LEFT AND RIGHT VENTRICLE TRANSCRIPTOMES IN UNUSED HUMAN DONOR HEARTS

Poster Contributions

Hall C
Sunday, March 30, 2014, 3:45 p.m.-4:30 p.m.

Session Title: Approaches to Advanced Heart Failure: From VAD, Transplant, Palliative Care to New Percutaneous Therapies
Abstract Category: 12. Heart Failure and Cardiomyopathies: Clinical
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Background: Left (LV) and right (RV) ventricular transcriptome differences have not been reported in human donor (DON) hearts.

Methods: We performed RNAseq (30M target reads/cDNA library, paired-end 50 bp Illumina HiSeq 25009 sequencing) on 5 unused DON LVs and RVs. We used DESeq to determine log2fold differences of differentially expressed genes (DEGs, adjusted p < 0.05) and Ingenuity for network exploration.

Results: There were 24 LV vs RV DEGs including 5 non-coding (nc) RNAs. The top ten protein-coding DEGs included EREG (log2fold, -3.2), ANKRD2 (-2.0), SLC47A1 (-1.6), DPP6 (3.4), CLIC6 (-1.8), TRHDE (3.4), RABDAP1L (-1.1), HCN2 (1.9), IRX2 (2.8) and C5orf38 (2.1). ncRNAs (EnsEMBL GRCh37, release 67) included miRNA precursors 252194 (-2.2) and 252967 (-4.2), rRNA pseudogenes 241115 (-2.1) and 240117 (-2.1) and lncRNA 241530 (-1.8). Top canonical pathways included noradrenaline/adrenaline and serotonin degradation and TGFβ signaling with upstream regulators 9-hydroxyoctadecadienoic acid, EIF3I, PRCC, DYNLRB1 and ING2. The top network was “cell death/survival, cardiovascular disease” with central roles for TNF, SERPINE1 and EREG (Figure: red, upregulated; green, downregulated; orange, predicted activated; blue, predicted inhibited).

Conclusion: LV vs RV DON transcriptome DEGs include protein coding genes, novel non-coding RNAs, pseudogenes which may inform the risks of ischemic injury and/or dysfunction following transplantation.