clarified, and the same level of achievement as PIEZO-ICSI or even better can be expected. In the future, expanding the application range of this method to cases with normal egg membranes, along with further consideration as to whether NBP-ICSI can improve culture achievement or not, is desired.

ART LAB - SPERM

P-433 Wednesday, October 16, 2019 6:30 AM

WHAT IS THE BEST SPERM SOURCE AND METHOD OF SPERM SELECTION IN CASES WITH ABNORMAL SEMINAL OXIDATION-REDUCTION POTENTIAL (ORP) LEVELS ON THE DAY OF ICSI?

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OBJECTIVE: To investigate whether PICSI or TESA is better for the selection of sperm in cases of abnormal seminal ORP levels for ICSI patients .

DESIGN: Prospective randomized trial, which included 74 patients undergoing ICSI at a busy Fertility Clinic, Cairo, Egypt, from January 2018 to January 2019. ClinicalTrials.gov ID: NCT03360526.

MATERIALS AND METHODS: A total of 74 patients with sperm counts of more than $5x10^6$/mL and an ORP of more than 1.42 mV/10^6/mL were included in the study. Male partners were examined for infertility and seminal ORP was measured using the MiOXSYS analyzer. PICSI® dishes (Origio, Knardrupvej, Denmark) were prepared by hydrating the hyaluronan microdots with medium followed by incubation for sperm binding at 30°C. Sperm were checked for the hyaluronan binding capacity, immobilized and injected into mature oocytes. TESA was done by testicular tissue aspiration followed by sample processing and oocyte injection. Seminal ORP was tested in the same ejaculate that was used for ICSI and patients with abnormal ORP were randomized into two arms, PICSI (n=40) and TESA (n=34). Embryological parameters included: fertilization, cleavage, blastulation and good quality blastocyst rates were recorded. Pregnancy was followed up after 15 days of embryo transfer and pregnancy rate calculated. All statistical calculations were done using SPSS (Statistical Package for the Social Science; IBM Corp, Armonk, NY, USA) release 22 for Microsoft Windows.

RESULTS: There were no significant differences in the female age (30.1±4.58 vs. 29.2±4.16 yrs.) (P=0.3569), male age (36.4±5.87 vs. 34.6±6.44 yrs.) (P=0.2041), seminal ORP values (5.8±6.22 vs. 5.8±7.99 mV/10^6 sperm/ml) (P=0.9808) and the number of mature injected oocytes (15.7±7.8 vs. 16.8±7.7) (P=0.5631) between the PICSI and TESA groups, respectively. The blastulation rates between PICSI and TESA showed a significant difference (60.2% vs. 48.4%; P=0.0114). In contrast no difference in ORP level s was seen between PICSI and TESA, for fertilization (79.8% vs. 80.7%), cleavage (73.4% vs. 73.8%), high quality blastocyst (57.2% vs. 51.9%), pregnancy (67.8% vs. 50%), implantation (41.6% vs. 36.6%), and ongoing pregnancy rates (94.7% vs. 84.6%). There were also no correlations between ORP levels and fertilization (P=0.1523 R=-0.1792), cleavage (P=0.1475, R=-0.1724), blastulation (P=0.1763, R=-0.1623), and the percentage of high quality blastocyst formation (P=0.0902, R=-0.2055). The mean ORP level for the pregnant group was 6.36± 6.98 mV/10^6 sperm/ml as compared to6.39± 8.81 mV/10^6 sperm/ml in the non-pregnant group (P=0.9891).

CONCLUSIONS: The use of PICSI as a sperm selection method in patients with abnormal seminal ORP levels may result in better selection of sperm and improved blastulation rate. Thus, contrary to reports in the literature that TESA-retrieved sperm are unexposed to seminal reactive oxygen species, our study failed to show the advantage of TESA over PICSI dishes.

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INVESTIGATION OF DEEP LEARNING BASED DETECTION OF SPERM MORPHOLOGICAL DEFECTS.

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OBJECTIVE: Sperm selection in intracytoplasmic sperm injection (ICSI) is generally performed by embryologists' subjective visual inspection, and developing the method of an objective sperm selection and evaluation is necessary. In this study, we focused on the evaluation of sperm morphology and aimed to investigate the method to detect morphological abnormalities by computer analysis using deep learning models and to evaluate their performances.

DESIGN: We extracted still images of sperms from the videos, which were recorded during ICSI, and embryologists inspected the sperm morphology. We constructed models from these still images and embryologists' inspection results. We evaluated the accuracy to detect morphological defects and visualized the important region for prediction of abnormality by these models.

MATERIALS AND METHODS: We used a set of 1,095 images of morphologically normal sperms, which succeeded in fertilization, and another set of 475 images of morphologically abnormal sperms, which were not used for ICSI. Embryologists visually inspected these sperms and identified their morphologically abnormal sites. We conducted 2 kinds of classification. The first is whether the sperm has morphological defects. The second is which portion has morphological defects among 3 classes of the head only, both head and neck, and none. These images were analyzed with 2 kinds of convolutional neural network (deep learning) models, which were a simple model with 9 hidden layers and the VGG16 model with 22 hidden layers and pre-trained parameters in the transfer learning. We compared these model performances and examined the accuracy improvement in image size and class weight adjustment in inverse proportion to imbalanced data.

RESULTS: The discrimination accuracy on the morphological abnormality of the sperm in the VGG16 model was 95.6% (AUC 0.988) in 224 pixels square images, and this was better than that of the 9 hidden layers model (Accuracy 83.2%, AUC 0.959). The abnormal site classification accuracy in the VGG16 model was 87.1% (AUC 0.958). The class weight adjustment could improve the accuracy in neither the VGG16 model nor the 9 hidden layers model. On the other hand, we got similar accuracy using 64 pixels square images but we found that the models learned background noises in images through visualization of the important region.

CONCLUSIONS: We confirmed that the deep learning models on sperm morphology can properly identify morphological defects at high accuracy. This suggested that these models will be able to support in selecting objectively morphologically normal sperm in the future. Our models could work well even in class-imbalanced data, and the class weight adjustment was not necessary for imbalanced data. However, if the image resolution is insufficient for appropriate learning, these models could not learn well even if the accuracy of the model was high. Therefore, the visualization of important region is needed for validation of learning models. In this study, the number of samples is limited at a single facility, and we are going to add much more samples in multiple facilities to validate our method.

SUPPORT: Miraca Research Institute G.K.

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DEFECTS IN SPERM CAPACITATION AND FERTILIZING ABILITY ARE HIGHLY PREVALENT IN MEN UNDERGOING FERTILITY WORKUPS, EVEN IF NORMOSPERMIC.

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Cap-Score (%)	PGP (%)	% of men having fertility exams (n=1610)	% normospermic men having fertility exams (n=948)	% men having fertility exams >10M TMC (n=1489)	% fertile men (n=76)
≤ 18	≤ 19	8	6	7	1
19 - 25	20 - 29	28	27	28	9
26 - 31	30 - 39	32	32	32	14
32 - 36	40 - 49	17	19	18	36
37 - 42	50 - 59	9	10	9	24
> 42	≥ 60	6	6	6	16

OBJECTIVE: Semen analysis (SA) fails to evaluate fertilizing ability and best identifies extreme infertility cases. Cap-Score™ functionally assesses sperm capacitation/male fertility and prospectively predicts pregnancy. Here, we examine the association of SA, Cap-Score, and Cap-Score's relationship with the probability of generating pregnancy in 3 cycles (PGP; Schinfeld et al., 2018), in men having fertility exams vs fertile men.

DESIGN: Correlation study: Cap-Score, PGP and SA metrics were compared in 1610 men questioning fertility vs 76 fertile men (pregnant partner or recent father).

MATERIALS AND METHODS: Semen was collected from men having SA because of fertility concerns (9 clinics; 10/2016 to 3/2019). Volume, concentration and motility were assessed (WHO criteria; morphology omitted due to variable methods). Fixed samples were shipped to Androvia for Cap-Score and PGP determination. Fertile men were assessed previously (WIRB 20152233). **Table 1** was designed with even PGP bins and evaluated by Chi-square.

RESULTS: 59% (948/1610) of men having SA were normospermic (volume, concentration, motility). Compared to fertile men ($p<0.001$), more men having fertility exams had Cap-Scores ≤ 31 (PGP bins of ≤ 19, 20-29 and 30-39). Fewer than expected had Cap-Scores ≥ 32 (PGP bins of 40-49, 50-59 and ≥ 60). This distribution revealed a high prevalence of reduced capacitation/fertilizing ability in men having fertility exams. Defects in sperm function were equally prevalent regardless of passing any single or multiple SA metrics, or those having >10 million total motile cells (TMC; $p=0.990$).

CONCLUSIONS: Of normospermic men having fertility exams, 65% (616/948) had Cap-Scores ≤ 31 (PGP ≤ 39%); in contrast, only 25% of fertile men (19/76) scored in this range. Conversely, only 35% (332/948) of normospermic men questioning their fertility had Cap-Scores ≥ 32, in contrast to 75% of fertile men. These data support reports that reduced sperm function/fertilizing ability is common in men questioning their fertility and cannot be detected by traditional SA, contributing to the high percentage of men diagnosed with idiopathic infertility. In men having fertility exams, reduced Cap-Scores were detected equally in normospermic men vs all men examined. These data show that a test of sperm capacitation offers a powerful complement to traditional SA, capable of identifying normospermic men with reduced sperm fertilizing ability.

Reference: Schinfeld et al.Â Cap-Score™ prospectively predicts probability of pregnancy. Molecular Reproduction and Development. 2018; 85 (8-9), 654-664

SUPPORT: Androvia LifeSciences LLC.

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PATERNAL CONTRIBUTION TO EARLY EMBRYONIC DEVELOPMENT IN SEVERE MALE FACTOR PATIENTS. Jenna Friedenthal, MD,[a] Dmitry Gounko, MA,[b] Joseph A. Lee, BA,[b] Christine Briton-Jones, PhD, HCLD,[b] Alan B. Copperman, MD.[a] [a]Icahn School of Medicine at Mount Sinai, New York, NY; [b]Reproductive Medicine Associates of New York, New York, NY.

OBJECTIVE: Current evidence suggests that the maternal genome is primarily responsible for embryonic development until the cleavage stage, at which time, expression of paternal genes occurs along with activation of the embryonic genome [1]. Theoretically, sperm could influence earlier post-fertilization events, since defects in the sperm centrosome have the potential to compromise early cell division. Additionally, sperm DNA damage has been shown to adversely affect embryo quality as early as day 2 of development [2]. Evidence regarding the association between severe male factor infertility and embryonic development, embryonic aneuploidy, or clinical outcomes within in vitro fertilization (IVF) cycles utilizing intracytosplasmic sperm injection (ICSI) is contradictory [3]. Thus, we sought to assess the relationship between severe male factor infertility and early embryonic development in an IVF model that includes ICSI and preimplantation genetic testing for aneuploidy (PGT-A).

DESIGN: Retrospective cohort study.

MATERIALS AND METHODS: Our study included patients at a single academic center who underwent IVF-PGT-A cycles from 2011 to 2019. ICSI was used in all study cases. Patients were divided into 2 cohorts: severe oligospermia (<5 million/mL), and normal semen analyses (SA) (≥5 million/mL). The primary outcome was cleavage rate (CR). Secondary outcomes were fertilization rate (FR), blastulation rate (BR), euploid rate (ER), ongoing pregnancy/live birth rate (OP/LBR), and clinical loss rate (CLR). Student's t-test, chi-squares, and multivariate logistic regression analyses were used for statistical analysis, with $p<0.05$ considered significant.

RESULTS: A total of 3,029 patients underwent 3,488 IVF-PGT-A cycles during the study period, leading to 4,716 single, euploid frozen embryo transfers. In our unadjusted analysis, the FR and CR were significantly lower in the severe oligospermia group compared to the normal SA group (FR 82.30% vs 77.78%, $p<0.0001$; CR 99.25% vs 98.23%, $p = 0.007$). There were no significant differences in BR, ER, or clinical pregnancy outcomes between the groups. After performing an adjusted analysis that controlled for confounding variables, a significant difference in CR between the oligospermia group and the normal SA group ($\beta = 0.99$, $p = 0.03$) remained.

CONCLUSIONS: In the largest study to date evaluating the association between the paternal genome and embryonic development, we demonstrated that oligospermic samples are associated with impaired early embryo development. Our results provide new insight into the role of the paternal genome in embryonic development prior to activation of the embryonic genome. Future studies should aim to examine more closely paternally-derived genomic actions, including epigenetic factors such as paternal centrosome function, chromatin packaging, or histone modification, which impact successful cell division and growth prior to the cleavage stage in severe male factor patients. Our findings may lead to a better understanding of the ways in which maternal-paternal genomic interactions drive early embryonic development.

References: 1. Schultz, R.M., *The molecular foundations of the maternal to zygotic transition in the preimplantation embryo.* Hum Reprod Update, 2002. **8**(4): p. 323-31.

2. Simon, L., et al., *Paternal influence of sperm DNA integrity on early embryonic development.* Hum Reprod, 2014. **29**(11): p. 2402-12.

3. Mazzilli, R., et al., *Effect of the male factor on the clinical outcome of intracytoplasmic sperm injection combined with preimplantation aneuploidy testing: observational longitudinal cohort study of 1,219 consecutive cycles.* Fertil Steril, 2017. **108**(6): p. 961-972.e3.

SUPPORT: None.

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DOES THE USE OF MICROFLUIDIC SPERM SORTING FOR THE SPERM SELECTION IMPROVE IVF SUCCESS RATES IN MALE FACTOR INFERTILITY? Pinar Ozcan, MD, Assoc. Prof.,[a] Taha Takmaz, MD,[a] Melis Gokce Kocer Yazici, MD,[b] Oya Akcin Alagoz, MD, Assoc. Prof.,[c] Mert Yesiladali, MD,[b] Cem Neset Fıçıcıoğlu, MD,