Genotype and gene expression correlates in human placentas: NCS Project 2-18

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Introduction: The human placenta plays a critical role in the maintenance and parturition process of pregnancy. Genetic factors are known to play a role in many common diseases associated with pregnancy including preterm birth and preeclampsia. To develop a resource for understanding normal gene expression and its correlates with genotype and to investigate gene expression differences in pathological placenta states we have created a bank of placentas collected both with the NCS and locally.

Methods: We have conducted preliminary gene expression profiling on a global basis for term placentas in labor and no labor deliveries using RNA sequencing of amnion, chorion and decidua. For NCS samples we did RT-PCR to assay gene expression and TaqMan assays for genotype determination.

Results: We studied 8 SNPs in 4 candidate genes (*PGR*, *OXTR*, *PLA2G4A*, *PTGER2*) for genotype and expression using placentas from the NCS prepilot study. Our work shows that gene expression in different placental tissues correlate better with each other than with other tissues and that there are unique tissue specific gene profiles associated with placental tissue.

Conclusions: Based upon the limited prepilot data set, the NCS collection should provide material that is robust for both genetic and gene expression studies. The outcomes of this work from the Pilot and Main Studies will be provided on publically accessible web sites and extended to additional tissue and gestational ages.