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Resumo	Background: Since patients with cystic fibrosis with different Cystic Fibrosis Transmembrane Regulator (CFTR) genotypes present a wide response variability for modulator drugs such as Orkambi®, it is important to screen variants in candidate genes with an impact on precision and personalized medicine, such as Solute Carrier Family 26, member 9 (SLC26A9) gene. Methods: Sanger sequencing for the exons and intron-exon boundary junctions of the SLC26A9 gene was employed in nine individuals with p.Phe508del homozygous genotype for the CFTR gene who were not under CFTR modulators therapy. The sequencing variants were evaluated by in silico prediction tools. The CFTR function was measured by cAMP-stimulated current (ΔIsc-eq-FSK) in polarized CFTR of human nasal epithelial cells cultured in micro-Ussing chambers with Orkambi®. Results: We found 24 intronic variants, three in the coding region (missense variants - rs74146719 and rs16856462 and synonymous - rs33943971), and three in the three prime untranslated region (3' UTR) region in the SLC26A9 gene. Twenty variants were considered benign according to American College of Medical Genetics and Genomics guidelines, and ten were classified as uncertain significance. Although some variants had deleterious predictions or possible alterations in splicing, the majority of predictions were benign or neutral. When we analyzed the ΔIsc-eq-FSK response to Orkambi®, there were no significant differences within the genotypes and alleles for all 30 variants in the SLC26A9 gene. Conclusions: Among the nine individuals with p.Phe508del homozygous genotype for the CFTR gene, no pathogenic SLC26A9 variants were found, and we did not detect associations from the 30 SLC26A9 variants and the response to the Orkambi® in vitro.
Fomento	