

Pharmacogenetic Testing for Fluoropyrimidines at Instituto Nacional de Câncer, Brazil

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The present letter focuses on the pharmacogenetic (PGx) testing of variants of the *dihydropyrimidine dehydrogenase* (*DPYD*) gene available at Instituto Nacional de Câncer (INCA), Rio de Janeiro, for cancer patients who are candidates for treatment with the fluoropyrimidines 5-fluorouracil (5-FU) and/or capecitabine.¹ The rationale for *DPYD* genotyping is as follows: *DPYD* encodes the enzyme dihydropyrimidine dehydrogenase (DPD), which accounts for approximately 85% of 5-FU elimination in humans; consequently, reduction in or absence of DPD activity due to reduced or no-function *DPYD* variants leads to 5-FU accumulation and increased risk of toxicity. This also affects patients treated with capecitabine, since 5-FU is capecitabine's active metabolite.

The original *DPYD* genotyping panel adopted at INCA assessed 4 single-nucleotide polymorphisms (SNPs) listed in the Clinical Pharmacology Implementation² (CPI) and the Dutch Pharmacogenomic Working Group³ (DWPG) guidelines, namely rs391820 (*DPYD**2A), rs55886062 (*DPYD**13), rs56038477, and rs67376798. After genotyping 230 patients, we reported minor allele frequencies (MAFs) of rs391820, rs67376798, and rs56038477, similar to other Brazilian cohorts,^{4,5} whereas rs55886062 was consistently absent.⁶

Based on these data and on the current structure of the Brazilian population,⁷ our *DPYD* genotyped panel was updated by replacing rs55886062 with rs115232898, a reduced-function SNP,⁸ tightly linked to African ancestry, listed among the Tier-1 variants in the Joint Consensus for *DPYD* genotyping recommendations.⁹ As the present letter is written, 285 patients have been genotyped at INCA for rs115232898 and 4 were heterozygous for the variant T allele (MAF = 0.74%); of notice, these 4 patients self-identified as Black (*Preto*, in Portuguese), according to the race/skin color classification of the Brazilian Census.

At MAF = 0.74%, rs115232898 was the second most common SNP of the *DPYD* genotyping panel; only rs56038477

was detected at a higher MAF (1.07%) in our cohort. The rs56038477 SNP is commonly used to identify the reduced-function *DPYD HapB3* haplotype, based on the assumption of its complete linkage disequilibrium (LD) with rs75017182 (c.1129–5923C > G), which defines the *HapB3* haplotype. However, a recent report¹⁰ of incomplete, albeit extensive ($D' = 0.985$) LD between these two SNPs prompted the suggestion that, in rare cases, the recommendation for reduced fluoropyrimidine dosing, based on the rs56038477 genotype, would be inappropriate and could negatively impact the drug response. This concern led us to genotype rs75017182 in all patients who had received fluoropyrimidine dosing recommendations based on the rs56038477 genotype. This analysis verified a perfect LD between the two SNPs: the 6 patients heterozygous for rs56038477 were also carriers of rs75017182 in heterozygosis, whereas all other patients had the reference allele in homozygosis at both loci. Perfect LD of these two SNPs in Brazilians may also be inferred from their identical MAF (0.43%) in a large, admixed cohort of elderly individuals.¹¹ Thus, we feel confident about fluoropyrimidine dosing recommendations based on rs56038477 as a surrogate marker for *DPYD HapB3*.

Collectively, the genotyping panel for the 4 SNPs (rs391820, rs55886062, rs56038477, and rs115232898) currently in use at INCA identified 10 patients as carriers of 1 of the reduced or no-function *DPYD* alleles, plus 1 patient heterozygous for rs3918290 and rs56038477. These patients were assigned the intermediate (IM; $N = 10$; frequency: 3.5%) and the poor DPD metabolizer phenotype (PM; $N = 1$; frequency: 0.4%) respectively, and received recommendations for fluoropyrimidine initial dosing according to the CPI² and DWPG³ guidelines. These data were then used to predict the diagnostic performance of 12 commercial laboratories offering *DPYD* tests in Brazil, identified through

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an internet search.¹² Five of these laboratories genotype all SNPs in our panel; thus, they are expected to reproduce our results. By contrast, the other 7 laboratories do not include rs56038477 nor rs115232898 in their genotyping panels and would misclassify 9 of the 10 IMs as normal metabolizers (NMs), and, most importantly, misclassify the high-risk PM patient as IM. This high rate of misclassification (90.9%) derives from the fact that the missing rs56038477 and rs115232898 SNPs are the most prevalent in our patient cohort, as aforementioned. This analysis extends to Brazilian patients the reported concerns regarding the limitations and variability in *DPYD* variant detection by commercial laboratories in the United States, and the potential deleterious impact on PGx-informed dosing recommendations for fluoropyrimidines.¹³

In conclusion, the implementation and updating of PGx testing of *DPYD* variants at INCA conforms to the requirement/recommendation by several drug regulatory agencies (such as the European Medicines Agency [EMA], the United States Food and Drug Administration [FDA], and Health Canada/Santé Canada [HSCS]) for *DPYD* genotyping prior to fluoropyrimidine administration.¹⁴ Accordingly, the Brazilian Health Regulatory Agency (Agência Nacional de Vigilância Sanitária, ANVISA, in Portuguese) package insert for capecitabine states that “the test for DPD deficiency should be considered according to the local availability and current guidelines.”¹⁵ However, the package insert for 5FU¹⁶ makes no reference to *DPYD* or DPD testing.

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Conflict of Interests

The author has no conflict of interests to declare.

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