Potential of genomics for discovering addiction

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Abstract: Addiction, in contrast to diseases like cancer, has been traditionally studied using limited subsets of genes and signaling molecules. The advances in genomics now allow relatively easy identification of disease-related genes, many of which are potentially unexplored in different aspects of addiction. DNA array technology makes it feasible to investigate thousands of gene products simultaneously after drug exposure. Deep sequencing of genomes coupled with whole-genome linkage and association analyses help us better understanding of addiction biology by distinguishing the genes contributing to tolerance, sensitization, dependence, craving and relapse [1, 2]. Increasing evidence suggests that splice variants of neurotrophic factors and receptors may play an important roles in addiction [3, 4]. Further, intermediate phenotypes have prepared a bridge among functional alleles and different phenotypes and offer the golden opportunity in genome-wide analyses. On the other hand epigenomic studies are appealing as diseases like addiction last for long periods [1]. A general understanding of the addiction biology will also shed light on the mechanisms of other mental disorders such as depression, anxiety, schizophrenia and other overlapping conditions.

Keywords: Genomics; Addiction; Epigenomic

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