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disease with the MAGE expression profile in primary tumor tissue, venous blood, and bone marrow aspirates of cancer patients in several cohorts. Subsequently, a detailed statistical assessment of the data sets has to be done, and the proposed method for summarizing the patterns of MAGE expression may be helpful for the generation of a later decision model. However, far more clinical experience is needed with this approach, and quantitative data will have to be included in the final analysis as relevant carrier of additional information.

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Pneumothorax Following Transthoracic Fine-Needle Aspiration of the Lung

To the Editor:

We read with interest the article by Choi et al¹ (November 2004) concerning the incidence and risk factors of delayed pneumothorax after transthoracic fine-needle aspiration (FNA) of pulmonary lesions guided by a variety of radiologic techniques. The article is both well written and informative. As the authors indicate in their discussion, it is a common practice to obtain a chest radiograph typically 4 h after percutaneous transthoracic needle aspiration.²

The incidences of early and delayed pneumothorax in the study by Choi et al were 18.6% and 3.3%, respectively. However, all of the patients in their study who required tube thoracostomy for delayed pneumothorax were symptomatic. This represents <1% of their study population. Interestingly, none of the patients in this study with delayed pneumothorax had undergone CT-guided FNA. We have previously reported that immediate pneumothorax develops in 17.2 to 24.1% of patients undergoing CT-guided FNA.^{3,4} In our studies, delayed pneumothorax occurs in 2.5 to 3.1% of patients who underwent this procedure. Moreover, delayed pneumothorax requiring intervention with pleural space evacuation occurred in 1.3 to 1.6% of patients.

While we agree the conclusion of Choi et al that late pneumothorax is clinically important, the practice of obtaining a delayed

postprocedure chest radiograph after CT-guided FNA does not appear to be an efficient use of resources. Based on our research, chest radiography appears to add little information regarding lung expansion to that obtained by CT at the end of CT-guided FNA. Instruction to seek medical attention in the event of symptoms of pneumothorax appears to be a more effective method of addressing this potential complication.

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To the Editor:

In our study (November 2004),¹ most transthoracic needle biopsies were performed by fluoroscopic and ultrasonography guidance. Only 4.5% of the transthoracic needle biopsies (21 of 458) were performed with CT scan guidance. Therefore, it is difficult to compare our data to the data of Byrd et al² and Shantaveerappa et al.³

Definitely, CT scanning is more sensitive than a posteroanterior chest radiograph for the detection of pneumothorax. After the analysis of our data, we had a suspicion that a delayed pneumothorax was simply so small and localized that it would go undetected by a posteroanterior chest radiograph at 4 h but would be detectable by CT scan if one were performed.

However, according to his previous work, delayed pneumothorax still occurred in 4 of 158 patients (2.5%) even though a CT scan was performed after the CT scan/fine-needle aspiration.³ This rate is not so different from that in our study¹ (3.3%; 15 of 458). The study by Shantaveerappa et al³ helps us to resolve our suspicion. Furthermore, the rate of intervention was even higher (all patients, 1.7% [2 of 158]; patients with delayed pneumothorax, 50% [2 of 4]) in their study³ than that in ours (all patients, 0.65% [3 of 458]; patients with delayed pneumothorax, 20% [3 of 15]).¹ I think that the two studies showed quite similar data but different interpretations.

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Interleukin-1 β Gene Polymorphisms Associated With COPD

To the Editor:

We read with interest the article by Hegab et al.¹ Although interleukin (IL)-1 β is also thought to be one of the important cytokines in COPD, Joos et al² failed to show the relationship between functional single nucleotide polymorphisms at the IL-1 β promotor gene at position -511. However, since their

reports were published, there was an explosion of reports revealing the association between IL-1 β -511 polymorphisms and a variety of diseases ranging from psychological³ to dental disease.⁴ Therefore, completely healthy elderly people were recruited from a large health survey in the Sendai area.

To elucidate the genotype of IL-1 β polymorphisms at positions -31 and -511, polymerase chain reaction and restriction enzyme fragment length polymorphisms were performed on blood samples.^{2,3} Table 1 shows the characteristics of 85 COPD patients and 68 healthy subjects and the distribution of IL-1 β -511 and -31 genotypes in these two groups. The T allele at -511 SNP ($p = 0.02$) was overrepresented in the healthy control subjects. The homozygote subjects were particularly at lower risk for COPD, with an odds ratio of 0.43 for -511 C/C and T/C. Although IL-1 β -31 and -511 loci had linkage disequilibrium, there were no differences on the C allele -31 and genotyped frequency of IL-1 β between the COPD patients and the control subjects.

Different from the report Joos et al,² we showed a significant association between only the T allele at -511 SNP and susceptibility to COPD. First, because both the COPD patients and the control subjects were elderly, we suspect that the IL-1 β -511 loci strongly affects susceptibility to COPD with chronic inflammation for a long time. Second, since there is much evidence linking IL-1 β -511 polymorphisms and other diseases,^{3–5} healthy elderly smokers who have not had these diseases may have the T allele at -511 SNP. Since there were no differences in the distribution of IL-1 β polymorphisms at position -31 between the COPD patients and the control subjects, we believe that our sample size was not large enough to detect small differences between the two groups.

Table 1—IL-1 β Genotypes in Healthy Control Subjects and COPD Patients*

Characteristics/Polymorphism	Control Subjects (n = 68)	Patients (n = 85)	p Value	Odds Ratio	95% Confidence Interval
Age, yr	65.6 ± 10.6	66 ± 8.6	0.80		
Pack-years	44 ± 17	47 ± 14	0.67		
Gender					
Male	66 (97.1)	82 (95.3)			
Female	2 (2.9)	3 (4.7)	0.83		
Pulmonary function					
FVC (% of predicted)	98 ± 5	84 ± 7	0.11		
FEV ₁ /FVC, %	95 ± 5	47 ± 2	0.01		
IL-1 β -511 (T-C)					
Genotypes					
T/T	25 (36.8)	17 (20.0)	0.02	0.43	0.20–0.89
T/C	29 (42.6)	42 (49.4)	0.40	1.31	0.69–2.50
C/C	14 (20.6)	26 (30.6)	0.16	1.70	0.80–3.59
Alleles					
C	57 (41.9)	94 (55.3)			
T	79 (58.1)	76 (44.7)	0.02	0.58	0.37–0.92
IL-1 β -31 (T-C)					
Genotypes					
C/C	20 (29.4)	20 (23.5)	0.41	0.74	0.36–1.52
T/C	32 (47.1)	40 (47.1)	0.79	0.92	0.48–1.75
T/T	16 (23.5)	25 (29.4)	0.41	1.35	0.65–2.81
Alleles					
C	72 (52.9)	80 (47.1)			
T	64 (47.1)	90 (52.9)	0.31	1.27	0.81–1.99

*Data are presented as mean ± SEM or No. (%) unless otherwise indicated.

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