DETECTING SEQUENCE VARIATION IN RAPIDLY EVOLVING GENES, X. Hou[1], M. Chen[2], M. delaBastide[2], Z. Xuan[2], J. Parla[2], L. Cardone[2], D. Rebolini[2], S. Pierce[2], W. R. McCombie*[2]
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The chromosomal DNA sequence of chimpanzee (*Pan troglodytes*) and human (*Homo sapiens*) differ by only 1.23% based on nucleotide substitutions. Positive natural selection during the evolution creates a great separation between the two species. It is hypothesized that genes that are rapidly changing during the evolution of primates could be related to brain functional disorders such as schizophrenia. Genome-wide *in-situ* exon capture combines the advantages of microarrays and massively parallel sequencing to enrich a desired non-repeat fraction of the genome, enabling focused and efficient resequencing of the targeted genes for *de novo* discovery of disease-related mutations. As a way of assessing the population variation of rapidly evolving genes in normal humans, we used the method above to perform deep sequencing on selective genes both in populations of unaffected human individuals and of chimpanzee. We have identified many single nucleotide polymorphisms (SNP) amongst several genes that are essential for apoptosis and cellular vitality.