

Summary of detection of mitochondrial mutations in preeclampsia

We hypothesized that placentas from patients with preeclampsia harbor more mutations, which may lead to poor placentation. To prove this hypothesis, we first extracted DNAs from placentas in patients with preeclampsia and full term delivery (FTD). We then sequenced the whole mitochondrial genome and identified mutations by Phred/Phrap. Currently, we have sequenced mitochondrial genome from 16 preeclampsia and 14 full term delivery patients. To our surprise, patients with preeclampsia contain 10% less mutations (12.5 vs 14.2 per patient). We further compared mutations in three groups: structural proteins, rRNAs, and tRNAs. Both preeclampsia and FTD patients shared same amounts of mutations (10.3 per patients). However, PE patients have less nonsynonymous mutation (3.8 vs 5.1 per patients). Preeclampsia patients contained much less mutations in rRNAs (1.8 vs 3.1 per patient), but no difference in conserved mutations (0.37 vs 0.36 per patient). Preeclampsia patients contained much less mutations in tRNAs (0.44 vs 0.85 per patient), and less conserved mutations in tRNAs (0.25 vs 0.67 per patient). We need larger samples to further evaluate significance of single mutations or mutations in each individual gene. Our next step is to sequence 100 more samples in both preeclampsia and FTD.