Gynecology, Medical University Vienna). Women were eligible for enrollment if they had conceived spontaneously within a maximum period of six months. A history of autoimmune diseases, chemotherapy, radiation, ovarian surgery and polycystic ovary syndrome precluded inclusion. Study subjects were then stratified as follows: Group 1, age 18-30 years; Group 2, 31-36 years; and Group 3, 37-40 years. AMH measurements were performed using the DSL Active MIS/AMH assay by Beckman Coulter Inc., USA.

Results: Mean AMH levels declined with advancing female age from Group 1 to Group 3 from 1.19 ng/ml to 0.95 ng/ml and 0.62 ng/ml. AMH levels were not statistically associated with day of blood draw or pregnancy characteristics, such as fetal gender, fetal weight or mode of delivery. AMH levels were, however, at all ages universally lower than reported in the literature for infertile patients.

Conclusions: As previously reported in infertile population, fertile women also demonstrate declining AMH levels with advancing age. Uniformly lower levels at all ages than previously reported in infertile women suggest, however, that puerperal AMH, contrary to prior reports, appears suppressed. AMH levels, thus, do not appear as stable under all hormonal influences as previously reported.

O-007 Nomogram for the decline in serum Anti-mullerian hormone across the reproductive lifespan

S.M. Nelson1, C.M. Messow2, A.M. Wallace3, R. Fleming4, A. McConnachie5
1University of Glasgow; Reproductive & Maternal Medicine 3rd Floor QEB, Glasgow - Scotland, United Kingdom
2University of Glasgow; Robertson Centre for Biostatistics, Glasgow - Scotland, United Kingdom
3University of Glasgow; Clinical Biochemistry, Glasgow - Scotland, United Kingdom

Introduction: Serum anti-Mullerian hormone (AMH) levels and follicle numbers decrease with age. We hypothesised that the decline in AMH would mirror the relationship between the follicle cohort and age, and that AMH would exhibit non-linear decay.

Materials and Methods: A population of 9706 women attending infertility clinics in the UK with an AMH measured by the DSL assay and a date of birth recorded. The data was split randomly into a training cohort of 4854 women to develop alternative models for the decline in circulating AMH with age and a separate cohort of 4852 women for independent validation of these models. In both datasets, linear, biphasic linear, exponential, power, and quadratic models were compared in terms of the distribution of model residuals, graphically and in terms of the sum of absolute and squared residuals, the proportion of variance explained (R²), and the Akaike and Bayesian Information Criteria (AIC, BIC). In addition, non-parametric smoothed estimates of model residuals in relation to age were generated, with confidence bands, to assess bias across the age distribution. The best performing model was used to construct an age related AMH nomogram.

Results: In the training cohort, the non-linear models were superior to the simple linear model, with little difference in goodness-of-fit between the non-linear alternatives. This was confirmed by validation in a separate cohort. However, the biphasic linear model is conceptually less valid than models employing a smooth association with age. Furthermore, the differential and power models were considerably more complicated to fit and to generate age-specific norms. Consequently, the quadratic model offers the most pragmatic approach for development of an age related AMH nomogram. All models tended to fit poorly at the extremes of the age range, but results were similar when these extremes were excluded.

Conclusions: AMH concentrations decline in a non-linear manner with increasing reproductive age which is well described by a quadratic curve. The quadratic model was used to construct an age related AMH nomogram.
Introduction: Development of new, non-invasive quantitative methods for oocyte evaluation will be valuable to determine the reproductive potential of a patient’s oocyte cohort. Animal model provided evidence that measurements of the metabolic activity of oocytes and embryos could be predictive of embryonic developmental potential. Oxygen consumption has been regarded as the best indicator of overall metabolic activity and a valuable parameter for evaluating oocyte quality. Our objective is to evaluate the diagnostic value of oocyte oxygen consumption rate measurements as a quality marker by correlating respiration rates with stimulation parameters and reproductive outcome.

Material and Methods: A prospective cohort observational study was undertaken on 349 oocytes from 56 couples included in an egg donation program. Inclusion criteria were: first ICSI cycle, embryo transfer 72 hours after ICSI. Exclusion criteria included patients with endometriosis, ovarian hyper stimulation syndrome, hydrosalpinx, obesity and maternal age over 45 years old (aging uterus).

We considered for the study any independent variables related to the developmental embryos: fertilization, cell number 48 hrs and 72 hrs after fertilization, fragmentation, multiclnucleation, and similarity of blastomere size, and other parameters related to the stimulation procedure; days of stimulation, serum Estradiol and Progesterone levels, and total number of MII oocytes obtained. The oocytes were cultured in specially designed polymer trays with microwells which were placed in an embryo resiprometer (Unisense, Fertilitech, Aarhus). Oxygen concentration gradients ensuing in the microwells due to oocyte consumption of oxygen were measured and the respiration rate in femtomol per second (fmol/sec) were calculated automatically at preset time intervals. In each experiment empty microwells devoid of metabolic activity were used as negative controls. Statistical analysis was performed using ANOVA, linear and logistic regression, with oocyte respiration (fmol/sec) as the dependent variable.

Results: The results showed different values of respiration depending on type of gonadotrophins used: when donors were stimulated with FSH, we observed higher oocyte oxygen consumption compared with the use of FSH + hMG or hMG only, (5.68 fmol/sec SD = 1.34, 4.97 fmol/sec SD = 1.22, 4.81 fmol/sec SD = 1.09 respectively P < 0.05). A longer stimulation combined with a lower dose of gonadotrophins increased the respiration rates, more days of stimulation were correlated with higher levels of respiration (r = 0.104 p = 0.026). Finally a higher estradiol levels in blood serum correlated with a lower level of oxygen consumption (r = 0.133 p = 0.013).

With regards to reproductive outcome we observed different levels of respiration within the same cohort of oocytes, and a higher rate of respiration was seen for fertilized oocytes compared with unfertilized, degenerated or those exhibiting abnormal fertilization OR = 1.34(OR 1.037-1.732, P = 0.014). With respect to the quality of embryos at 48 and 72 hours after fertilization we observed a higher rate of oocyte respiration in good quality embryos (i.e. embryos with 3-5 cells on day 2 and > 6 cells on day 3, < 20 % fragmentation, no multiclnucleation and even blastomere size), but the difference was not significant. Finally when we evaluated the relationship between embryo implantation and oocyte respiration rate we found higher respiration rates with the implanted embryos compared to those that not; 6.21 fmol/sec SD = 0.849, 5.23 fmol/sec SD = 0.345, respectively (p < 0.030).

Conclusions: Oxygen consumption measurements may be used to evaluate implantation potential for individual oocytes, by single measurement of the eggs before their manipulation. The used equipment provided a non-invasive and consistent measurement of individual oocytes respiration rates without affecting the subsequent development of the embryo. These characteristics make this technology a promising tool to evaluate oocyte quality and for assessing embryo quality in the future.

O-010 Near-infrared (NIR) analysis of day 5 embryo culture media from cohorts of patients’ embryos

D. Sakka1, M. Henman2, P. Harrison3, L. Botros1, M. Henson1, K. Judge1, P. Roos1
1Molecular Biometrics Inc., Research and Development, New Haven CT, USA.
2Sydney IVF, IVF Laboratory, Sydney NSW, Australia

Introduction: The complication of greatest consequence in IVF treatment is the high multiple pregnancy rate. Multiple pregnancies carry a higher incidence of complications and, hence, lead to higher health care costs. Single embryo transfer (SET) is the only effective way to minimize the risk of multiple pregnancies. As only one embryo is transferred during SET, the identification of the embryo with an optimum implantation potential becomes critical. Currently this is based largely on the morphological characteristics of an embryo. Non-invasive metabolomic profiling of embryo culture media using NIR spectroscopy assesses modifications of the chemical composition of the embryo’s surrounding medium and generates a Viability Score. This methodology has been presented as an adjunct to morphology in improving the identification of the most viable embryo for transfer (Seli et al. 2009). The objective of this study was to assess the Viability Score for individual patients’ cohorts of Day 5 embryos and determine whether differences in scores could have an impact on the fate of an individual embryo’s chances of selection.

Material and Methods: Embryos were group cultured in 20μl of Cook® cleavage medium until Day 3 and then individually in Cook® blastocyst medium. Embryos were selected for transfer or cryopreservation based on a Day 5 morphology assessment. After transfer up to 5 embryo media samples and blank controls were assessed using the ViaMetrics®-ETM NIR spectral analysis platform in the clinic, as a part of a beta testing phase of the diagnostic equipment and procedure. This diagnostic equipment and procedure examine individual metabolomic profiles of media samples using NIR spectroscopy. Biomarkers indicative of viability have been previously identified by examining the NIR spectra of negative and positive FCA outcome groups. Partial Least Squares, a Multivariate Regression, proprietary bioinformatics and leave-one-out cross-validation were used to develop a predictive algorithm that generates the Viability Score. In total, 439 embryos were assessed from 114 patients. The metabolomic profile of the embryo culture media samples was expressed as a Viability Score, which reflects the implantation potential of an embryo.

Results: A mean of 3.9 Day 5 embryos (range 1 – 5) were assessed for each patient. Analysis of all 439 samples yielded Viability Scores ranging from 0.02 to 1.03. The mean (± SD) Viability Score was 0.52 ± 0.16. Within an individual patient’s cohort of embryos, the average variability in the Viability Score was 0.29 ± 0.17. In this study, there was no significant difference found among mean Viability Scores across blastocyst morphology grades: Grade 1 (n = 66: 0.52 ± 0.15), Grade 2 (n = 187: 0.50 ± 0.15), and Grade 3 (n = 171: 0.51 ± 0.17). However, the embryos which ranked highest by Viability Score were selected for transfer only 26% of the time (31/119). This indicates that in 74% of the cases another embryo may have been indicated for selection using the Viability Score.

Conclusions: The current study shows that Day 5 embryos of varying morphology display a wide variation in their metabolomic Viability Scores. The data further show that the Day 5 embryo with the best morphology within the cohort also had the best Viability Score in only 26% of the cases. Based on published literature examining the value of metabolic and/or metabolomic profiling, this study supports the concept that choosing embryos with the best metabolic and/or metabolomic profile within a cohort, in addition to morphology, could have a significant impact on the identification of the best embryo for SET. Prospective trials are in process where this technology is used to select the most viable embryo within a cohort.

Reference:

Support: Molecular Biometrics, Inc

O-011 Subcellular dynamics of the maternal survival factor BCL2L10 in human pre implantation embryos

J.F. Guerin1, Y. Guillemín2, A. Cornut3, A. Aouacheria3
1Hôpital Femme Mère Enfant, Reproductive medicine, Bron-69500, France
2Institut de Biologie et Chimie des Protéines, CNRS UMR 5086, Lyon F-69367, France

Abstracts of the 26th Annual Meeting of ESHRE, Rome, Italy, 27 June – 30 June, 2010

Introduction: Apoptosis, a form of cell death by self-destruction, has been reported in human oocytes and during early embryo development both in vitro and in vivo. Recent evidence suggests that the developmental potential of the embryo could be related to its apoptosis rate. Thus, the investigation of apoptosis-related genes and mechanisms in early embryos is crucial. Bcl-2 family proteins are major regulators of cell death and survival. Among the members of the Bcl-2 family, the survival factor Bcl2L10 is abundantly and selectively expressed in human oocytes (1). The aim of the present work was to examine BCL2L10 specific expression and subcellular localization in early human embryos.

Material and Methods: Embryos were donated with fully informed consent by patients being treated by IVF or ICSI procedure. The research protocol has
been authorized by the French Biomedicine Agency. A total of 43 embryos were used including appropriate controls. Thirteen of these embryos were considered to be of high quality since they originated from supernumerary embryos which were selected then frozen at 4-cell stage or blastocyst stage in order to be transferred later in the uterus of the female partner. Thirty were deselected poor quality embryos (not chosen for transfer or freezing) or were early-arrested embryos (discarded after 3 days of fertilization). Embryos were fixed with 4% paraformaldehyde, permeabilized, blocked, and processed for double immunolabeling with selected primary antibodies and Alexa-conjugated secondary antibodies. For staining of DNA, the preparation was treated with TO-PRO-3 iodide or DAPI nuclear stain. To release calcium from internal stores and induce cell death, embryos were incubated with thapsigargin (1 μM, 1h) prior to fixation and immunofluorescence analysis. Confocal analysis was performed on Zeiss (LSM510) or Leica (TCS-SP2) confocal microscopes. Three-dimensional reconstructions were created from sequential confocal sections.

Results: Although BCL2L10 was detected in all tested embryos, they exhibited variability in BCL2L10 pattern at the subcellular level depending mostly on embryo quality. In healthy embryos, the BCL2L10 protein clearly co-localized with mitochondria that were identified using anti-mitoHsp70 antibody. Two-thirds of the embryos exhibited morphological fragmentation. In these embryos, we observed coexistence of blastomeres showing BCL2L10 positive expression, some embryonic cellular bodies exhibiting high fluorescence intensity, with blastomeres or fragments negative for BCL2L10. Strikingly, bright fluorescence was detected in the nuclei of at least one-third of the poor-quality embryos whereas nuclear labeling was absent in intact viable embryos. Degenerating embryos showing a strong nuclear staining for BCL2L10 exhibited a fainter mitochondrial signal. Subcellular localization of BCL2L10 was also affected by thapsigargin treatment, indicating that external apoptotic stimuli lead to internal defects in BCL2L10 expression.

Conclusions: While the BCL2L10 mRNA is a maternal transcript, the BCL2L10 protein is detected in human preimplantation embryos at least until the blastocyst stage. BCL2L10 appears to be differentially distributed at the subcellular level between viable embryos and nonviable or arrested embryos. We suggest that implications of not only aberrant gene expression but also abnormal protein subcellular redistribution should be established in pathological conditions resulting in embryo arrest. In that respect, whether embryo quality is related to an exclusive mitochondrial localization of BCL2L10 requires further study.


**O-012 Identification of possible biomarkers of embryo viability in the human embryonic secretome: preliminary results**


1 Sapienza Institute - Educational and Research Center in Assisted Reproduction, Scientific Department, Sao Paulo, Brazil
2 Fertility - Assisted Fertilization Center, IVF Laboratory, Sao Paulo, Brazil
3 Fertility - Assisted Fertilization Center, Scientific Department, Sao Paulo, Brazil
4 State University of Campinas, Institute of Chemistry, Campinas, Brazil
5 Waters Corporation, Mass Spectrometry Applications Research and Development Laboratory, Barueri, Brazil
6 Alfenas Federal University, Department of Exact Sciences, Alfenas, Brazil
7 Fertility - Assisted Fertilization Center, Clinical Department, Sao Paulo, Brazil

Introduction: The classic proteomics approach involves two-dimensional polyacrylamide gel electrophoresis. Nevertheless, limited success in the field of embryology is achieved due to the large amount of protein needed for the analysis, and due to the extensive sample manipulation workflow. Advances in proteomic technologies, especially involving nano ultra-high pressure chromatography (nanoUPLC) and mass spectrometry (MS), have allowed the use of minimal sample amount and the efficient identification of an increased number of proteins. Therefore, nanoUPLC-MS allows the non-invasive profiling of the human embryonic secretome, which involves proteins produced by the embryos and secreted into their surrounding environment. This strategy can provide the identification of biomarkers to be used as a powerful tool for embryo pregnancy prediction, leading the selection of the best embryo for transfer. The aim of this study was to identify differential secreted proteins in culture media samples used for embryo culture of patients undergoing intracytoplasmic sperm injection (ICSI) using data independent scanning based on UPLC-MS.

**Material and Methods:** Seventeen embryos from 8 patients undergoing ICSI were split according to the pregnancy outcome: positive (n = 9) and negative (n = 8). After fertilization assessment the culture media were refreshed and the embryos were cultured for more 48 hours. After embryo transfer, the remaining culture media were collected and the samples were pooled and precipitated using a solution containing 10%(v/v) trichloroacetic acid in acetone. Samples were prepared until final protein concentration was 1μg/μl and were enzymatically digested with trypsin. NanoUPLC (nanoAcquity™) tandem nanoESI with MS² acquisitions were performed with a Qq-IMS-oaTOF Synapt HDMS™ mass spectrometer (Waters, Manchester, UK). Protein identifications and quantitative data package were generated by dedicated algorithms with ProteinLynxGlobalServer v.2.4 Expression² software and the UniProtKB/Swiss-Prot database. Only proteins in attendance scores and confidence higher than 99% were considered in order to accept these database searches.

Results: It was observed unique proteins secreted by the embryo in positive and negative-pregnancies groups. The protein Jumonji (JARID2) was only observed in the positive-pregnancy group. Jumonji is a nuclear protein essential for cardiovascular, central nervous system and liver development at mouse embryogenesis. This protein is a Polycomb Repressive Complex 2 component, which modifies chromatin to silence many embryonic patterning genes, acting as a negative regulator of cell proliferation signaling. Exclusively at the negative-pregnancy group, there was a release of Testis-specific gene 10 protein (TSGA10), a perinuclear protein which has a key role in spermatogenesis. Its expression occurs during developmental stages of mouse embryos, in actively dividing and fetal differentiating tissues. This expression pattern suggests that it may be involved in active cell division, differentiation, and migrating cells.

Conclusions: Our data show that nanoUPLC-MS² technology is a valuable technique able for characterizing the human embryonic secretome. Our results suggest that competent embryos have a differential protein expression, with some proteins secreted into the surrounding culture medium being potential biomarkers. These results can also increase the understanding of early embryonic cellular processes correlated to pregnancy outcome. Embryo viability has been associated with a quiet rather than active metabolism, as RNA transcripts are more frequently up-regulated in oocytes and embryos before the embryonic genome activation presenting lower developmental potential. This pattern may also be related to protein function, since Jumonji protein, only observed at positive-pregnancy group, acts as a gene expression repressor. Otherwise, TSGA10 protein, whose detection was only at negative-pregnancy group, enhances cell division and differentiation, therefore it enhances gene expression. Secretome analysis may assist embryo selection based on morphological assessment in revealing secreted factors that reflect developmental competence and viability, and could predict a successful pregnancy, leading to single embryo transfer. This study will be sustained to confirm and seek for more interesting biomarkers in our results.

**O-013 The number of infiltrating leukocytes in follicular fluid could be used as a novel marker to predict the developmental competence of mature oocytes**

T. Ishikawa1, Y. Nakajo1, M. Ota1, M. Doshida1, M. Toy1, K. Kyono1

1 Kyono ART Clinic, Gynecology, Sendai, Japan

Introduction: The selection of embryos (oocytes) is currently based on morphological criteria in assisted reproductive technology. With the development of elective single embryo transfer, non-invasive and more quantitative methods of embryo selection, which have the ability to predict developmental competence, have been required. The microenvironment of ovarian follicle controls the oocyte maturation and the acquisition of developmental competence of nurturing oocyte. Hence, follicular fluid (FF) must include valuable information which could provide us with novel markers of oocyte viability. In this study, we focused on infiltrating leukocytes in FF and investigated the correlation between leukocyte population and the developmental competence of metaphase II (MII) oocytes.

Material and Methods: We examined 46 natural (unstimulated) menstrual cycles of 40 couples with unknown infertility causes at our clinic between August 2008 and November 2009. The patients underwent transvaginal ultrasound and serum hormone analysis. The ovulation was triggered with gonadotrophin-
releasing hormone agonist (Buserecure: Fuji Pharma Corp., Japan) intranasally, as soon as a follicle of > 18 mm was observed under ultrasonography. The oocyte retrieval (OPU) was scheduled 36 h after the trigger. IVF and following embryo culture were carried out with conventional methods. Fertilization was assessed 20 h after insemination, and embryo development was evaluated on days 2, 3, 5 and 6, and blastocysts were cryopreserved. FF was obtained at OPU. Leukocytes were separated from FF using Polymorph Rep (Axis-shield, Poc), centrifuged in phosphate-buffer-saline (PBS) twice, and suspended in 100μl of PBS. 1μl aliquots of cell suspension were applied for preparation of Diff-Quik (DQ) stained smears. The number of leukocytes was counted, and they were classified into mononuclear leukocytes or polymorphonuclear leukocytes on DQ stained smears. An accurate number of infiltrating leukocytes was determined by subtracting contaminated leukocyte count from the leukocyte count on stained smears.

Results: The mean age (means ± SD) of the patients was 33.1 ± 2.9 years (range: 28 - 37 years). OPU was performed in 40 cycles, but six cycles were cancelled due to abnormal hormone levels. In each of the 33 cycles (cases), one oocyte was successfully retrieved, and a total of 25 embryos developed to early cleavage stage (75.6%). A total of 14 embryos had developed into blastocysts on day 5 to day 6 (56.0%). The accurate number of infiltrating leukocytes was possible to determine in 26 (of 40) cycles. In these 26 cycles, contaminated leukocyte count from peripheral blood were below 10^5 cells per follicle (peripheral blood volume < 2μl). The cycles were classified into two groups as follows: group 1, developed into the blastocyst stage (n = 8); group 2, arrested in early cleavage stage-pronuclear stage, unfertilized oocytes, and retrieved no oocyte (n = 18). There was no significant difference between groups 1 and 2 in both leukocyte count and mononuclear leukocyte count. In contrast, there was a significant increase in polymorphonuclear leukocyte count of group 1 compared to that of group 2 (101.6 ± 47.6 x 10^3 versus 8.2 ± 8.6 x 10^3; P < 0.001).

Conclusions: This is the first report to show that the number of infiltrating polymorphonuclear leukocytes in FF could be associated with the blastocyst formation of MI oocyte. The hypothesis that ovulatory follicles become inflamed has been supported by previous reports. Therefore, the ovulation is controlled with a large variety of cytokines and chemokines which accelerate polymorphonuclear leukocyte migration. It is possible that polymorphonuclear leukocyte count could be used as a novel marker to predict the developmental competence of MI oocytes.

O-014 Gene expression of hormones and hormone receptors and growth factors and receptors in 8Cell human embryos - their role in early embryonic development

P. Drakakis1, A. Vismas2, G. Partsinevelos3, B. Desmarais4, R. Blets5, K. Kallianidis6, D. Lourad6, A. Antsaklis7, A. Kiessling8
1 “Alexandra” General Hospital of Athens. Recurrent Miscarriage Unit 1st Ob/Gyn Dept, Athens University Medical School
2 Bedford Stem Cell Research Foundation, Bedford Stem Cell Research Foundation, Somerville Massachusetts, U.S.A.

Introduction: The 8Cell stage human embryo was recently reported to over-express circadian oscillators and cell cycle drivers, such as cyclin E and Myc, and undereexpress cell cycle checkpoints, such as RB and WEE1. These findings indicate the totipotent embryo cells may not require hormone or growth factor stimulation for cell cycle progression.

Material and Methods: Using GO terms, Reactome and KEGG we have compiled a list into 249 genes and hormone receptors and 479 growth factors and receptors to query our database, 8CFES (8Cell/fibroblasts/embryonic stem cells), comprised of six whole genome microarrays: RNAs from two pools of 8Cell human embryos, fibroblasts before and after induced pluripotency, and two lines of embryonic stem cells (hES), hES01 and H9. The 8Cell microarray studies were reviewed and approved by institutional review boards in both Boston, MA and Athens, Greece.

Results: Several hormones and receptors were essentially silent on all six 8CFES microarrays, including: AMH/AMHR2; CAGA/LHCRG; FSHB/FSHR; GH/GHR; PRL/PRLR; PTH/PTH2R; PGR, RARB, THR8, TSHR, GIPR, OXTR. Several hormone/receptor genes were detected at low (< 500 FUs) levels on the 8Cell and hES arrays, including: CGB2, CCKAR, CSH1, EPO, INHA, INS/INSR, PENK, PRLHR, RORA and SCT. Twenty four genes were detected at moderate (500-4999 FUs) levels, including: CORT, FST, PRLH (8Cell only), GNRH2, IGF2R, RARA, RXRB, and THRAP1. Five hormone/receptor and related genes were detected at high (>5000 FUs) levels for hES and 8Cells: TRIP12, RBBM14/COAA, NUP62, PGRMC2, ACVR2B. Fifty four genes were differentially expressed between hES and 8Cells, of which two were allelic variants (NR2C1 and RXRA). Eighteen were under-detected at least 7-fold on the 8Cell arrays, including ESSRA, GAL, TRIP6, UCN2, THRAP3, and STC2 and ADM, both detected at highest levels in the fibroblasts. Several hormone genes were over-detected at least 7-fold on the 8Cell arrays although their receptors were silent or at low levels, including: CGB, CCK, GIP, OXT, NCOA6 and THRAP2.

Many growth factors and receptors were essentially silent or detected at low levels on all 8CFES arrays except the fibroblast array, including: FGFl-4,-5,-6, -7,-10,-11,-16,-17,-20,-21,-22,-23 and FGF8A, NR2L1,BMP1,-2,-3,-5,-8A, -10, -11, -12, -19, -20, -25, -27, -28, -30; BMP1B, -2, DKK1, -2, -4, -EDN2; FAS/FASLG; GDF1,-2,-5,-6, -8,-10; NRG2; OGN; PDGFA,-B,-C/PDGFBRA, -B; TGFA,-B1,-B3/TGFB1R; TNRFSF1B, -9,-11,-14, -17, -19; WISP1,-3; EGFR, NOV, TGFB2, GMGFI, EPSP, NRPI, CD97, CXCL1, KITLG, NGFB/NGFR; VEGFA. Fifty one genes were detected at moderate fluorescence levels in 8ES and hES, including LRPI0, CD47, BCA1, FIBP, S100A6, FGRFR1, -3, KIT; LIFR; NODAL; NENF, SOCS1, IN2; TNFRSF1A, -10B, -19L, -25. Thirteen genes were detected at high levels on 8CFES arrays, including: FGG3; BMP5B; and CD4. Forty two genes were silent or detected at least 7-fold lower in the 8Cells than hES, including: BMP7, DKK3, FGF2, -13, -19, -FRG1R1, -2; GDF3; GDFN; LEFTY1, -2; and TGFDR1. Fifty eight genes were greater than -7-fold higher in 8Cells than hES, including: AP15; BMP5,-15, CDR1; EGF; EGF5L, GDF9; GRB2, -7; PDGFR. Several growth factor genes were over-detected on the 8Cell arrays, but their receptors were silent or at low levels, including BMP6,-15 and EGF.

Conclusions: Taken together, the data suggest the totipotent 8-Cell blastomeres over-express some nuclear receptors/transcriptional activators, some conserved hormones, but not their receptors, and a few growth factors, but fewer receptors, suggesting a lack of autocrine hormone or growth factor signaling.

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SELECTED ORAL COMMUNICATION SESSION

SESSION 04: NOVEL TECHNIQUES FOR SPERM SELECTION

Monday 28 June 2010 10:00 - 11:30

O-015 Spermatic vein embolization improves semen quality in infertile men

S. Figueredo1, A.P. Sousa3, B. Paradu8, V. Carvalheiro6, T. Almeida Santos1
1 Coimbra University Hospital, Department of Reproductive Medicine, Coimbra, Portugal
2 Coimbra University Hospital, Department of Urology, Coimbra, Portugal
3 Coimbra University Hospital, Department of Radiology, Coimbra, Portugal

Introduction: Varicocele is considered a major cause of male infertility, with an overall prevalence rate of 40% in men being treated for primary infertility and of 80% in men with secondary infertility. Varicocele causes a progressive deterioration of seminal quality, its repair seeming to improve spermatogenesis. However this assumption remains controversial.

The aim of this study was to assess the effect of spermatic vein embolization with coils in semen quality in a population of infertile men.

Material and Methods: A retrospective cohort of 34 infertile men of mean age 33.64 ± 4.41 years who underwent spermatic vein embolization with coils between February 2008 and September 2009 in Coimbra’s University Hospital was evaluated for semen characteristics according to WHO 1999 criteria. All patients underwent a complete history, physical examination, hormone profile and genetic testing if needed (karyotype and Y microdeletions).

Embolization with coils of the internal spermatic vein was performed after vasography. Semen analysis was performed before embolization and repeated 4-6 months after the procedure. A positive effect of the procedure was considered when seminal parameters rose from abnormal to normal values (WHO, 1999).

Results: Significant improvement was observed in mean sperm concentration, motility and morphology after spermatic vein embolization. After this procedure, sperm concentration increased from 27.49 ± 3.97 x10^6/mL to 36.36 ± 7.36 x10^6/mL (p < 0.05); sperm rapid progressive motility rose from...