

## A Systematic Approach to Integrate Traditional Chinese Medicine and Western Medicines by Studying Comorbidity Mechanism of Adolescent Idiopathic Scoliosis and Primary Amenorrhea

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**SUMMARY.** This study was planned to explore the potential mechanism of comorbidity between adolescent idiopathic scoliosis (AIS) and primary amenorrhea (PA) by network biology method. In the first step, the Genecards database was searched to obtain the disease targets of AIS, PA and Mayer-rokitans Kuster-Hauser syndrome (MRKH). In the second step, the Venn diagram was used to correlate the targets of AIS, PA and MRKH to obtain common targets. The third step is to submit the common targets to the String platform, build a protein-protein interaction network (PPI), and click on the Cluster button for clustering. Finally, use String plug-in analysis to perform biological enrichment and pathway analysis of key targets, download biological processes, molecular functions, and cellular components (Gene Ontology) TSV files, and download KEGG Pathways and Wiki Pathways files, as well as diseases associated with genes and human phenotype data, and finally visualize the data with the help of bioinformatics. A total of 5227 targets were obtained for AIS, 1561 targets for PA, and 697 intersection targets, and then 20 key targets were obtained by intersection with 52 targets of MRKH. Submit it to the String platform to draw the PPI network, involving a total of 19 nodes and 35 edges, and MCODE analyzes 3 major modules. According to the results of GO bio-enrichment analysis, it was found that comorbid genes mainly act on nuclear chromatin and protein-DNA complexes, affect the activity of DNA-binding transcription factors and participate in the morphogenesis of human tissues and organs, especially the genitourinary system and the central axis bone development. The KEGG pathway analysis targets are related to the WNT signaling pathway, which can affect the regulation of stem cell pluripotency. In addition, the Wiki pathway is mainly involved in mammalian sexual development, affecting the differentiation of osteoblasts and the occurrence of the kidney. Most likely to cause diseases of the reproductive system, and phenotypes with abnormal uterine and skeletal morphology. The integration of gene-protein interactions and metabolic pathways can systematically reflect the co-morbidity mechanism of AIS and PA. The high fitting of pathway gene targets can be used from the perspective of integrating traditional Chinese medicine and Western medicine, the macro and micro refer to each other and explain.

**RESUMEN.** Este estudio se planeó para explorar el mecanismo potencial de comorbilidad entre la escoliosis idiopática adolescente (AIS) y la amenorrea primaria (AP) mediante el método de biología de redes. En el primer paso, se buscó en la base de datos de Genecards para obtener los objetivos de enfermedad de AIS, PA y el síndrome de Mayer-rokitans Kuster-Hauser (MRKH). En el segundo paso, se utilizó el diagrama de Venn para correlacionar los objetivos de AIS, PA y MRKH para obtener objetivos comunes. El tercer paso es enviar los objetivos comunes a la

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plataforma String, crear una red de interacción proteína-proteína (PPI) y hacer clic en el botón Cluster para agrupar. Por último, use el análisis de complemento String para realizar enriquecimiento biológico y análisis de rutas de objetivos clave, descargar archivos TSV de procesos biológicos, funciones moleculares y componentes celulares (Ontología de genes) y descargar archivos KEGG Pathways y Wiki Pathways, así como enfermedades asociadas, con genes y datos de fenotipo humano, y finalmente visualizar los datos con la ayuda de la bioinformática. Se obtuvieron un total de 5227 objetivos para AIS, 1561 objetivos para PA y 697 objetivos de intersección, y luego se obtuvieron 20 objetivos clave por intersección con 52 objetivos de MRKH. Envíelo a la plataforma String para dibujar la red PPI, que involucra un total de 19 nodos y 35 bordes, y MCODE analiza 3 módulos principales. De acuerdo con los resultados del análisis de bioenriquecimiento GO, se encontró que los genes comórbidos actúan principalmente sobre la cromatina nuclear y los complejos proteína-ADN, afectan la actividad de los factores de transcripción que se unen al ADN y participan en la morfogénesis de los tejidos y órganos humanos, especialmente el sistema genitourinario y desarrollo óseo del eje central. Los objetivos del análisis de la vía KEGG están relacionados con la vía de señalización WNT, que puede afectar la regulación de la pluripotencialidad de las células madre. Además, la vía Wiki está involucrada principalmente en el desarrollo sexual de los mamíferos, lo que afecta la diferenciación de los osteoblastos y la aparición del riñón. Lo más probable es que cause enfermedades del sistema reproductivo y fenotipos con morfología uterina y esquelética anormal. La integración de interacciones gen-proteína y vías metabólicas puede reflejar sistemáticamente el mecanismo de comorbilidad de AIS y PA. El alto ajuste de los objetivos genéticos de la ruta se puede utilizar desde la perspectiva de integrar la medicina tradicional china y la medicina occidental, la macro y la micro se refieren entre sí y se explican.

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