

ACU&MOX-DATA: a platform for fusion analysis and visual display acupuncture multi-omics heterogeneous data

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Abstract

A new network platform named ACU&MOX-DATA (<http://cbcb.cdutcm.edu.cn/ACU&MOX-DATA/>) was recently set up and introduced. The purpose of this website is to integrate and analyze multi-omics data of acupuncture and moxibustion and serve as a disease, clinical, and laboratory experiment public database. Some existing functions and the future plan of the website were also discussed. This platform can help researchers to integrate analyses and visual interpretation of key scientific issues in acupuncture & moxibustion under the guidance of traditional Chinese medicine theory through heterogeneous and multi-level data fusion analysis.

Keywords: Acupuncture and moxibustion, Integrate analysis, Multi-omics, Platform

Graphical abstract: <http://links.lww.com/AHM/A41>.

With the wide application of high-throughput technology, a large quantity of data is obtained from different levels, such as the genome, transcriptome, proteome, epigenome, metabolome, and metagenomics^[1]. Additionally, clinical and laboratory data such as neuroimaging and pathological information, which matches with multi-omics data is also increasingly accumulated. These data constitute multi-level and heterogeneous data, the integration analysis of which will help researchers gain a deeper understanding of biological processes and molecular mechanisms and provide new ideas for in-depth interpretation of biological phenomena or diseases^[2-3].

Acupuncture is one of the most distinctive traditional Chinese medicine therapies and has been used for thousands of years to treat diseases and regulate the balance in body by stimulating the acupoint with needles or a lit mugwort stick. However, the mechanism of action remains unknown as acupuncture is not clearly

understood. It is thus difficult to use Reductionism methods to accurately explain how acupuncture works and where it takes effect as it has multi-target, multi-form, and multi-level characteristics. In recent years, the use of multi-omics technology to study the principle and mechanism of acupuncture has grown in popularity^[4]. However, these studies often explain the role of acupuncture from one or two omics levels, which is a minor step toward the goal of understanding the whole acupuncture network. Additionally, although the combination of multiple omics may solve a few problems to an extent, complex acupuncture theories, such as the state and synergistic effect of acupoints, and how to conduct integration or fusion analysis remains a challenge.

Here, we present the ACU&MOX-DATA website (<http://cbcb.cdutcm.edu.cn/ACU&MOX-DATA/>), which was developed using the python Django framework. Its specific interface is written in html, CSS, and JavaScript (Figure 1). The ultimate goal of the platform is to achieve integrated analyses and visual interpretation of key scientific issues on acupuncture under the guidance of traditional Chinese medicine through heterogeneous and multi-level data fusion analysis. At present, the work has already made initial progress. Two key functional interfaces were established: One interface is the acupoint efficacy exploration interface, where researchers can select different diseases, different acupoints, different intervention parameters (such as acupuncture/moxibustion, acupuncture frequency, etc), and different target organs based on the existing data on the website, and comprehensively analyze the impact of the above factors on acupoint efficacy. The other one is for analyzing the characteristics and mechanisms of acupuncture and moxibustion. For instance, researchers can analyze the main differential genes or covariant genes changed after acupuncture intervention. These results will provide a reference for the subsequent selection of acupuncture points or methods of acupuncture, and help explore the mechanism of acupuncture (Figure 2).

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Figure 1. Home page of ACU&MOX-DATA website (<http://cbcb.cdutcm.edu.cn/ACU&MOX-DATA/>).

Another important function of the ACU&MOX-DATA website is to help researchers develop new strategies for acupoint combination research. Previously, if researchers wanted to know why two or more acupoints were used together to achieve better therapeutic effects, they would have to study each acupoint individually, and then combine them according to their common targets or pathways. This research strategy is more likely to verify the existing law of the acupoint combination use rather than create a new method for finding new combination mode of synergistic acupoints in treating disease. Therefore, it is difficult to break through the already existing acupoint combination of experience and theories. However, if we use a platform such as ACU&MOX-DATA, the research strategy will be transformed toward identifying the core mechanism or core symptom of the disease, finding the acupoint group that can affect the core mechanisms or core symptoms through network backtracking, and then optimizing the acupoint group through certain screening processes, so that the acupoint combination formula can be obtained. Thus, it is relatively easy to find the rule of acupoint synergistic effect, which can be verified later in clinical practice. It is undoubtedly very useful for promoting the development of acupoint combination use (Figure 3).

In the future, the platform will connect with the public database, improve the user's personalized data upload path, and further solve the technical bottleneck of integration the clinical or laboratory data with multi-omics data. This platform is expected to become an important support for the development of acupuncture in the era of massive data availability. Additionally, this database will promote innovative development and enhance the influence of discipline development of acupuncture.

Conflicts of interest statement

The authors declare no conflict of interest.

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Author contributions

Qiaofeng Wu and Shuguang Yu instructed the website construction. Qiaofeng Wu drafted the paper. Shuqing Liu, Ruibin Zhang, Qiang Tang, Longcong Dong, and Sihui Li provided data and participate in performing the study. All authors read and approved the final manuscript.

Ethical approval of studies and informed consent

All procedures were approved by The Committee on Ethical Use of Animals of Chengdu University of Traditional Chinese Medicine and the Ethics Committee for Animal Care and Use of Sichuan University. All procedures were conducted in accordance with the guidelines of the National Institutes of Health Animal Care and Use Committee (No. 2020267A).

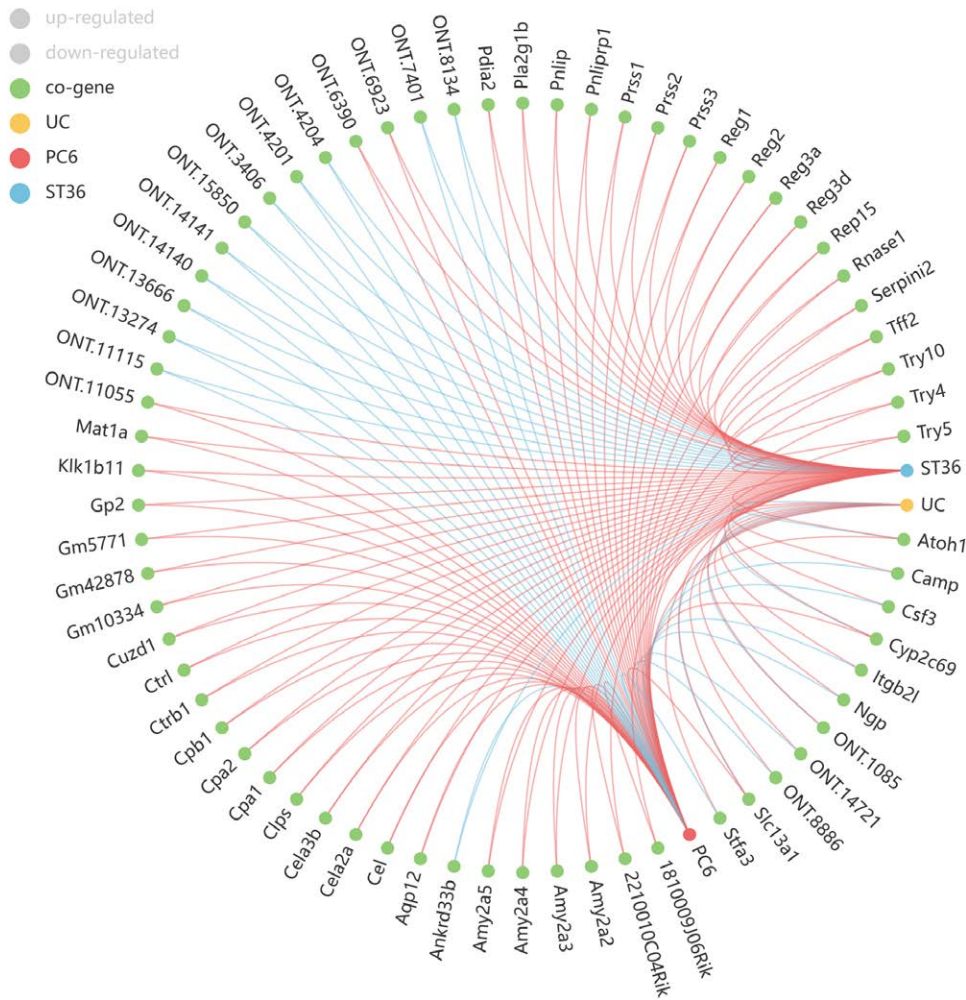


Figure 2. Differential coexpression genes (co-gene) analysis after moxibustion at Zusanli (ST36) or Neiguan (PC6). The data comes from the C57BL/6J mice model of UC, only showing the top 100 genes. UC: ulcerative colitis.

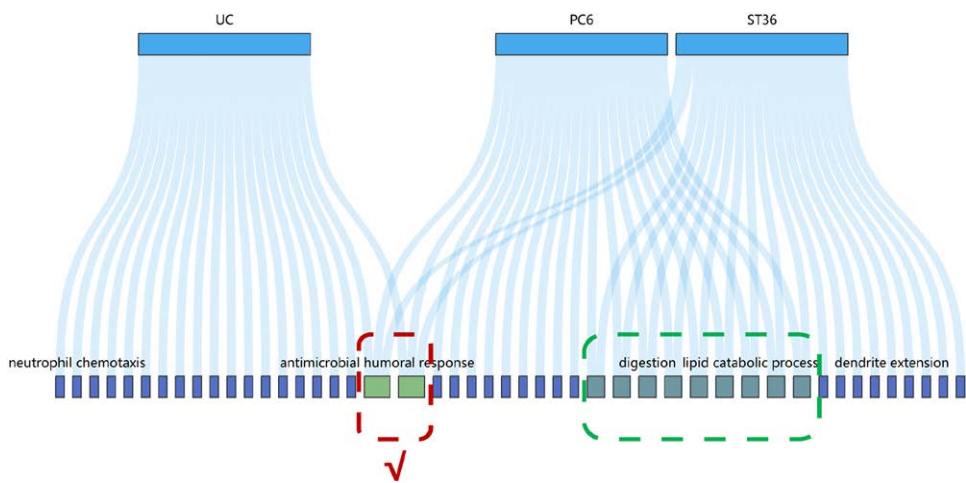


Figure 3. New strategy for acupoint synergistic effect research. Take Zusanli (ST36) and Neiguan (PC6) as an example, we first analyze the pathways affected by ST36 and PC6, respectively, then backtrack the pathway mechanisms according to the network affected by both acupoints. Next, we can infer their synergistic effect, data also comes from UC mice. UC: ulcerative colitis.

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Data availability

On reasonable request, the corresponding author will provide the datasets used and/or analyzed in this study.

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