BRL) supplemented with 10% FCS (Gibco BRL), 0.01 iu porcine FSH ml–1 (Sigma), and 0.01 iu equine LH ml–1 (Sigma) per well and then cultured for 22 h (39°C, 5% CO2 in humidified air).

Pre-LH group. Immediately after ovariectomy, COCs were aspirated from putative preovulatory follicles > 8 mm and were included in the experiment on the basis of a minimum of three layers of compact cumulus investment.

Fig. 1. Schedule of treatments for superovulation with a fixed LH surge to collect prematured oocytes from FSH-treated cows for in vitro maturation (pre-LH) or in vivo maturation (post-LH), and subsequent simultaneous in vitro fertilization (IVF). FSH: administration of eight consecutive, decreasing doses of FSH; time: the time relative to start of in vitro maturation (start of IVM); PG: administration of prostaglandin; GnRH: administration of GnRH; LH surge: start of in vivo maturation: the time at which the maximum of the GnRH-induced LH surge occurs, starting in vivo maturation; OVX: ovariectomy.

Collection of oocytes and in vitro maturation

In vitro group. Bovine ovaries were collected in a thermos flask at a local abattoir from Holstein Friesian cows of unknown reproductive status and were then transported to the laboratory. Cumulus–oocyte complexes (COCs) were aspirated from 3–8 mm follicles, but only those with a multi-layered compact cumulus investment were used for the experiments. An average of ten usable COCs was collected per ovary. Selected COCs were rinsed once with Hepes-buffered M199 supplemented with 10% fetal calf serum (FCS; Gibco BRL, Paisley) and once with maturation medium. Groups of 35 oocytes were randomly allocated to wells of four-well culture plates (Nunc A/S, Roskilde) containing 500 µl maturation medium (M199; Gibco BRL) supplemented with 10% FCS (Gibco BRL), 0.01 iu porcine FSH ml–1 (Sigma), and 0.01 iu equine LH ml–1 (Sigma) per well and then cultured for 22 h (39°C, 5% CO2 in humidified air).

Pre-LH group. Immediately after ovariectomy, COCs were aspirated from putative preovulatory follicles > 8 mm and were included in the experiment on the basis of a minimum of three layers of compact cumulus investment.
COCs of one cow were then processed in one well for in vitro maturation similar to the COCs of the in vitro group.

**Post-LH group.** Immediately after ovariectomy at 24 h after the LH surge, COCs matured in vivo were aspirated from preovulatory follicles > 8 mm and were selected for the experiment based on an expanded cumulus-cell mass. COCs with a compact cumulus investment and degenerated oocytes were discarded. Selected COCs from each cow were kept together in maturation medium in a single well until fertilization.

The interval between ovariectomy and transfer of COCs to maturation (pre-LH group) or fertilization (post-LH group) medium was 30–40 min. The duration of maturation was 24 h for the pre-LH group (in vitro) and 24 h in vivo (ovariectomy 24 h after the LH surge). Ovulation of fully matured oocytes occurs 24 h after the LH surge (Dieleman et al., 1983a). Maturation was assessed by determining expansion of the cumulus cells. Cytological studies have revealed that in our system > 80% of the oocytes reach the metaphase II stage.

**In vitro fertilization and embryo culture (IVF and IVC)**

Procedures for in vitro fertilization (IVF) were performed as described by Izadyar et al. (1996). In brief, matured oocytes of the in vitro, pre-LH and post-LH groups were fertilized in wells of four-well culture plates. All oocytes were fertilized at the same time with the same batch of sperm suspension (20 × 10^6 cells ml⁻¹) 20 μl containing the sperm pellet. COCs were transferred to 0.5 ml cups in a minimum volume (≤ 5 μl) of PBS with 0.1% (w/v) PVA and frozen at –80°C. Analysis of cultured embryos was confined to those of morphological grades I and II (Robertson and Nelson, 1998).

**Selection of the embryos for RT–PCR**

For each gene, embryos from as many different cows as possible were analysed. Furthermore, similar numbers of embryos collected on days 7 and 8 were assigned to each mRNA analysis. Depending on the type of gene, four to five transcripts were analysed per embryo and at least five embryos per gene were determined. The relative abundance of mRNAs from the six different genes important in the development of a preimplantation embryo was determined in single bovine blastocysts by semi-quantitative RT–PCR.

**Isolation of RNA**

Poly(A)⁺ RNA from a single embryo was isolated using a Dynabeads mRNA DIRECT kit (Dynal A.S., Oslo). RNA was isolated following the manufacturer’s instructions with minor alterations (Wrenzycki et al., 1999). In brief, frozen embryos were thawed by adding 30 μl lysis buffer (100 mmol Tris–HCl l⁻¹, pH 7.5; 500 mmol LiCl l⁻¹; 10 mmol EDTA l⁻¹, pH 8; 1% (w/v) LiDS; 5 mmol dithiothreitol l⁻¹). As an internal standard, 1.0 pg rabbit globin RNA (Life Technologies BV, Eggenstein) was added to each embryo. The samples were mixed for 10 s, centrifuged for 15 s at 12 000 g, and left for 10 min at room temperature. Dynabeads (5 μl; Dynal) were added and mixed for 5 min at room temperature. The samples were put in the magnetic separator to remove the lysis buffer and leave the Dynabeads. The Dynabeads were washed four times, once with 40 μl washing buffer A (10 mmol Tris–HCl l⁻¹, pH 7.5; 0.15 mol LiCl l⁻¹; 1.0 mmol EDTA l⁻¹; 0.1% (w/v) LiDS) and three times with 40 μl washing buffer B (10 mmol Tris–HCl l⁻¹, pH 7.5; 0.15 mol LiCl l⁻¹; 1.0 mmol EDTA l⁻¹). After removal of washing buffer B, 11 μl sterile H₂O was added and incubated at 65°C for 2 min to elute mRNA from the Dynabeads. The cups were put into the magnetic separator again; the supernatant was removed and immediately used for reverse transcription.

**Reverse transcription**

Poly(A)⁺ RNA isolated from a single embryo was reverse transcribed into cDNA in a total volume of 20 μl. The reaction mixture consisted of 1 × RT buffer (50 mmol KCl l⁻¹; 10 mmol Tris–HCl l⁻¹, pH 8.3; Perkin Elmer Biosystems, Vaterstatten), 5 mmol MgCl₂ l⁻¹, 1 mmol of each dNTP l⁻¹ (Amersham, Brunswick), 2.5 μmol random hexamers l⁻¹ (Perkin Elmer), 20 iu RNase inhibitor (Perkin Elmer) and

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50 μl MuLV reverse transcriptase (Perkin Elmer). The samples were centrifuged for 15 s at 12 000 g and were overlaid with mineral oil to prevent evaporation. One sample was prepared with 1.0 pg rabbit globin RNA and 10 μl H₂O. As negative controls, tubes without an RNA sample and tubes with an RNA sample, but without reverse transcriptase, were analysed. The reverse transcription reaction was carried out in a thermocycler (Biometra Triothermoblock; Biometra, Göttingen) for 10 min at 25°C, 60 min at 42°C, and 5 min at 99°C, and was kept on ice once the reaction was completed.

**PCR**

Immediately after reverse transcription the samples were subjected to PCR amplification. PCR was performed with a volume of the reverse transcriptase reaction corresponding to 0.1 (desmocollin 2 and Glut-1), 0.2 (heat shock protein, E-cadherin and poly(A) polymerase) and 0.4 (plakophilin) embryo equivalents in a final volume of 50 μl, containing 1 x PCR buffer (20 mmol Tris–HCl l–1; 50 mmol KCl l–1, pH 8.4; Life Technologies), 1.5 mmol MgCl₂ l–1, 200 μmol of each dNTP l–1 and 1 μmol of each sequence-specific primer l–1 (0.5 μmol l–1 for globin primers). A ‘hot start’ PCR was performed to obtain specific amplification. During the ‘hot start’ 1 μl Taq DNA polymerase (Life Technologies) was added at 72°C. The sequences and positions of the primers used, the annealing temperature, the fragment sizes of the expected products and the sequence references are shown (Table 1). The products of each primer pair were sequenced to confirm the identity of the RT–PCR fragments.

Running a linear cycle series established the optimal cycle number at which the transcript was amplified exponentially for the PCR reaction. The PCR programme started at 97°C for 2 min, decreased to 72°C for 2 min (hot start) and was followed by a number of cycles, which depended on the gene (Table 1), of 15 s at 95°C for denaturation, 15 s at the annealing temperature of the specific gene (Table 1) and 15 s at 72°C for primer extension. After finishing these cycles a final extension of 5 min at 72°C was performed, followed by cooling to 4°C. A PTC-200 thermocycler (MJ Research, Watertown, MA) was used.

**Detection and semi-quantification of RT–PCR products**

RT–PCR product (25 μl) with 5 μl of 10 × loading buffer (0.25% (w/v) xylene cyanol and 25 mmol EDTA l⁻¹ in 50% (w/v) glycerin) was loaded on to a 2% (w/v) agarose gel in TBE buffer (90 mmol Tris l⁻¹; 90 mmol borate l⁻¹; 2 mmol EDTA l⁻¹, pH 8.3) containing 0.2 μg ethidium bromide ml⁻¹ and subjected to electrophoresis. The concentration of ethidium bromide in the running buffer and the gel was the same. After electrophoresis at 100 V for 5 min and at 80 V for 40 min, the fragments were visualised on a 312 nm UV transilluminator. A CCD camera (Quantix; Photometrics, Munich) and IP Lab spectrum (IP Lab Gel; Signal Analytics Corporation, Vienna, VA) were used to digitize the image of the gel. Densitometric scanning using a computer-assisted image analysis system (IP Lab Gel; Signal) was used to quantify the signal intensity of each band. The relative abundance of the mRNA of the different genes was estimated by dividing the intensity of the band of the gene of interest by the intensity of the globin band from the same sample.

The recovery rate of the RNA was estimated for all of the embryos. It was calculated as the ratio between the intensity of the globin bands with and without RNA extraction. On average, 42% of the poly(A)+ RNA of the blastocyst was extracted, which is similar to percentages obtained by Wrenzycki et al. (1999).

**Statistical analysis**

Rates of blastocyst formation were analysed with logistic regression and P ≤ 0.05 was considered significant. For the relative abundance of the gene transcripts, an analysis of variance was performed using the nlme library of S-PLUS 2000 with random cow effects (Pinheiro and Bates, 2000). Data are presented as mean ± SEM.

**Results**

**Response to superovulation treatment (pre-LH and post-LH groups)**

No LH surge was observed in peripheral blood of cows in the pre-LH group (Fig. 2). The cows that were treated with GnRH (post-LH group) showed a clear LH surge at 2 h after the administration of GnRH; in cows from which embryos were collected for RT–PCR, maximum LH concentration was 24.5 ± 2.5 μg I⁻¹ (n = 7; Fig. 2).

Signs that an LH surge had occurred before the implant was removed were observed in four cows: cumulus cells were moderately expanded in two cows from the pre-LH group and two cows of the post-LH group had already ovulated. Oocytes from these animals were excluded from the experiment.

The superovulation response in the pre-LH and the
post-LH groups was 30.3 ± 10.5 (mean ± SD, n = 6) and 23.1 ± 10.0 (mean ± SD, n = 7) follicles > 8 mm on average per cow, respectively.

Oocyte recovery and in vitro culture

In the pre-LH group, 166 COCs were collected from 182 follicles of preovulatory size from six cows (recovery rate 91.2%). COCs that did not have an intact multi-layered compact cumulus investment or that already showed cumulus expansion were excluded (n = 26) from analysis. In the post-LH group, 136 oocytes were collected from 162 follicles of preovulatory size from seven cows (recovery rate 84.0%). Denuded oocytes and COCs not showing cumulus expansion (n = 20) were excluded. In the in vitro group, 333 oocytes were collected and used for IVM, IVF and IVC.

Cleavage rates on day 4 of culture were similar in the three IVC groups (average 75%; Table 2). On day 7 after

---

**Table 1. Primers used for PCR**

<table>
<thead>
<tr>
<th>Genes</th>
<th>Primer sequence and positions</th>
<th>Number of cycles</th>
<th>Annealing temperature (°C)</th>
<th>Fragment size (bp)</th>
<th>Sequence references (EMBL accession number)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Desmocollin 2</strong></td>
<td>5’ primer (2085–2109): CTCCGGCCGATGACAAAGTGATTC 3’ primer (2503–2527): GCGCATCTCTTCTCTCGTATTGTAT</td>
<td>31</td>
<td>57</td>
<td>443/397 (insertion of 46 bp, 2396–2441)</td>
<td>Koch et al. (1992) (M81190)</td>
</tr>
<tr>
<td><strong>Plakophilin</strong></td>
<td>5’ primer (1337–1361): CGGCTGACCCGGAGGTTCCTTTCTTA 3’ primer (1580–1604): CGGTGAGGGTGGCGGCGTTGTA ACTCTTGCTGTAAT</td>
<td>35</td>
<td>64</td>
<td>268</td>
<td>Heid et al. (1994) (Z37975)</td>
</tr>
<tr>
<td><strong>Poly(A) polymerase</strong></td>
<td>5’ primer (886–915): TTTCTCAGTTTGCTGATTCGATGCTCACGATGGCTGATCC 3’ primer (1108–1137): TGGAGATCTGGTTGGGTATGCTGTGTAAT</td>
<td>35</td>
<td>57</td>
<td>252</td>
<td>Raabe et al. (1991) (X63436)</td>
</tr>
</tbody>
</table>
insemination, most (60–80%) of the blastocysts had already formed. Rates of blastocyst formation at day 7 were significantly (P < 0.05) different in the pre-LH, post-LH and in vitro groups. The overall rate of blastocyst formation was significantly (P < 0.05) higher in the pre-LH group (50%; Table 2) than in the post-LH (31.0%) and in vitro groups (26.4%). Most of the blastocysts in the three IVC groups were already expanded: 64.3, 52.7 and 54.5% for pre-LH, post-LH and in vitro group embryos, respectively.

Relative abundance of genes in single blastocysts derived from different oocyte origins

For RT–PCR products (Fig. 3), the bands represent gene transcripts derived from 0.1–0.4 parts of a bovine blastocyst. As negative controls, RNA or reverse transcriptase was omitted during the reverse transcription reaction. No amplified products were found at any time in the negative controls during these experiments.

Table 2. Rates of blastocyst formation after in vitro culture (IVC) and IVF of in vivo- or in vitro-matured oocytes obtained from preovulatory follicles from FSH-stimulated cows compared with the rates of in vitro-matured oocytes from 3–8 mm follicles

<table>
<thead>
<tr>
<th>Number of oocytes after IVF, day 1*</th>
<th>Number of cleaved embryos on day 5 (%)</th>
<th>Number of blastocysts</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Day 7† (%)</td>
<td>Day 8 (%)</td>
</tr>
<tr>
<td>Pre-LH (after in vitro maturation)</td>
<td>140</td>
<td>123 (87.9)</td>
</tr>
<tr>
<td>Post-LH (after in vivo maturation)</td>
<td>116</td>
<td>85 (73.3)</td>
</tr>
</tbody>
</table>

3–8 mm follicles

After IVM

<table>
<thead>
<tr>
<th>Number of oocytes</th>
<th>Number of cleaved embryos on day 5 (%)</th>
<th>Number of blastocysts</th>
</tr>
</thead>
<tbody>
<tr>
<td>333</td>
<td>233 (70.0)</td>
<td>55 (16.5)c</td>
</tr>
</tbody>
</table>

*Oocytes were collected from preovulatory follicles before (pre-LH) or 24 h after (post-LH) an induced LH surge. Day 1 is start of IVC. Percentages of cleavage and blastocyst formation are calculated relative to the number of (non)-fertilized oocytes at day 1 of IVC.

†At day 7 of IVC, blastocysts were collected and stored for RT–PCR, and morulae and early blastocysts were cultured for an additional day and collected as blastocysts at day 8.

a–c Values with different superscripts within a column are significantly different (P < 0.05).

Fig. 3. Expression of six genes important to development as detected by RT–PCR in a 0.1 to 0.4 proportion of a single bovine blastocyst; digitalized image after electrophoresis on an agarose gel containing ethidium bromide. PCR products are indicated at the top for heat shock protein 70.1 (HSP), poly(A) polymerase (polyA), glucose transporter 1 (Glut-1), desmocollin 2 (Dc-2), E-cadherin (E-cad) and plakophilin (plako), and for the RNA extraction control globin (– Ext: without extraction; + Ext: with extraction). Expected fragment sizes are indicated at the bottom; bpl: 100 bp ladder as marker for fragment size.

Fig. 4. Relative abundance of transcripts of six genes important to development as detected by semi-quantitative RT–PCR in single bovine blastocysts originating from oocytes subjected to different modes of maturation. Embryos were derived from: (i) immature oocytes from 3–8 mm follicles after IVM, IVF and IVC (in vitro group; ); (ii) prematurely oocytes from preovulatory sized, FSH-stimulated follicles after IVM, IVF and IVC (pre-LH group; ); (iii) prematurely oocytes from preovulatory sized, FSH-stimulated follicles after in vivo maturation, IVF and IVC (post-LH group; ); and (iv) similar oocytes to those in (iii) but also with fertilization and development entirely in vivo (in vivo group; ). Bars represent the mean ± SEM relative abundance of a number of blastocysts as indicated in the bars; each value was the mean of at least five different cows. Asterisks indicate difference from all groups: *P < 0.1; **P < 0.05.
The relative abundance of Glut-1 was significantly \((P < 0.05)\) higher in the \textit{in vivo} group compared with the pre-LH, post-LH and \textit{in vitro} groups (Fig. 4). The relative abundance of desmocollin 2 and plakophilin tended to be higher in the fourth group (\textit{in vivo}) compared with the other three groups, although this difference was not significant. No significant differences were detected in any of the gene transcripts between the three \textit{in vitro} groups (\textit{in vitro}, pre-LH and post-LH groups; Fig. 4).

**Discussion**

In the present study the effects of different maturation regimens of bovine oocytes on the relative abundance of transcripts from six genes important in development in blastocysts were investigated. \textit{In vitro} conditions have profound effects on the patterns of expression of a range of gene transcripts in bovine and murine embryos (Ho et al., 1994, 1995; Niemann and Wrenzycki, 2000). The present data show for the first time that prematuration–maturation does not necessarily affect the relative abundance of the genes and indicate that \textit{in vitro} maturation may not be the critical factor contributing to variation in mRNA content between \textit{in vitro}- and \textit{in vivo}-derived embryos. The differences between \textit{in vivo}- and \textit{in vitro}-derived blastocysts were probably not due to variation in the rates of development. In parallel experiments, blastocysts derived \textit{in vivo} and \textit{in vitro} as well as those derived from pre-LH and post-LH groups had similar numbers of cells.

The semi-quantitative RT–PCR assay used in the present study provides sensitive and highly reproducible results from both pooled and single bovine embryos. It has constantly been updated and increased in sensitivity (Wrenzycki et al., 1999, 2001a,b, 2002). The validity of the assay has been demonstrated previously and revealed efficient amplification of both the globin standard and the RNA of choice (Wrenzycki et al., 2000). Its accuracy compares favourably with current real-time RT–PCR techniques (Stenman et al., 1999). Similar to endpoint RT–PCR, real-time RT–PCR uses standards against which the amounts of mRNA of the genes of choice are compared (Freeman et al., 1999; Bustin, 2000; Steuerwald et al., 2000). The densitometric analysis of ethidium bromide-stained agarose gels described in the present study is a well established and sensitive enough approach to detect even subtle differences in amounts of mRNA in different biological materials (Grover et al., 2001; Ringhoffer et al., 2001). The degree of variation with this approach is rather small (Grover et al., 2001), but can be further decreased by an optimized real-time RT–PCR protocol (Bustin, 2000). We have calculated the number of replicates necessary to obtain statistically significant differences to accommodate any inherent variability. This approach has recently proven valid for single bovine cloned and IVP embryos (Wrenzycki et al., 2001b, 2002). The differences in patterns of expression described previously were related to the increased incidence of the large offspring syndrome in offspring derived from IVP or cloned bovine embryos (Niemann and Wrenzycki, 2000; Niemann et al., 2002). Even subtle changes in patterns of expression of specific genes were shown to have marked biological effects such as predisposition to tumourigenesis (Yan et al., 2002) and may be causally involved in large offspring syndrome.

The mRNAs measured in blastocysts in the present study were probably transcribed during embryonic development and did not represent mRNAs that remained from the maternal mRNA pool. Plakophilin, desmocollin 2 and E-cadherin are predominantly expressed from the morula stage onwards (Wrenzycki et al., 1999, 2001a). The mRNAs of glucose transporter 1 and poly(A) polymerase were found throughout early development up to the blastocyst stage, which is indicative of both maternal and embryonic origin, with a burst after maternal–embryonic transition of genomic activity (Wrenzycki et al., 1999). The different amounts of mRNA observed in blastocysts derived from oocytes matured \textit{in vitro or in vivo} in the present study are supported by findings from histological and biochemical studies. Embryos developed \textit{in vitro} frequently form the blastocoel earlier than \textit{in vivo}, without proper compaction, and have fewer cells than do \textit{in vivo}-grown embryos (Van Soom et al., 1997b). Desmocollin 2 and plakophilin molecules are involved in intercellular communication structures and compaction (Collins et al., 1995). The lower expression of desmocollin 2 and plakophilin observed in blastocysts of the \textit{in vitro} group might explain the impaired compaction in embryos produced \textit{in vitro}. Differences in metabolism between bovine embryos produced \textit{in vitro} and those developed \textit{in vivo} have been detected, especially with regard to lactate production and glucose metabolism (Khurana and Niemann, 2000). The decreased amount of glucose transporter 1 in \textit{in vitro} embryos found in the present study probably reflects differences in energy metabolism between blastocysts developed \textit{in vitro} and \textit{in vivo}.

A novel aspect of the present study was related to expression of the panel of genes in blastocysts derived from prematured oocytes (pre-LH group) and oocytes matured \textit{in vivo} (post-LH group). The results of the present study indicate that blastocysts developed from pre-LH and post-LH oocytes are not different with respect to patterns of gene expression from those derived from oocytes that lacked a period of prematuration and \textit{in vivo} maturation. Nevertheless, the mode of oocyte prematuration and maturation may affect the developmental competence after cleavage into morulae and blastocysts (Hyttel et al., 1997).

The rate of blastocyst development in the pre-LH group was higher than in the \textit{in vitro} group, which is in accordance with earlier observations and confirms the stimulatory effects of prematuration on oocyte developmental competence. The rate of blastocyst development in the post-LH group differed from recent findings in which exceptionally high rates of blastocyst development were found (Van de Leemput et al., 1999; Hendriksen et al., 2000). When two cows with low rates of blastocyst development were excluded from analysis, the rate of
blastocyst development of the post-LH group increased to approximately 45% and the relative abundance of the genes did not change significantly. The high proportion of well-expanded blastocysts indicates the inherent high capacity of the blastocysts for development.

The results of the present study indicate that in vitro maturation – as the first step in IVP of embryos – has improved significantly (Bavister, 1995; Keskinetepe and Brackett, 1996). Blastocysts derived from oocytes that were matured differently, but cultured identically, did not show significant differences with respect to the panel of gene transcripts investigated in the present study. The differences may therefore be related to the in vitro conditions imposed on fertilized oocytes. This contention is supported by previous findings for sheep and cattle, in which zygotes were subjected to different culture conditions and developed abnormal phenotypes (Young et al., 1998; Sinclair et al., 2000). Nevertheless, it could be useful to analyse gene expression in oocytes immediately after completing different maturation protocols. However, this would require a different panel of gene transcripts to be informative, including genes involved in cell cycle regulation, meiotic competence and cumulus expansion. Little is known about transcriptional activity in bovine oocytes. Duration of oocyte maturation and quality of COCs affected transcription of cyclooxygenase-2 and various prostaglandin E receptors in in vitro culture (Calder et al., 2001). Furthermore, it would be interesting to determine rates of transcription in the embryos in which development was arrested at an early stage and thus did not reach the blastocyst stage.

In conclusion, the difference in the relative abundance of the six gene transcripts found between blastocysts produced in vitro and in vivo can probably be attributed to embryo culture conditions after maturation and fertilization. Prematuration and maturation are thought to be critically involved in the ability of the oocyte to support early development (Sirard and Blondin, 1996; Hyttel et al., 1997; Rizos et al., 2002). Whether blastocysts derived from oocytes matured in vivo or in vitro differ with regard to quality has yet to be determined. It should be noted that this study was limited to a panel of six gene transcripts and it is possible that other gene transcripts would behave differently. cDNA array technology enables simultaneous determination of a potentially unlimited number of gene transcripts and it has already been applied to the diagnosis of various forms of human cancer, human autoimmune diseases and the characterization of murine embryonic stem cells (Alizadeh et al., 2000; Kelly and Rizzino, 2000; Rogge et al., 2000). A prototype of a suitable cDNA array for single bovine embryos has recently become available (Brambrink et al., 2002) and its broader application will also improve determination of patterns of gene expression in embryos derived from IVP or cloning.

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