



Expression profiling based on coexpressed modules in obese prepubertal children

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ABSTRACT. The aim of this study was to identify related genes and the underlying molecular mechanisms in obese patients who show a series of clinical and metabolic abnormalities known as metabolic syndrome. We identified expression profiles through a coexpression network. In addition, a similarity matrix and expression modules were constructed based on domain and pathway enrichment analysis. The genes in module 1 were mainly involved in the metabolism of xenobiotics by cytochrome P450, aldosterone-regulated sodium reabsorption, and focal adhesion owing to the presence of aldo/ketoreductase, basic helix-loop-helix, von Willebrand factor, Frizzled-related domain, and other domains. The genes in module 3 may be involved in cell cycle (hsa04110) and DNA replication (hsa03030) pathways through mini-chromosome maintenance, serine/threonine protein kinase, the protein kinase domain, and other domains. We analyzed the published molecular mechanisms of obesity and found many genes and pathways that have not been given enough attention and require further confirmation.

Keys words: Obesity; Coexpression network; Cell cycle; Pathway enrichment analysis