Conclusions: In compromised monochorionic twins showing UA-AREDF in donor or smaller twin, postoperative lower CPR could be a useful predictive index for the subsequent fetal demise after laser surgery. Such low CPR value might reflect severe insufficient placental function or residual placental territory in donor or smaller twins.

OC18.06
Management of selective intrauterine growth restriction with abnormal Doppler in monochorionic diamniotic (MCDA) twin pregnancies

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Objectives: Review outcome following interventional and expectant management of MCDA twin pregnancies complicated with selective intrauterine growth restriction (sIUGR) and absent or reverse end-diastolic flow (AREDF) in the umbilical arteries.

Methods: All cases of sIUGR defined as abdominal circumference <5th centile and AREDF before 26+6 weeks, between 2011 and 2017. Management options included selective fetoscopic laser coagulation (SFLC) of inter-twin anastomoses, cord coagulation (CC), or expectant management (EM). Discordance in EFW and positive a-wave on the ductus venosus (DV) at diagnosis were considered as potential predictors for perinatal survival.

Results: Of 108 cases, 13, 50 and 45 were managed by SFLC, CC and EM. Overall survival was 23%(6/26), 40%(40/100) and 77.8%(70/90) respectively. The discordance in EFW at diagnosis was more marked and negative a-wave in DV was more prevalent in both intervention groups. Intrauterine demise of the co-twin occurred in 30.8%(4/13), 10%(5/50) and 6.7%(3/45) respectively and was associated with demise of the smaller twin following SFLC and EM in 76.9%(10/13) and 17.8%(8/45) respectively. AC < 3 z-scores and absent a-wave in the ductus venosus were predictive of spontaneous demise in the EM group. Mean gestational age at delivery was 30 (29-32), 35 (32-35) and 32 (29-32) weeks following SFLC, CC and EM respectively.

Conclusions: SFLC yielded poor results. Expectant management is a valid option as some will improve and allow a favourable neonatal outcome with few spontaneous fetal demise during follow-up. However, in cases with high discordance, AREDF and abnormal DV Doppler, CC should be considered to protect the co-twin.

OC18.07
Reduced ventricular strain initiates cardiovascular compromise in monochorionic pregnancies

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Objectives: We hypothesised reduced ventricular strain is the first cardiovascular response of the recipient fetus to developing Twin–twin transfusion syndrome (TTTS). Resultant impaired ventricular filling reduces the usual right to left atrial shunt, leading to right ventricular volume loading, increased venous pressure and decompensation.

Methods: We enrolled 150 monochorionic diamniotic pregnancies (MCDA) into a prospective cohort study (2015-2018). Our sonographers were taught to optimise 4-chamber clips during routine bi-weekly surveillance for TTTS development. Twin pairs were deidentified and separately imported into speckle-tracking software (Cardiac Performance Analysis, TomTec, Germany). Global peak systolic left and right ventricular strain (LV, RV) was analysed offline by two experienced co-authors, blinded to twin-type or pairing.

An interim cross-sectional analysis was performed using Wilcoxon signed ranks test for paired-twin analysis and significance of 2-tailed test, p<0.05. Nine pregnancies developed TTTS, we excluded one with TAPS. Mean values, prior to TTTS onset, were compared with 32 uncomplicated MCDA controls matched for gestational age (GA), with known outcomes.

Results: Mean GA (SD) at TTTS onset was 20.4 (2) weeks; GA at scan prior to TTTS onset was 18.7 (2.3) versus 19.9 (1.6) in controls. Median interval between scan and TTTS onset was 7 days (4-35). No controls had weight discordance >22%. No significant inter-twin pair differences in strain were detected.

Conclusions: Twins destined to be recipients had lower strain values than their co-twin. The small sample prohibits firm conclusions, but the findings are consistent with reduced strain in the recipient fetus before TTTS develops.

Supporting information can be found in the online version of this abstract

OC19: MANAGING COMPLICATIONS IN EARLY PREGNANCY

OC19.01
Cell-free DNA in the detection of chromosomal aneuploidies in early fetal demise and miscarriage

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Objectives: To assess the possibilities of cell-free DNA (cDNA) testing in case of early fetal demise and miscarriage.

Methods: This prospective study was started in March 2017. Pregnancies with diagnosed missed abortion or miscarriage between 5 and 12 weeks were included. For each case, the maternal blood sample was taken, cDNA was isolated from maternal plasma and the whole-genome sequencing using next-generation semiconductor sequencing was performed. The results were assessed using exponentially weighted moving average charts which enables to look at the distribution of reads alongside the chromosome 1-22 and X. Furthermore, the decidual tissue samples were taken during surgical evacuation of the uterus. They were checked for the maternal contamination and subsequently assessed using multiplex QF-PCR (chromosome 2,7,13,15,16,18,21,22) and some cases also with SNP array.

Results: 47 samples from nonviable pregnancies were analysed. The average gestation age was 8.1 weeks. In 34 (72%) cases the fetal fraction was sufficient (>4%) and cDNA results could be evaluated. Out of these, euploid fetus was detected in 21 (62%) cases. The remaining 13 (38%) cases showed chromosomal anomalies. These were Trisomies 4,14,15,16,18,21 and monosomy X, confirmed also by QF-PCR or SNP array. In addition to QF-PCR panel, cfDNA was isolated from maternal blood sample was taken, cfDNA was isolated from maternal plasma and the whole-genome sequencing using next-generation semiconductor sequencing was performed. The results were assessed using exponentially weighted moving average charts which enables to look at the distribution of reads alongside the chromosome 1-22 and X. Furthermore, the decidual tissue samples were taken during surgical evacuation of the uterus. They were checked for the maternal contamination and subsequently assessed using multiplex QF-PCR (chromosome 2,7,13,15,16,18,21,22) and some cases also with SNP array.

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