metaplasia/dysplasia or clonal patches. We speculate that the molecular changes in the airway epithelium of an affected bronchiole in the context of constrictive bronchiolitis might account for the increased risk of developing non-small-cell lung carcinoma in our patient, although this association requires further confirmation.

In conclusion, constrictive bronchiolitis should be included as a differential diagnosis of DCLD and it is speculated that it may determine an increased risk of lung cancer.

References

Martina Rodrigues de Oliveira, Alexandre Franco Amaral, Ellen Caroline Toledo do Nascimento, Carlos Roberto Ribeiro Carvalho, Bruno Guedes Baldi

a Divisão de Pneumologia, Instituto de Coracao, Hospital das Clinicas HCFMUSP, Faculdade de Medicina, Universidade de Sao Paulo, Sao Paulo, SP, Brazil
b Departamento de Patologia, Hospital das Clinicas HCFMUSP, Faculdade de Medicina, Universidade de Sao Paulo, Sao Paulo, SP, Brazil

* Corresponding author.
E-mail address: bruno.guedes2@terra.com.br (B.G. Baldi).

© 2018 SEPAR. Published by Elsevier España, S.L.U. All rights reserved.

Calcified Pulmonary Nodules in an Oncological Patient

Nódulos pulmonares calcificados en un paciente oncológico

Dear Director:

A 50-year-old female patient underwent thoracic and abdominal computed tomography examinations for oncological follow-up. The images showed multiple lung nodules, some of which were calcified (Fig. 1A and B), a calcified hepatic mass, and an exosplenic osteolytic lesion with internal foci of calcification on the ischiopubic ramus of the right hip (Fig. 1C). The patient had undergone colonoscopy 3 years previously due to rectal bleeding, which showed an exophytic and stenosing rectal lesion. The biopsy findings were compatible with well-differentiated tubular adenocarcinoma. Surgical resection confirmed the anatomopathological

Fig. 1. Chest computed tomography with axial (A) and coronal (B) reconstruction showing multiple pulmonary nodules, some with calcification (arrows). Note also in B a calcified mass in the right lobe of the liver (arrowheads). In C, computed tomography of the pelvis with coronal acquisition MIP reconstruction, showing an osteolytic lesion with internal foci of calcification (arrows) and invasion of surrounding soft tissue. In D, histological section of the pulmonary nodule demonstrating atypical neoplastic glands infiltrating the connective tissue amid desmoplastic stroma. Note also the amorphous basophilic material, compatible with extracellular deposition of calcium adjacent to the neoplastic process (arrows; hematoxylin and eosin stain, × 100).
Changes in the Melting Peak of Hybridization Probes Used for Genotyping in Alpha-1 Antitrypsin Deficiency Do Not Always Imply Errors

To the Editor,

Molecular analysis of the gene that encodes alpha-1 antitrypsin (AAT; SERPINA1 gene) is the gold standard for the identification of allelic variants.1 The different molecular methods that can be used for this purpose include hybridization probes or HybProbes,2 which provide real-time PCR tracking. Once the amplification process is complete, these probes identify the genetic variants present in a particular region within the amplicon. This is a homogeneous genotyping test, that is to say, the entire process occurs in a single tube with no additional manipulation between the start of the test and the observation of the results. However, while it is a very reliable technique, errors may sometimes occur, especially in the interpretation of the results.3

We performed an analysis of the prevalence of non-S/S and non-Z/Z variants of the SERPINA1 gene in a clinical population from La Palma (Canary Islands, Spain) by recruiting a series of 1510 patients regardless of the reason that led them to the pulmonology clinic. We identified 7 subjects in whom the peaks in the melting charts displayed by the HybProbe probes designed to identify the non-S/S variants showed a shift in respect of normal charts (Fig. 1). These 7 patients had been diagnosed with various respiratory diseases, such as diffuse interstitial lung disease, sleep apnea–hypopnea syndrome, and chronic obstructive pulmonary disease.

To rule out an error in the genotyping process due to differences in the saline concentration of the 7 DNA samples involved, these were prepared and analyzed again. In the new analysis, the real-time PCR genotyping platform software (LightCycler 480) continued to allocate these samples to a different genotype group than those defined by the standards, using the computer application’s...

References


Carla dos Santos Rossi,b Thiago Franchi Nunes,a Edson Marchiori,c,a

a Instituto de Tratamento do Côncamo, Campo Grande, MS, Brazil
b Universidade Federal de Mato Grosso do Sul, Campo Grande, MS, Brazil
c Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil

c Corresponding author.
E-mail address: edmarchiori@gmail.com (E. Marchiori).

1579–2129
© 2018 SEPAR. Published by Elsevier España, S.L.U. All rights reserved.