DPYD pathogenic variants associated with fluoropyrimidines toxicity

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Background: Genetic variants in dihydropyrimidine dehydrogenase gene (*DPYD*) coding for the key enzyme (DPD) of fluoropyrimidines (FPs) catabolism. *DPYD* contributes to the development of severe FPs-related toxicity, and pathogenic *DPYD* variants detection reduces side effects and complications associated with FP-toxicity. The allelic frequency of these variants in the Mexican population is currently unknown.
Methods: The study was carried out at the Centro Universitario Contra el Cáncer (CUCC) of the Universidad Autónoma de Nuevo León (UANL) in Monterrey México. Genomic DNA was isolated from 154 subjects using the QIAamp DNA Blood Midi kit (QIAGEN) following the manufacturer's recommendations. We analyze the variants c.1156G->T, c.2846A->T, and c.1129-5923C->G by qPCR using predesigned probes. For the remaining genomic variants (c.1905+1G->A, c.1679T->G, c.1898delC and c.299_302delTCAT), we design sequencing oligos using the software Oligo Primer v.7®. The allele frequency was calculated for each variant.
Results: We analyzed a total of 154 samples to detect the seven variants analyzed. So far, only 2 samples have been found that presented the variant c.1129-5923C>G in a state of heterozygosis, representing 1.2987% of the total of our population.
Conclusions: The allele frequency for the variant c.1129-5923C->G was higher than reported in other populations. So this allele is more common in our population, which could attribute to the large percentage of side effects in our patients. However, more studies and increasing the number of samples are needed to establish DPYD the allele frequency more precisely.