From the authors:

We would like to thank S. Greco and coworkers for their comments on our paper about the predictive value of bronchoalveolar lavage (BAL) cell differentials in the diagnosis of interstitial lung disease (ILD) [1]. In their study, which they discuss in their letter to the Editors, they tested the feasibility of our data for the differential diagnosis of pulmonary tuberculosis (TB) and sarcoidosis. In contrast to our study, they retrospectively analysed 88 patients with biopsy-proven sarcoidosis and 76 patients with culture-positive pulmonary TB.

First of all, we agree with the major points of their study. The high grade of lymphocytosis (>50%) is the best predictor for sarcoidosis, and the presence of elevated neutrophils rendered the diagnosis of sarcoidosis very unlikely. In our experience and clinical practise, however, the proportion of TB with a comparable ILD pattern seems to be extremely low. In our own hospital (Hospital Grosshansdorf, Center of Pneumology and Thoracic Surgery, Grosshandorf, Germany), >100 patients per year are treated for TB. Within the study interval of 7 yrs (~700 TB patients), only seven of these patients showed a clinical and/or radiological pattern of ILD [1].

Although many clinicians use BAL fluid to confirm the diagnosis of TB microbiologically, it does not seem to be the only diagnostic tool that can be used to confirm TB. In addition, other diseases with an ILD pattern (nonsarcoid ILD) are much more frequent than TB with an ILD pattern. In our study [1], nonsarcoid ILD is not equal to TB with an ILD pattern. Therefore, the lower predictive value seen in the study by S. Greco and coworkers is not unexpected.

Our analysis was carried out in a manner similar to that adopted by most clinicians in the diagnostic process, with a special emphasis on interstitial lung disease. The use of cut-off values in the interpretation of bronchoalveolar lavage cellular results seems to be more practical compared with the use of a discriminant score.

L. Welker
Laboratory of Cytology, Hospital Grosshansdorf, Center of Pneumology and Thoracic Surgery, Grosshandorf, Germany.

REFERENCES

1 Welker L, Jorres RA, Costabel U, Magnussen H. Predictive value of BAL cell differentials in the diagnosis of interstitial lung disease. *Eur Respir J* 2004; 24: 1000–1006.

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The prevalence of ΔF508 in primary osteoporotic patients

To the Editors:

We read with great interest the paper by KING *et al*. [1] in a recent issue of the *European Respiratory Journal*. The authors found a strong association between reduced bone mineral density (BMD) and carrier state of ΔF508 cystic fibrosis (CF) allele (the most common cystic fibrosis transmembrane regulator (CFTR) gene variant) in an adult CF population. Their results suggest that reduced BMD in CF appears to have a genetic component, independent of the disease severity and nutritional deficits. This fascinating observation is in line with the results found by our group [2]. It was found that healthy mothers of CF children (who are obligate heterozygous carriers of a CFTR mutation) have lower than normal BMD values. Furthermore, a correlation with the BMD values of their CF children was demonstrated. Although there are no data on the role of the CFTR gene in bone, it has been reported that not only BMD but also the bone structure of patients with CF was altered compared with healthy individuals [3].

These data further support a possible genetic component in the development of a CF-associated bone deficit. If so, one can speculate that the presence of a single diseased CFTR gene may contribute to the development of osteoporosis in the otherwise healthy adult population.

In a pilot study, we tested the prevalence of the ΔF508 CFTR gene mutation in subjects with severe primary osteoporosis. A total of 137 Caucasian post-menopausal females (aged 46–80 yrs) with osteoporosis were enrolled. Osteoporosis was defined by a T-score of ⩽-2.5 at the lumbar spine and/or hip sites. Individuals with secondary causes of osteoporosis or bone loss were excluded. All study participants gave informed consent. The prevalence of the ΔF508 variant of CFTR gene was screened by capillary electrophoresis [4].

Three patients with a single ΔF508 allele were detected, which corresponds to the prevalence observed previously in the general Hungarian population [5]. These patients did not suffer from a more severe form of osteoporosis than those without a CFTR gene mutation.

These results do not support the hypothesis that the ΔF508 mutation is more common among females with primary osteoporosis. However, a serious limitation of this study is that the number of patients was too low to establish any association between the heterozygosity for the ΔF508 allele and the epidemiology of primary osteoporosis. Given the frequency of the ΔF508 allele in Hungary (3.5%) [5], the number of patients in this study would have been enough to reveal a four-fold difference when the expected allele frequency is 14%, with a power of 85%, among patients with osteoporosis in the