Case report

Alpha-1-Antitrypsin Deficiency Associated with the Mattawa Variant

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Article history:
Received 4 April 2013
Accepted 9 May 2013
Available online 20 November 2013

Keywords:
α-1-antitrypsin deficiency
Mattawa
Spanish Registry of patients with α-1-antitrypsin deficiency

Abstract

The most common deficiency alleles for α-1-antitrypsin deficiency (AATD) are Pi*S and Pi*T, but there are also other deficiency variants. This case report describes the first two cases of AATD detected in Spain resulting from the combination of a null Mattawa allele with a normal Pi*M, and a rare Mmalton. Both cases were initially diagnosed as Pi*M by isoelectric focusing (IEF), but the low serum AAT values led us to suspect the existence of rare deficiency alleles that were undetectable using this technique, and to performing molecular analysis of the gene, which provided the correct diagnosis. Inconsistencies between serum AAT values and the phenotype should make one suspect the existence of one of these rare alleles.

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Case report

Case 1

The first patient was a 47-year-old woman, non-smoker, with essential hypertension, recurrent bronchitis since age 25, and exertional dyspnea in the last 3 years.

Her spirometry was normal (FVC 96%, FEV1 105%, FEV1/FVC 84%), but her carbon monoxide diffusing capacity (DLCO) and transfer coefficient (KCO) were 68 and 61% of their respective theoretical values. Chest computed tomography (CT) showed an accentuated bronchial pattern with no signs of bronchiectasis or emphysema. Liver function tests were normal. The serum AAT concentration was 73.7 mg/dL (reference values: 103–200), consistent with partial AAT deficiency, but the phenotype labeled as PI‘MM did not agree with the AAT concentrations. It was therefore decided to perform gene sequencing of the AAT in peripheral blood, in which a PI‘Nullmattawa allele was detected. This mutation is characterized by the insertion of a nucleotide within the coding region of exon 5, and results in a frameshift that creates a premature stop signal at position 376 (p.Leu353PhefsX24). This finally translates into a very unstable truncated protein that is degraded inside the hepatocyte and is undetectable in serum10 (Fig. 1).

The second allele of the patient contained a normal variant in exon 5, consisting of a substitution of a cytosine (C) for an adenine (A) in nucleotide 1200 of the cDNA, generating the replacement of a glutamic acid (Glu) by an aspartate (Asp) in codon 400 (c. 1200A>C/p.Glu400Asp), which corresponded to an M3 allele. Therefore, this is a PI‘M3Nullmattawa heterozygous genotype, with moderately reduced serum AAT levels.

Case 2

Another carrier of the Nullmattawa allele was identified from the REDAAT database.10

The patient was a 67-year-old woman with a history of pleuropulmonary tuberculosis, with documented bacteriological cure. She suffered frequent respiratory infections. Functional parameters were consistent with severe airway obstruction (FEV1: 620 ml and FVC: 1280 ml, 22% and 39% of the theoretical values, respectively). High resolution computed tomography (CT) showed diffuse centrilobular and paraseptal emphysema and diffuse cylindrical bronchiectasis. No result indicating liver involvement was detected at any time.

Her serum AAT concentrations were 43 mg/dL. IEF suggested a PI‘M3MM phenotype, but as it did not correspond with the serum AAT concentrations, a genetic study was performed. This detected a PI‘Mmalton allele (deletion of residue 52, p.Phe52del)11 and a PI‘Nullmattawa allele, the combination of which explained the patient’s low serum AAT concentrations.

Discussion

The exceptional nature of the null alleles (estimated prevalence 100–200 times lower than the Z alleles) precludes us from having precise knowledge of their clinical impact and real incidence. Nevertheless, it is important to take them into account, as they can create diagnostic confusion if genomic studies are not performed.

The Mmalton allele (also known as Mccoliari and Mnichan) was first described in 1987 and, like the Z gene, produces a poorly folded protein. Around 80%–90% of this variant polymerizes in the hepatocyte without being secreted into the blood, where it expresses levels less than 15% when in homozygosity. It is associated with a high risk of pulmonary emphysema and liver disease.11,12

The Mattawa allele (and in general any null allele) codes for a truncated protein, with major conformational changes, which is degraded intracellularly without having the opportunity to aggregate, and hence expresses undetectable serum AAT concentrations. This means that homozygotes have a very high risk of emphysema, but not of liver disease.

In conclusion, in our patients, the discrepancy between the IEF phenotype and the serum AAT concentrations led us to suspect the existence of rare alleles. Molecular analysis of the gene finally provided the correct diagnosis, as stated in the recommendations.2

Conflict of Interest

The authors declare no conflict of interest.

Acknowledgements

The authors thank Dr. Ignacio Blanco for his important contribution to the writing of this article.
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