Conclusion In addition to knockout of the E1B coding cassette, siRNA mediated E1B also serves as an approach to prepare oncolytic adenovirus.

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08 STUDY OF TOTAL FLAVONOIDS FROM MAO DONGQING IN CEREBRAL ISCHEMIA REPERFUSION MODELS

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Objective Mao Dongqing (MDQ) is the dried root of Ilex pubescens Hook. et Arn. It is a renowned traditional Chinese medicine which has been used for the treatment of acute and chronic cardio-cerebrovascular diseases in the clinic for many years. The aim of this study was to further understand the effect of total flavonoids from MDQ on cerebral ischemia reperfusion injury.

Methods Ginaton group (extract of ginkgo biloba leaves injection), the small, middle and large doses of total flavonoids from the MDQ group were given related drugs via intragastric administration before the operation. The sham operation group, ischaemic preconditioning model group and ischemia reperfusion group were given the same volume of 0.1% CMC daily for 10 days. After the last administration, animal models of cerebral ischemia reperfusion injury in mice were established using the method of blocking the bilateral common carotid artery for 10 min, restoring perfusion for 10 min, bilateral carotid artery occlusion for 10 min, and then reperfusion for 24 hours. Half of the brain was fixed in 10% formalin for HE staining. The other half of the brain was used to prepare brain homogenate, which was used to determine the content of ATPase, NO and NOS.

Results We found that the models with cerebral ischemia reperfusion injury in mice were copied successfully. Large and medium doses of total flavonoids from MDQ could significantly reduce the content of NO, tNOS, iNOS and increase the activity of ATPase in brain tissue of mice. Total flavonoids from MDQ could also reduce the pathological changes of the hippocampus and cortical neuron cells in the hippocampus of mice.

Conclusion The results of this study showed that the model of cerebral ischemia-reperfusion in mice was successful. The total flavonoids from MDQ could achieve the role of anti-cerebral ischemia injury by inhibition of the inflammatory cascade, improving the imbalance of oxygen supply and demand and the disorder of glucose metabolism, inhibiting the apoptosis of nerve cells during cerebral ischemia reperfusion injury. Acknowledgment National "Significant New Drug Creation" science and technology major special project ($2009Z \times 09103-324$).

09 EXPLORING THE GENOTYPE-PHENOTYPE ASSOCIATIONS OF COLORECTAL CANCER USING VECTOR SPACE MODEL

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Background Colorectal cancer is a malignant tumour which endangers human lives. With the rapid development of molecular medicine, a great deal of research related to clinic-omics data has been published. Mining the association of genotypephenotype data has been increasingly recognised as an effective way for early stage prediction of colorectal cancer.

Methods In this study, a literature text mining method was proposed for biomedical objects association using the Vector Space Model (VSM). For each article, we represented biomedical objects as the vectors of VSM. Gene symbols were denoted as the genotype objects, and the MeSH terms annotated from the literature were denoted as the phenotype objects. A TF-IDF algorithm was then used to quantitatively calculate the correlation between genotype and phenotype objects.

Results A total of 473 242 articles related to colorectal cancer were acquired from the MEDLINE database. We finally obtained 77 clinical terms and 490 genes highly related to colorectal cancer, resulting in 2125 associations between these clinical terms and genes. Biological pathway analysis by KEGG database demonstrated that genotype-phenotype association mining from our study covers all stages of the development of colorectal cancer, a number of which were at the early stage. These findings might become a beneficial complement of cancer translation research.

Conclusion Our study provides a biomedical literature mining method for cancer translational research such as construction of a precision medicine knowledge base, biomarker prediction/ evaluation, and knowledge discovery in texts.

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