

## Physiological Genomics Analysis for Mania: Supportive Evidence for Epigenetics Concept

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### ABSTRACT

**Background:** Mania is an important psychological problem. This disorder can be detected anywhere in the world. This psychological disorder becomes an important concern in modern psychological medicine. **Aims:** There are some researches on the pathogenesis of this disease; however, there is no clear-cut on its etiopathogenesis. The big query is on the genetic underlying of the mania. **Materials and Methods:** Here, the author uses the physiological genomics study to better understand the pathogenesis of mania. **Results:** According to this work, the physiogenomics relationship on chromosomes could not be identified. **Conclusion:** The result from this study shows that mania might not have a genetic, but epigenic origin, which is different from the well-known disorder in psychological medicine, Alzheimer's disease.

**Key words:** Mania, physiogenomics, relationship

### INTRODUCTION


Bioinformatics can help manipulate the data derived from Human Genome project and it can be useful for studying of etiopathology of disease in medicine.<sup>[1]</sup> Physiological genomics is the new technique that can be useful in tracing of function to gene for finding the relationship in pathophysiology aspect.<sup>[2]</sup> This can also be helpful in psychological medicine.

Mania is an important psychological problem.<sup>[3]</sup> This disorder can be detected anywhere in the world. This psychological disorder becomes an important concern in modern psychological medicine. There are some researches on the pathogenesis of this disease; however, there is no clear-cut on its etiopathogenesis.<sup>[3]</sup> The big

query is on the genetic underlying of the mania. Here, the author uses the physiological genomics study to better understand the pathogenesis of mania.

### MATERIALS AND METHODS

This work used a simulation-based physiogenomics analysis by consomics technique.<sup>[4]</sup> The protocol used in this work is similar to the previous reports using the main physiogenomics tool, PhysGen. Conceptually, the test for relevancy or relationship between function and gene was carried out using the computational physiogenomics tool. The basic strategy, Targeting Induced Local Lesions in Genomes assay that helps detect allelic series of induced point mutations in genes of interest was mainly used.<sup>[4,5]</sup> In this work, the primary template was human genome similar to previous referencing studies.<sup>[6-8]</sup> The input ontology term is "Mania" gene in range v 2.02 with length 1 Mbp was applied and the outputs are gene with specific physiogenomics score (degree of correlation, significant if this score is more than 1). All steps in this work followed the previously published referencing reports<sup>[6-8]</sup> (see the previous published papers for more details).

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## RESULT

According to this work, the physiogenomics relationship on chromosomes could not be identified.

## DISCUSSION

Although mania is a well-known psychological disorder, its exact etiopathogenesis has never been clearly mentioned.<sup>[9]</sup> The genetic contribution is widely discussed for the possibility;<sup>[9]</sup> however, there has never been previous physiogenomics clarification. It is still a big question in psychological medicine that mania has its genetic root or not. Analysis of gene expression in mania with special focus on physiogenomics can help answer this problem.

Here, the author used the physiogenomics approach to study mania and no physiogenomics relationship can be identified. In fact, there are few reports on genetic underlying of mania. The potential that CACNA1C might be a genetic risk factor for mania has been recently published.<sup>[10]</sup> However, based on the present work, no evidence of physiogenomics relationship can be identified. Therefore, the emerging concept of epigenetics root of mania should be considered.<sup>[11]</sup> The recent molecular psychiatry report by Kaminsky *et al.* can be the good supportive evidence for this claim.<sup>[12]</sup> In that work, “epigenetic differences at HCG9” was found.<sup>[12]</sup>

The result from this study shows that mania might not have a genetic but epigenic origin, which is different from the well-known disorder in psychological medicine, Alzheimer’s disease.<sup>[8]</sup>

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