Errata

Wadelius M, Chen LY, Lindh JD, et al. The largest prospective warfarin-treated cohort supports genetic forecasting. *Blood*. 2009;113(4):784-792.

On page 786 in the 22 January 2009 issue, there is an error in the *P* value required for significance, which reads "of less than .001." The correct *P* value is "of less than 2.9×10^{-4}." In the "Methods" section, the fourth sentence under the heading "Statistical analysis" reads, "M_{eff} was 172 in our study and hence a *P* value of less than .001 was required for significance." The sentence should have read, "M_{eff} was 172 in our study and hence a *P* value of less than 2.9×10^{-4} was required for significance."

On page 788, there is an error in the TIR calculations. The "Results" section, under the heading, "Time in range," reads, "During the first 3 months, the median time in range, 2 to 3 (TIR), was 67% (average, 65%). *VKORC1* rs9923231 G>A had a nominal effect on TIR during the first 3 months ($P = .003$, and for rs2359612 C>T $P = .002$). Average TIR was the highest (70%) in A/A individuals (in LD with rs2359612 T/T) and the lowest (64%) in G/G individuals (in LD with rs2359612 C/C). *CYP2C9**2 and *3 also nominally affected this outcome ($P = .041$). TIR was the lowest in *3/*3 individuals (average, 53%), and relatively high in *2/*3 heterozygotes (average 67% to 72%). After correction for multiple testing ($P < .001$), no candidate gene was significantly associated with TIR during the first 3 months.

"The median time in range 2 to 3 during the entire treatment period was 64% (average, 61%). When the 39 patients with a target INR outside 2.4 to 2.6 were removed, the overall average TIR increased by 0.1%. *VKORC1* rs9923231 was significantly associated with overall time in range ($P = 1.68 \times 10^{-4}$, and for rs2359612 $P = 1.47 \times 10^{-4}$). As above, average TIR was the highest (65%) in A/A individuals (rs2359612 T/T) and the lowest (60%) in rs9923231 G/G individuals (rs2359612 C/C). *NR1I3* SNP rs3003596 was almost significantly associated with overall TIR after correction for multiple testing ($P = .001$). *CYP2C9* was not associated with overall TIR."

The content should have read, "During the first 3 months, the median time in range, 2.0 to 3.0 (TIR), was 70% (average, 67%). *VKORC1* rs9923231 G>A had a nominal effect on TIR during the first 3 months ($P = .004$, and for rs2359612 C>T $P = .001$). Average TIR was the highest (71%) in A/A individuals (in LD with rs2359612 T/T) and the lowest (65%) in G/G individuals (in LD with rs2359612 C/C). *CYP2C9**2 and *3 also affected this outcome ($P = .001$). TIR was the lowest in *3/*3 individuals (average, 50%), and relatively high in *2/*3 heterozygotes (average 69% to 71%). After correction for multiple testing ($P < 2.9 \times 10^{-4}$), no candidate gene was significantly associated with TIR during the first 3 months.

"The median time in range 2.0 to 3.0 during the entire treatment period was 74% (average, 71%). *VKORC1* rs9923231 was significantly associated with overall time in range ($P = .001$, and for rs2359612 $P = 7.45 \times 10^{-4}$). As above, average TIR was the highest (75%) in A/A individuals (rs2359612 T/T) and the lowest (69%) in rs9923231 G/G individuals (rs2359612 C/C). *CYP2C9**2 and *3 was associated with overall TIR ($P = .002$). TIR was again lowest in *3/*3 individuals (average, 58%) and highest in *2/*3 heterozygotes (mean, 73% for all). After correction for multiple testing ($P < 2.9 \times 10^{-4}$), no candidate gene was significantly associated with overall TIR."

Garcia JS, Medeiros BC, Appelbaum FR. *Blood* consult: monosomal karyotype acute myeloid leukemia. *Blood*. 2012;119(24):5659-5660.

On page 5659 in the 14 June 2012 issue, there is a typographical error in the karyotype reported. In the "Case presentation" section, the fifth sentence of the first paragraph reads, "Cytogenetic analysis revealed the following karyotype: 45,XY,del(5)(q11.2q35),+8,der,(12)der (16;18)(p10;q10),-7,-17[17]/46,XY[3]." The sentence should have read, "Cytogenetic analysis revealed the following karyotype: 45,XX, del(5)(q11.2q35),+8,der(12)?,der(16;18)(p10;q10),-17[14]/44,idem,-2,del(4)(q31.1),-7,-10,-13,+3mar[3]/46,XX[3]."