

# Assembling the jigsaw puzzle of drug addiction

January 5 2008

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Using an integrative meta-analysis approach, researchers from the Center for Bioinformatics at Peking University in Beijing have assembled the most comprehensive gene atlas underlying drug addiction and identified five molecular pathways common to four different addictive drugs. This novel paper appears in PLoS Computational Biology on January 4, 2008.

Drug addiction is a serious worldwide problem with strong genetic and environmental influences. So far different technologies have revealed a variety of genes and biological processes underlying addiction. However, individual technology can be biased and render only an incomplete picture. Studying individual or a small number of genes is like looking at pieces of a jigsaw puzzle - only when you gather most of the pieces from different places and arrange them together in an orderly fashion do interesting patterns emerge.

The team, led by Liping Wei, surveyed scientific literature published in the past 30 years and collected 2,343 items of evidence linking genes and chromosome regions to addiction based on single-gene strategies, microarray, proteomics, or genetic studies. They made this gene atlas freely available in the first online molecular database for addiction, named KARG ([karg.cbi.pku.edu.cn](http://karg.cbi.pku.edu.cn)), with extensive annotations and friendly web interface.

Assembling the pieces of evidence together, the authors identified 18 molecular pathways that are statistically enriched in the addiction-related

genes. They then identified five pathways that are common to addiction to four different substances. These common pathways may underlie shared rewarding and response mechanisms and may be targets for effective treatments for a wide range of addictive disorders.

Source: Public Library of Science

Citation: Assembling the jigsaw puzzle of drug addiction (2008, January 5) retrieved 18 April 2024 from <https://medicalxpress.com/news/2008-01-jigsaw-puzzle-drug-addiction.html>

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