

**COMPARATIVE TRANSCRIPTOME ANALYSIS IN CHIMPANZEE TRIO**

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Transcriptome can be defined as the total set of transcripts in a given cell or a population of cells (e.g., tissue). Using mRNA-sequencing (mRNA-seq) technology, which sequences the transcripts with massively parallel DNA sequencing (new generation sequencer: NGS), we can see the dynamics of transcripts among different type of cells (e.g., cancer cells vs. normal cells) or different organisms (e.g., human brain vs. chimpanzee brain). Here we used this mRNA-seq for transcriptome analysis of leukocyte in a chimpanzee trio (father-mother-child). We obtained 3~5 Gb from each individual by Illumina-GAI sequencer and found about a hundred thousand SNPs against a reference chimpanzee genome sequence (panTro2). Moreover we found ten thousands and several thousands of expression SNPs (expSNPs) and several thousands of expression INDEL (insertions and deletions) on average among trio, and revealed that expSNPs are more enriched on 3'-UTR than CDS or 5'-UTR, suggesting a major role of expSNPs as a gene expression regulator. Besides that, NGS enables us to quantify a level of gene expression in an allele-specific way, and it is thus possible to estimate relative contribution of *cis* and *trans* mutations for gene expression divergence, and more importantly, to detect candidate imprinting genes straightforwardly. At present, we have thousands of such expSNPs in the data. Further analysis as well as conjunction with human trio data could help us to get a comprehensive understanding for precise dynamics of transcriptome both intra- (trio) and inter- (humans and chimpanzees) specific levels.

Keywords: chimpanzee, comparative transcriptome, SNPs, new generation sequencer