

Analysis of the Molecular Role of COMT in Bipolar Disorder

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Background and Objective: Bipolar disorder is a chemical imbalance of neurotransmitters in the brain. This mental condition causes dramatic mood swings characterized by episodes of elation and high activity alternating with periods of low mood and low energy. Bipolar disorder affects approximately 5.7 million American adults, or about 2.6 percent of the U.S. population age 18 and older in a given year (Kessler and Chiu, 2005). Many genes have been implicated in bipolar disorder. The objective of this research was to accumulate all of the information contained in the various databases on *COMT* to include its structure, polymorphisms, phenotypic variations between male and female, and population diversity as it pertains to allelic frequencies and use this information to interpret the generated multiple sequence alignment and phylogenetic tree.

Methods: Sequences were selected from the Universal Protein Resource Database. A Unix-based T-Coffee multiple sequence alignment was viewed using GeneDoc with MEME Pattern identification and matching. TreeView Software was used to generate a phylogenetic tree.

Results: A T-Coffee multiple sequence alignment displays the most common *COMT* polymorphism and a phylogram displays a phylogenetic tree. Various databases reveal African-American allelic frequencies for the single nucleotide polymorphism, Rs4680, covering the most common MB-*COMT* Val158Met polymorphism.

Discussion and Conclusions: The addition of genotypes from African-American patients diagnosed with bipolar disorder will allow for a more thorough conclusion.