[BIOINFO 2023]

Transcriptome-based systematic analysis of the molecular mechanisms of Bojungikki-Tang on immune cell networks

Sang-Yun Kim[1¶], Jin-Mu Yi[2¶], Hee-Rim Yeo[1], Musun Park[3], Mi-Kyung Jeong[2*] and Sang-Min Park[1*]

1College of Pharmacy, Chungnam National University, Daejeon 34134, Republic of Korea

2KM Convergence Research Division, Korea Institute of Oriental Medicine, Daejeon 34054, , Republic of Korea

3KM Data Division, Korea Institute of Oriental Medicine, Daejeon 34054, Republic of Korea

¶ These authors contributed equally to this work.

* Co-Correspondence to: Sang-Min Park, Ph.D. and Mi-Kyung Jeong, Ph.D

Immunotherapy with immune checkpoint inhibitors, including anti-PD-1 antibodies, has improved cancer treatment, increasing long-term survival rates for patients. However, immunotherapy has relatively low response rates, leading to exploration of combination therapies to address this limitation [1]. Previous studies have demonstrated the effectiveness of combining Bojungikki-Tang (BJIKT) with anti-PD-1 antibodies in modulating immune function and inhibiting tumor growth. In this study, we used drug-induced transcriptome analysis to investigate the molecular mechanisms behind these synergistic effects of BJIKT [2, 3]. Large-scale transcriptome data were generated for five immune cell types treated with BJIKT, four key herbs from BJIKT (Astragalus mongholicus Bunge, Atractylodes japonica Koidzumi, Glycyrrhiza uralensis Fisher, and Panax ginseng C. A. Meyer), and various combinations of these herbs. Differential expression analysis and pathway enrichment analysis revealed that BJIKT enhances the tumor microenvironment, influencing immunological functions within a network of interactions between the five immune cell types and cancer. These findings may contribute to the development of herbal medicine-based immunotherapy combinations.

Keywords : Herbal medicine, Transcriptome, Immunotherapy, Combination therapy, Pathway analysis