automated and manual segmentations. METHODS/STUDY POPULATION: Twenty placentas from singleton pregnancies between 11-14 weeks' gestation were manually and automatically segmented from 3D ultrasound volumes. Automated segmentations were produced by a trained convolutional neural network pipeline. Dice overlap scores and volumes were computed between manual and automated segmentations. Deformable medial modeling was applied to both manual and automated segmentations to produce the following metrics: maternal and chorionic surface areas (SA), thickness, circumference, and diameter along the generated medial surface. Placental non-planarity was also determined as the greatest medial surface height difference. A paired t-test and simple linear regression was performed between manual and automated segmentations for each shape metric. RESULTS/ANTICIPATED RESULTS: Mean placental volume measurements between manual and automated segmentations were similar, with a percent difference of 3.28% and a mean Dice overlap score of 0.85 ± 0.07. There were strong, statistically significant ($p < 0.01$) linear correlations with chorionic and maternal SA, SA difference, thickness, circumference, medial surface diameter, and medial surface height difference. No significant differences were noted with chorionic SA, thickness, circumference, maximum medial surface diameter, or medial surface height difference. However, statistically significant differences ($p < 0.01$-0.03) were noted in maternal SA, SA difference, and mean medial surface diameter. Despite these differences, mean percent difference for all morphometric parameters was less than or equal to 10%. DISCUSSION/SIGNIFICANCE: A deformable medial model evaluate unique global and regional shape placental features with highly correlated values between manual versus automated placental segmentations. However, clinical studies are needed to determine if minor differences would impact the clinical utility of these features as potential indicators of placental function.

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Does incorporation of plasma biomarkers to the Lung Injury Prediction Score improve the predictive value for development of acute respiratory distress syndrome?*

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OBJECTIVES/GOALS: To determine if incorporating specific laboratory values and plasma biomarkers (club cell secretory protein (CC16), matrix metalloproteinase 3 (MMP3), interleukin 8 (IL-8), protein C) to the Lung Injury Prediction (LIP) Score improves the predictive value for development of acute respiratory distress syndrome (ARDS) in ICU patients. METHODS/STUDY POPULATION: Adult patients admitted to the ICU on supplemental oxygen over baseline requirement with a LIP Score ≥6 will be included. Patients admitted to the ICU >24 hours, end-stage renal disease, decompensated heart failure, or <100 µL plasma available will be excluded. Whole blood will be collected from the core lab, centrifuged, and plasma will be stored at -80°C. Protein biomarkers will be measured using enzyme-linked immunosorbent assay. Baseline characteristics, laboratory values, ventilator parameters, and clinical outcomes will be collected from the medical record. ARDS will be defined by the Berlin criteria. Machine learning methods will be used to identify the model with the highest predictive accuracy. Area under the receiver operating characteristic curve of each model will be compared to the LIP Score. RESULTS/ANTICIPATED RESULTS: Research is in progress. Plasma samples and clinical data have been collected for 148 of the 160 samples required to achieve power. Biomarker analysis will take place after sample collection is complete. We anticipate a machine learning model incorporating laboratory values and one or more plasma biomarkers into the LIP Score will outperform the baseline LIP Score for prediction of ARDS development. DISCUSSION/SIGNIFICANCE: Delayed diagnosis and intervention contribute to poor ARDS outcomes. Current predictive models for ARDS have low accuracy and enriching these models with plasma biomarkers may increase their predictive value. Development of accurate models may facilitate earlier ARDS diagnosis and intervention as well as enrichment strategies for ARDS trials.

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Developing Methods for High-Resolution Characterization of Plasma Cells*

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OBJECTIVES/GOALS: Antibodies play an important role in the pathogenesis of a wide range of diseases, including cancer, autoimmune diseases, and infections. There are currently no reliable methods to isolate and study specific plasma cell subpopulations as antibody production sources. We aim to develop methods to study plasma cells in high resolution. METHODS/STUDY POPULATION: We will use molecular cloning to engineer fusion proteins that would bind plasma cell proteins to study these cells based on their surface features. The first phase of our study consists of assessing the efficacy of this plasma cell isolation method in established cell lines (e.g., RPMI 8226) and also antibody-secreting cell lines that we are establishing as a part of this study. In the second phase of the study, we will assess the efficacy of this method by studying antigen-specific plasma cell populations in the bone marrow aspiration samples of 20 healthy volunteers using various assays, including ELISPOT, flow cytometry, and fluorescent microscopy. RESULTS/ANTICIPATED RESULTS: We have designed the constructs and have completed the cloning. The final plasmids have been verified using various restriction enzymes and Sanger sequencing. Following the transfection of Freestyle HEK 293F cells and isolation of respective proteins, we expect to be able to utilize these engineered proteins to differentiate various antibody-secreting plasma cells. We will use cell lines for proof-of-concept experiments and will subsequently move this method to human bone marrow samples. We expect to be able to visualize multiple specific antibody-secreting plasma cell populations using fluorescent microscopy and utilize this method to isolate them by cell sorting via flow cytometry. DISCUSSION/SIGNIFICANCE: We expect to be able to use this method to target specific plasma cell clones in the advancement of precision medicine regarding the treatment of plasma cell disorders (e.g., multiple myeloma) and also expand its use in other areas, such as antibody discovery and the assessment of the humoral immune responses in infectious diseases.

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