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STUDY ON THE SYNDROME BIOLOGICAL BASIS OF ESSENTIAL HYPERTENSION BASED ON LITERATURE MINING

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Objectives To investigate the syndrome biological basis of Essential Hypertension (EH) from the level of genes, proteins and signalling molecules by literature mining software, meanwhile to provide clues for experimental and clinical studies on the biological basis of EH syndrome.

Methods GenCLiP gene mining software was applied to search EH-related genes. Then download the up-to-date related literature for each gene from PUBMED. Automatically extracted keywords from the literature and manually curated the keywords, remove unrelated keywords, add diagnostic criteria symptoms of EH syndrome as new keywords based on the Clinical Guiding Principles of Traditional Chinese Medicine Research. Cluster analysis of genes with these keywords was conducted then to investigate current study on the pathogenesis of EH and the syndrome-related genes. What's more Ali Baba literature mining software was applied for further analysis of the detailed information of the genes, proteins and signalling molecules of each syndrome.

Results There are 446 genes related to EH. According to the results of cluster analysis, 14 genes were found closely related to the hyperactivity of liver fire syndrome of EH, GOLPH3, NR4A3, MDD1, MS, CYP2D6, MDD1, MS, CYP2D6, CYP3A4, TRIM21, ACE, ALRH, pLF and TAS2R38. The related signalling molecules and proteins are Phosphatidylinositol 4-kinases, mammalian target of rapamycin, growth-factor, GBF1, NPR3, MYO18A, pDZD2, ARL6IP5, TBC1D5, SCAMPs, C1orf122, calnexin, Sec2, SUB1, BLVRB, TR3, NGFI-B, Nor-1, oestrogen-receptor, N-acetyltransferase2, CYP2C19, APOE, cytochrome P450, vascular endothelial growth factor, total testosterones, growth hormone, TSHB, nitric oxide synthase, pPARA, p-glycoprotein inhibitor, Testosterone, AMG, progesterone receptor membrane component 2, pARP, ASB, SSA, SsbB, p53, BRCA2, NF-κ B, toll interacting protein, Interferon Regulatory Factor 1, Fas-associated death domain, TLR4, TRIB2, CENP-B, angiotensin-converting enzyme inhibitors, Angiotensin-Converting Enzyme 2 AT1, renin, Renalase, Angiotensin, Tph1, interleukin-2. Two genes, GOLPH3 and PLF, were found related to the syndrome of excessive accumulation of phlegm-dampness. The related signalling molecules and proteins are Phosphatidylinositol 4-kinases, mammalian target of rapamycin, growth-factor, GBF1, NPR3, MYO18A, pDZD2, ARL6IP5, TBC1D5, SCAMPs, C1orf122, calnexin, Sec2, SUB1, BLVRB. Nine genes were found related to the syndrome of Yin-yang concurrent deficiency, GOLPH3, CRP, NPPB, COPD, IGHE, ALB, ALRH, pLF and ACE. The related signalling molecules and proteins are tumour necrosis factor-α, metalloproteinase-9, cystatin C, B-type natriuretic peptide, adiponectin, Il-6, CR3, ADR2, leptin, Tnnc1, chloride channel, ATP2B1, Myl1, MTHFR, NPPA, prolactin, IGHEP1, IGHG3, IGHA1, IGHG2, EcoRI, IGHD, CYP2B6, cytochrome P450, SOD, Ferroportin1.

Conclusions Study on the biological basis of syndrome has always been the hot and difficult spots in TCM research. This study initially conducted research on the biological basis of EH syndrome from the level of gene, protein and signalling molecule by applying GenCLiP gene-mining software and Ali Baba literature mining software. The results also provide clues for experimental and clinical studies on the biological basis of EH syndrome.