and the remnant tendon sheath was significantly different from the adhesion between the tendon and the subcutaneous tissue. Histological observation: with time, fibrous connective tissue increased around the tendon, which was more pronounced between the tendon and the subcutaneous tissue than between the tendon and the remnant tendon sheath.

Conclusion Postoperative adhesions between the tendon and different tissues differ. More tissue adhesion formed between the tendon and the subcutaneous tissue than between the tendon and the remnant sheath.

20   GUT MICROBIOTA IN HUMAN ADULTS WITH IRRITABLE BOWEL SYNDROME DIFFERS FROM HEALTHY CONTROLS

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Background Recent evidence suggests that there is a link between irritable bowel syndrome (IBS) and microbiota in the gut. The onset and maintenance of IBS may be caused by gut microbiota, but the causes of the pathophysiology of this disorder are unknown.

Method 25 patients who fulfilled Rome III criteria for IBS and 29 age- and gender-matched healthy controls were chosen in this study. The total bacterial DNA isolated from the two populations was investigated through amplicon pyrosequencing of the V3–V4 regions of the 16S ribosomal RNA gene.

Results The composition of bacteria in the groups differed between healthy controls and IBS subgroups from phylum to the genus level. Synergistetes phylum ($p=0.016$), Bacilli class ($p=0.006$), Lactobacillales order ($p=0.006$), Enterobacteriales order ($p=0.02$), the families Streptococcaceae ($p=0.009$), Enterobacteriaceae ($p=0.02$), and Enterococcaceae ($p=0.001$), and the genera Streptococcus ($p=0.002$), Enterobacter ($p=0$), Klebsiella ($p=0.006$), and Enterococcus ($p=0.001$) exhibited higher levels in IBS patients compared with healthy controls. By contrast, Clostridia class ($p=0.024$), Betaproteobacteria class ($p=0.019$), Clostridiales order ($p=0.024$), the families Bacteroidaceae ($p=0.049$), Desulfovibrionaceae ($p<<0.01$), and Lachnospiraceae ($p=0.012$), and the genera Bacteroides ($p=0.049$) and Roseburia ($p=0.012$) had lower levels in IBS patients. The genera Turicibacter and Collinsella were most abundant in 51–60 year old patients, followed by 31–40 year old IBS patients. We also detected Acinetobacter and Campylobacter belonging to Proteobacteria phylum in female IBS patients, but not in male patients.

Conclusion There were differences in faecal microbiota between IBS patients and healthy controls. The faecal microbiota of patients with IBS is associated with significant increases in detrimental and decreases in beneficial bacterial groups.

21   EFFECT OF JINJIANG GRANULES ON INTESTINAL MUCOSAL IMMUNITY IN MICE MODEL

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Objectives To study the effect of Jinjiang granules on immune function in mice with hypoimmunity and to provide a basis for the application of Jinjiang granules in the early stage of clinical colds.

Methods KM mice (half male, half female) were randomly divided into 6 groups. The mice were given the drug once a day (normal control group and model group were given with physiological saline). The mice were weighed once every 3 days. Weight was adjusted to the drug volume. All the groups except the normal group were injected with cyclophosphamide to establish the mice model of hypoimmunity for 3 days. On the seventh day, two hours later the thymus, spleen and intestinal mucosa were obtained after intragastric administration to detect SIgA, Gln, TNF-α and IL-1β.

Results The mice models of hypoimmunity in mice succeeded. In the medication group the IL-1β and TNF-α levels improved and the SIgA and Gln levels were reduced to different degrees. In the treatment group there was a certain therapeutic effect on spleen and thymus tissue pathological changes. The best curative effect is the lentinan, followed by large dose of jinjiang group and medium dose of jinjiang group.

Conclusions Jinjiang granules can improve the immune function of the mice models of hypoimmunity. It also improves intestinal immune function. It prevents colds when given as the initial medicine.

22   IN VIVO EVALUATION OF ETHANOL EXTRACT OF FORSYTHIA SUSPENSA (THUNB.) VAHL (FRUIT) IN ANTI-INFLAMMATORY AND ANALGESIC ACTIVITIES

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Objectives The dried fruit of Forsythia suspensa (Thunb.) Vahl (FSTV) is a typical heat-clearing and detoxicating herb according to traditional Chinese medicine theory. This study was undertaken to evaluate the anti-inflammatory and analgesic activities of 85% ethanol extract of FSTV (FSTV-ET) in vivo.

Methods Conventional reflux extraction method was used to prepare FSTV-ET with a yield of 42.7%. The analgesic activity of FSTV-ET was evaluated using the hot plate test and acetic acid-induced abdominal writhing test, and the anti-inflammatory activity was evaluated by the xylene-induced ear oedema

model in female Kunming (KM) mice. Lipid peroxidation product malondialdehyde (MDA) and inflammatory mediator prostaglandin (PG) E2 were both detected using methods reported in the literature.

Results FSTV-ET exerted analgesic activity with a significant dose-dependent increase in latency in the hot plate test. The percentage inhibition suggested that FSTV-ET exhibited analgesic activity in the central nervous system. Meanwhile, FSTV-ET at 0.16, 0.32, and 0.64 g/kg strongly inhibited the acetic acid-induced writhing response. FSTV-ET also exerted analgesic activity in the peripheral nervous system. Moreover, FSTV-ET demonstrated a significant anti-inflammatory effect against xylene-induced oedema in a dose-dependent manner, and reduced MDA and PGE2 levels.

Conclusions These findings indicate that FSTV-ET can produce anti-inflammatory and analgesic activities in vivo, and the mechanism is likely to be related to inhibiting lipid peroxidation and inflammation.

23 STUDY ON MiRNAs PREDICTION AND CO-EXPRESSION PATTERNS OF THE HUMAN INTRONIC MiRNAs WITH THEIR HOST GENES

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Objectives MiRNAs are a set of endogenous non-coding RNAs with a length of about 22nt. They regulate the expression of the target mRNAs and are involved in many important biological processes including metabolism, defense against viruses, apoptosis and proliferation. In this paper we focus on two hotspot issues related to miRNAs, namely miRNAs prediction and the co-expression patterns prediction of the intronic miRNAs with their host genes.

Methods Firstly, a new method based on machine learning techniques is proposed to recognise the miRNAs. Couplet-syntax is introduced to depict local structure-sequence of pre-miRNA which is able to represent the most robust and intrinsic features of pre-miRNA. Feature selection algorithms based on filter models are proposed to achieve good comprehensive performance. Secondly, a new method based on multiple features extraction techniques is proposed to recognise the co-expression patterns of the intronic miRNAs with their host genes. The feature vectors were calculated from the genome coordinates data of human miRNAs which includes intronic miRNAs, miRNA-hosting introns, and miRNA-hosting genes. The ensemble features selection algorithm is used to obtain a subset of features with high correlation and stability.

Results The analysis and comparison of multi-group experiments show that we achieved the best features and models to predict miRNAs and the co-expression patterns of the intronic miRNAs with their host genes which are verified with promising results.

Conclusions This study not only provides some effective means for research on miRNAs prediction and co-expression prediction of intronic miRNAs with their host genes, but also gives some solid foundation for future research in this field.

24 DANGGUI SHAOYAO POWDER IMPROVES DIABETIC NEPHROPATHY WITHOUT ALTERING BLOOD GLUCOSE IN STREPTOZOTOCIN-INDUCED DIABETIC RATS

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Objectives Diabetic nephropathy (DN) is one of the most severe diabetic complications and is becoming a worldwide epidemic, accounting for approximately one-third of all cases of end-stage renal disease. In this study, we investigated its influence on Th1/Th2 cells balance, inflammation and lipid metabolism to assess whether Danggui Shaoyao Powder (DSS) ameliorates DN.

Methods Wistar rats were randomly divided into control group, model group, DSS group and benazepril group. The model group was induced by injection intraperitoneally with streptozotocin after high-calorie foods were given for 1 month. Animals were treated orally with saline, DSS and benazepril daily for 8 weeks. At the end of 8 weeks, blood glucose, 24 hour urinary protein (24 hour UPr), creatinine clearance rate (Ccr), total cholesterol (TC), triglyceride (TG), low-density lipoprotein (LDL), high-density lipoprotein (HDL), serum levels of interferon (IFN)-gamma, tumour necrosis factor (TNF)-alpha, interleukin (IL)−4, and IL-10 were measured. Glomerular morphology was observed by light microscopy.

Results Compared with rats in the control group, rats in the DN group had significantly increased 24 hour UPr, Scr, blood lipids and pro-inflammatory cytokines IFN-gamma and TNF-alpha secreted by Th1 cells. In addition, down-regulation of the proportion of Th2 cells and decrease of the anti-inflammatory cytokines IL-4 and IL-10 secreted by Th2 cells occurred. Compared with the model group, the DSS group had significantly decreased levels of 24 hour UPr, Scr, TC, TG, LDL, IFN-gamma and TNF-alpha, and increased IL-4 and IL-10. The renal pathological changes in the DSS treatment group were ameliorated.

Conclusion This study suggests that DSS could improve renal function in streptozotocin-induced DN model rats. The mechanism may be related to regulating the Th1/Th2 cell balance and improved lipid metabolism in DN rats.