

Correction to “Frequency of Undetected CYP2D6 Hybrid Genes in Clinical Samples: Impact on Phenotype Prediction”

In the article referenced above [Black JL 3rd, Walker DL, O’Kane DJ, and Harmandayan M (2012) *Drug Metab Dispos* **40**:111–119], Table 2, column 1, row 11 should read “Percentage of total samples ($n = 1390$) with CYP2D6*36 + *10-like ($n = 44$).” The corrected table is shown below.

In addition, the assignments of allele designations by the CYP2D6 Nomenclature Committee to the CYP2D7-2D6 hybrid allelic variants are undergoing revision. Readers are encouraged to refer to <http://www.cypalleles.ki.se/cyp2d6.htm> for the most recent nomenclature.

The online versions of this article have been corrected in departure from the original version.

The authors regret this error and apologize for any confusion or inconvenience it may have caused.

TABLE 2

Frequency of hybrid genes per sample type

The frequency of hybrids genes in CYP2D6*4 and CYP2D6*10 samples is reported for both heterozygous or homozygous and heterozygous alone. We did not determine whether one or both chromosomes contained a hybrid tandem in homozygous samples. For this reason, to determine the risk that a CYP2D6*4 or CYP2D6*10 allele is actually in a hybrid tandem arrangement, we determined the percentage of heterozygous samples for each, which had a hybrid tandem. The “Any homozygous genotype” row included any sample with an initial homozygous genotype except those with duplications. Finally, the frequency of hybrid genes in samples originally genotyped as having duplications is shown. The percentage of hybrid alleles in the 1390 samples is also shown by category, although note that the sample set was not from a random population but was purposefully enriched for samples with CYP2D6*4, CYP2D6*10, duplication, and homozygous genotypes; thus, frequency of hybrid genes in a general population is likely to be different.

| Category | <i>n</i> | % |
|--|----------|------|
| Heterozygous or homozygous CYP2D6*4 | 508 | |
| Containing CYP2D6*4N + *4-like | 9 | 1.8 |
| Containing CYP2D6*68 + *4-like | 109 | 21.5 |
| Percentage of total samples ($n = 1390$) with CYP2D6*4N + *4-like or CYP2D6*68 + *4-like ($n = 118$) | | 8.5 |
| Heterozygous CYP2D6*4 | 482 | |
| Containing CYP2D6*4N + *4-like | 7 | 1.5 |
| Containing CYP2D6*68 + *4-like | 83 | 17.2 |
| Heterozygous or homozygous CYP2D6*10 | 209 | |
| Containing CYP2D6*36 + *10 | 44 | 21.1 |
| Percentage of total samples ($n = 1390$) with CYP2D6*36 + *10-like ($n = 44$) | | 3.2 |
| Heterozygous CYP2D6*10 | 193 | |
| Containing CYP2D6*36 + *10 | 28 | 14.5 |
| Any homozygous genotype | 332 | |
| Containing CYP2D7-2D6 hybrid genes | 4 | 1.2 |
| Percentage of total samples ($n = 1390$) with CYP2D7-2D6 hybrid gene ($n = 4$) | | 0.3 |
| Any duplication sample | 341 | |
| Containing CYP2D7-2D6 + CYP2D6 hybrid tandem present | 25 | 7.3 |
| Percentage of total samples ($n = 1390$) with CYP2D7-2D6 + CYP2D6 or novel structure ($n = 25$) | | 1.8 |