Deep-belief network for predicting potential miRNA-disease associations.

Abstract
MicroRNA (miRNA) plays an important role in the occurrence, development, diagnosis and treatment of diseases. More and more researchers begin to pay attention to the relationship between miRNA and disease. Compared with traditional biological experiments, computational method of integrating heterogeneous biological data to predict potential associations can effectively save time and cost. Considering the limitations of the previous computational models, we developed the model of deep-belief network for miRNA-disease association prediction (DBNMDA). We constructed feature vectors to pre-train restricted Boltzmann machines for all miRNA-disease pairs and applied positive samples and the same number of selected negative samples to fine-tune DBN to obtain the final predicted scores. Compared with the previous supervised models that only use pairs with known label for training, DBNMDA innovatively utilizes the information of all miRNA-disease pairs during the pre-training process. This step could reduce the impact of too few known associations on prediction accuracy to some extent. DBNMDA achieves the AUC of 0.9104 based on global leave-one-out cross validation (LOOCV), the AUC of 0.8232 based on local LOOCV and the average AUC of 0.9048 ± 0.0026 based on 5-fold cross validation. These AUCs are better than other previous models. In addition, three different types of case studies for three diseases were implemented to demonstrate the accuracy of DBNMDA. As a result, 84% (breast neoplasms), 100% (lung neoplasms) and 88% (esophageal neoplasms) of the top 50 predicted miRNAs were verified by recent literature. Therefore, we could conclude that DBNMDA is an effective method to predict potential miRNA-disease associations.

PMID: 32866969 [PubMed — as supplied by publisher]

The clinical value of the changes of peripheral lymphocyte subsets absolute counts in patients with non-small cell lung cancer.

Abstract
INTRODUCTION: Immune function strongly influences the outcome of patients with non-small cell lung cancer (NSCLC). It’s vital to understand the immune state of patients through detecting the percentage and number of lymphocyte subsets accurately, and helpful to evaluate conditions of prognosis and adjust treatment for patients.

METHODS: We conducted a retrospective cohort study in First Teaching Hospital of Tianjin University of Traditional Chinese Medicine, Tianjin, China. The absolute counts and percentages of CD3+, CD3 + CD4+, CD3 + CD8+, B and NK cells were determined by single platform technologies. 172 patients received treatment including surgery or chemotherapy after surgery. The factors affecting disease progression were analyzed by Binary Logistic regression. Progression free survival (PFS) calculating survivals were with the method of Kaplan-Meier. The log-rank test and cox’s proportional hazard regression (enter method) were used for univariable and multivariable analyses respectively.

RESULTS: Relative to normal controls, patients with NSCLC at different stages showed decreased absolute lymphocyte count obviously, rather than lymphocyte percentages. Different treatments had unlike influence on the homeostasis of lymphocytes and the effects last for a long time. Logistic regression showed CD3 + CD4+ and CD3 + CD8+ could contribute to favorable prognosis. Multivariate analysis of prognostic factors of PFS showed CD3 + CD4+ cell was independent factor for predicting PFS.

CONCLUSIONS: The absolute count of CD3+, CD3 + CD4+, CD3 + CD8+, B and NK cells were better indication of the patient’s immune state than percentages of each lymphocyte subsets. Immune function was impaired in patients with non-small cell lung. The high level of baseline absolute CD3 + CD4+ cells count
Plasma enterobacterial ClpB levels and ClpB- and α-MSH-reactive immunoglobulins in lung cancer patients with and without anorexia.

Related Articles

Plasma enterobacterial ClpB levels and ClpB- and α-MSH-reactive immunoglobulins in lung cancer patients with and without anorexia.

Nutrition. 2020 Jul 22;78:110952

Authors: Molfino A, Amabile MI, Imbimbo G, Emiliani A, Ramaccini C, Lahaye E, Takagi K, Fetissov SO

Abstract

OBJECTIVES: Anorexia represents a common and debilitating clinical problem in patients with several forms of cancer, in particular lung cancer, but its mechanisms are not completely understood. Recently, the caseinolytic-protease-B (ClpB) homologue protein, produced by common gut bacteria, such as Escherichia coli, was identified as an antigen-mimetic of α-melanocyte-stimulating hormone (α-MSH), an anorexigenic neuropeptide. ClpB was previously detected in human plasma and displayed satietogenic properties; however, its possible relevance to cancer anorexia has not yet been investigated.

METHODS: To address this question, we analyzed plasma ClpB concentrations as well as levels and affinities of anti-ClpB and α-MSH-reactive antibodies in patients with lung cancer with and without anorexia as compared with body mass index-matched healthy controls with normal appetite.

RESULTS: We found that plasma ClpB concentrations were significantly lower in non-anorexic patients with cancer than those of the control group (P = 0.028). In contrast, patients with cancer and anorexia had lower levels of anti-ClpB immunoglobulins (Ig)M (P CONCLUSIONS: Taken together, the results revealed a reduced humoral immune response to ClpB in patients with cancer and anorexia, which may lead to an enhanced satietogenic effect of this enterobacterial protein contributing to the mechanisms of reduced appetite.

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PVT1 induces NSCLC cell migration and invasion by regulating IL-6 via sponging miR-760.

Related Articles

**Inherited rare, deleterious variants in ATM increase lung adenocarcinoma risk.**

J Thorac Oncol. 2020 Aug 28;:

Authors: Selvan ME, Zauderer MG, Rudin CM, Jones S, Mukherjee S, Offit K, Onel K, Rennert G, Velculescu VE, Lipkin SM, Klein RJ, Gümüş ZH

Abstract

INTRODUCTION: Lung cancer is the leading cause of cancer deaths in the world, and adenocarcinoma (LUAD) is its most prevalent subtype. Symptoms often appear in advanced disease when treatment options are limited. Identifying genetic risk factors will enable better identification of high-risk individuals.

METHODS: To identify LUAD risk genes, we performed a case-control association study for gene-level burden of rare, deleterious variants (RDVs) in germline whole-exome sequencing (WES) data of 1,083 LUAD patients and 7,650 controls, split into discovery and validation cohorts. Of these, we performed WES on 97 patients and acquired the rest from multiple public databases.

We annotated all rare variants for pathogenicity conservatively, using ACMG guidelines and ClinVar curation, and investigated gene-level RDV burden using penalized logistic regression. All statistical tests were two-sided.

RESULTS: We discovered and replicated the finding that the burden of germline ATM RDVs was significantly higher in LUAD patients versus controls (ORcombined=4.6; p=1.7e-04; 95% CI=2.2–9.5; 1.21% of cases; 0.24% of controls). Germline ATM RDVs were also enriched in an independent clinical cohort of 1,594 patients from the MSK-IMPACT study (0.63%). Additionally, we observed that an Ashkenazi Jewish (AJ) founder ATM variant, rs56009889, was statistically significantly more frequent in AJ cases versus AJ controls in our cohort (ORcombined=2.7, p=6.9e-03, 95% CI=1.3–5.3).

CONCLUSIONS: Our results indicate that ATM is a moderate-penetrance LUAD risk gene, and that LUAD may be part of the ATM-related cancer syndrome spectrum. Individuals with ATM RDVs are at elevated LUAD risk and can benefit from increased surveillance (particularly CT scanning), early detection and chemoprevention programs, improving prognosis.

PMID: 32866655 [PubMed — as supplied by publisher]

**Molecular characterisation and clinical outcomes in RET rearranged non-small cell lung cancer (NSCLC).**

Related Articles

**Molecular characterisation and clinical outcomes in RET rearranged non-small cell lung cancer (NSCLC).**

J Thorac Oncol. 2020 Aug 28;:


Abstract

INTRODUCTION: RET rearrangements are an emerging targetable oncogenic fusion driver in NSCLC. However, the natural history of disease and the activity of different classes of systemic therapy remains to be defined. Furthermore, molecular testing for RET is not yet routine and the optimal method of testing is unclear. We present a comparative analysis of molecular profiling with FISH or NGS and treatment outcomes.

METHODS: Retrospective analysis of patients treated at the National Cancer Centre Singapore. Baseline demographics and treatment outcomes were collected.

RESULTS: A total of 64 patients were included, with median age 62 years (range 25–85), 56% were female, 77% Chinese ethnicity, 95% adenocarcinoma and 69% never smokers. RET rearrangement was detected by FISH in 30/34 (88%) patients, NGS in 40/43 (93%) patients, and with discordant results in 7/13 (54%) patients tested with both methods. Of 61 stage IIIB/IV or recurrent patients, prevalence of CNS metastases was 31%, and 92% received palliative systemic therapy. OS was prolonged in selective RET TKI
treated versus untreated patients (median 49.3 vs. 15.3 months; HR 0.16, 95%CI 0.06−0.40, p