Title	The relationship between sputum microbial load and leucocyte count in stable bronchiectasis
Author(s)	Tsang, KWT; Ho, CS; Ho, PL; Yuen, KY; Ip, MSM; Lam, WK
Citation	The 2nd Medical Research Conference, Hong Kong, China, 25-26 January 1997, v. 19 n. 2 Supp, p. 25
Issued Date	1997
URL	http://hdl.handle.net/10722/54158
Rights	Creative Commons: Attribution 3.0 Hong Kong License

045

DOES GLUTATHIONE S-TRANSFERASE (GSTMI) GENE EXPRESSION HAVE A PROTECTIVE AND PROGNOSTIC ROLE IN NON-SMALL CELL LUNG CARCINOMA IN HONG KONG CHINESE PATIENTS?

WK Lam, H Ge[2], J Lee[3], MP Wong[4], WW Yew[3], ML Lung[2]. Depts of Medicine and [4]Pathology, University of Hong Kong, [2]Dept of Biology, HKUST, and [3]TB&Chest Unit, Grantham Hospital, Hong Kong.

Glutathione S-transferase (GST) enzymes catalyse glutathione-conjugation (detoxification) with substances including tobacco-related carcinogens such as benzo(a)pyrene. It has remained controversial whether GSTMI gene expression has a protective and prognostic role in non-small cell lung carcinoma (NSCLC).
Genomic DNA from normal lung tissues of 89 Chinese patients with NSCLC and the blood from 25 healthy persons was extracted and studied for GSTMI genotype using polymerase chain reaction technique. The patients included 52 men (average age 60.6±10.8 years, 85% smokers), and 37 women (average age 61.9±9.0 years, 23% smokers), and histologically 62/89 (70%) were adenocarcinoma and 21/89 (24%) were squamous cell carcinoma. The GSTMI null genotype appeared as a 160-base pair fragment while the GSTMI positive genotype contained both 232-base pair and 160-base pair fragments. The GSTMI null gene frequencies in lung cancer patients (59/89=66%) and healthy persons (17/25=68%) were similar, and there was no statistical difference between patients with different GSTMI genotypes in terms of age, sex, smoking history, histological type, disease staging and survival at 50-month post-operation.
It is concluded that GSTMI gene expression does not appear to have a protective or prognostic role in our NSCLC patients.

046

THE RELATIONSHIP BETWEEN SPUTUM MICROBIAL LOAD AND LEUCOCYTE COUNT IN STABLE BRONCHIECTASIS.

K.W.T. Tsang, C.S. Ho, *P.L. Ho, *KY Yuen, M. Ip, W.K. Lam. ***University Depts of Medicine & *Microbiology, University of Hong Kong, Hong Kong.***

Bronchiectasis is a respiratory disease in which chronic sputum production, resulting from chronic tracheobronchial infection and inflammation, is a disabling problem. The inflammatory component of bronchiectasis is considered to increase the susceptibility of the tracheobronchial tree to bacterial infection and colonization. This commonly held belief, however, has not been evaluated quantitatively. We have therefore performed this study to evaluate the relationship between some sputum inflammatory markers and microbial load. Sixteen patients (7F; mean age 54±3.9; mean FEV_1/FVC=1.3/2.0) who were in steady state idiopathic bronchiectasis were recruited into the study. Freshly produced sputum was serially diluted and cultured quantitatively on bacteriological agars (chocolate, blood, McConkey, Bacitracin, Mannitol and Cetrimide) at 37^0C for 24h and examined under by using haemocytometer and light microscopy for total leucocyte count. Non-selective sputum culture yielded $5.6x10^7$±1.10 colony forming units of bacteria (CFU)/ml. The weight of the 24h sputum (25.2±5.34g) correlated ($p<0.01$) with total sputum leucocyte count ($1.7x10^7$± 0.51 /ml) and total bacterial count ($5.6x10^7$±1.10CFU/ml) although there was no correlation between total sputum bacterial and leucocyte counts. This study provides evidence that the inflammatory element in bronchiectasis may be independent of the sputum bacterial load. Anti-inflammatory drugs should be tried on bronchiectasis.