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Leiden  
The Netherlands

**Publisher correction: anti-cancer treatment schedule optimization based on tumor dynamics modelling incorporating evolving resistance**

Yin, A.; Hasselt, J.G.C. van; Guchelaar, H.J.; Friberg, L.E.; Moes, D.J.

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**OPEN** **Publisher Correction: Anti-cancer treatment schedule optimization based on tumor dynamics modelling incorporating evolving resistance**

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Anyue Yin, Johan G. C. van Hasselt, Henk-Jan Guchelaar, Lena E. Friberg & Dirk Jan A. R. Moes


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The original version of this Article contained errors in Table 1 where the data was listed incorrectly in the column 'M-KRAS patients'. The original Table 1 and accompanying legend appear below.

The original Article has been corrected.

Parameters (units)	Description	Typical values		Reference
		WT-KRAS patients	M-KRAS patients	
$T_{s_0}$ (mm <sup>2</sup> )	Baseline of $T_s$ (clonal population that is sensitive to anti-EGFR inhibitor ( $D_1$ ))	5500	100	Data/Estimated value; Mutation was assumed to be acquired during treatment
$T_{R1_0}$ (mm <sup>2</sup> )	Baseline of $T_{R1}$ (clonal population that is resistance to $D_1$ but is sensitive to the second hypothetical treatment ( $D_2$ ))	0	1700	Data/Estimated value; Mutation was assumed to be acquired during treatment
$T_{R2_0}$ (mm <sup>2</sup> )	Baseline of $T_{R2}$ (clonal population that is resistance to both treatments)	0	0	Data/Estimated value; Mutation was assumed to be acquired during treatment
$M_{ctDNA1_0}$ (fragments/ml)	Baseline of mutant $KRAS$ ( $M_{ctDNA1}$ ) in ctDNA	0	500	Data/Estimated value; Mutation was assumed to be acquired during treatment
$M_{ctDNA2_0}$ (fragments/ml)	Baseline of a second hypothetical mutation ( $M_{ctDNA2}$ ) in ctDNA	0		Data/Estimated value; Mutation was assumed to be acquired during treatment
$k_{g1}$ (/week)	Growth rate constant of $T_s$	0.03		40
$k_{g2}$ (/week)	Growth rate constant of $T_{R1}$	0.021		43,44
$k_{g3}$ (/week)	Growth rate constant of $T_{R2}$	0.015		43,44
$k_{s1}$ (/week)	Tumor shrinkage rate constant due to $D_1$	0.1		Estimated value
$k_{s2}$ (/week)	Tumor shrinkage rate constant due to $D_2$	0.1		$k_{s1}$
$k_{M1}$ (/week)	Mutation rate from $T_s$ to $T_{R1}$ when $D_1=1$	0.05	0	Estimated value
$k_{M2}$ (/week)	Mutation rate from $T_{R1}$ to $T_s$ when $D_1=0$	0.03		Lower than $k_{M1}$ <sup>9</sup>
$k_{M3}$ (/week)	Mutation rate from $T_{R1}$ to $T_{R2}$ when $D_2=1$	0.05		$k_{M1}$
$k_{M4}$ (/week)	Mutation rate from $T_{R2}$ to $T_{R1}$ when $D_2=0$	0.03		$k_{M2}$
$H$	Hill coefficient	5		Visually matching the slope of data and the detectable time of mutant $KRAS$
$KT_{50}$ (mm <sup>2</sup> )	The size of tumor that provide half-maximal shedding rate of ctDNA	3500		Visually matching the slope of data and the detectable time of mutant $KRAS$
$k_{max_1}$ ((fragments/ml)/(week*mm <sup>2</sup> ))	Maximum shedding rate of $M_{ctDNA1}$	0.015	1.5	Visually matching the slope of data and the detectable time of mutant $KRAS$
$k_e$ (/week)	ctDNA eliminate rate constant	0.5		Visually matching the slope of data and the detectable time of mutant $KRAS$
$k_{max_2}$ ((fragments/ml)/(week*mm <sup>2</sup> ))	Maximum shedding rate of $M_{ctDNA2}$	0.015		$k_{max_1}$
IIV_ $B$ ( $\omega_1$ )	Standard deviation of IIV of baselines	0.6	1.5	Data
IIV_ $k_g$ ( $\omega_2$ )	Standard deviation of IIV of $k_g$	0.2		Data

**Table 1.** Parameters values of the developed model characterizing the dynamics of tumor size and mutation concentrations in metastatic colorectal cancer (mCRC) patients. ctDNA, circulating tumor DNA; IIV, interindividual variability; WT-KRAS patients, patients who were initially identified as  $KRAS$  wild-type in ctDNA; M-KRAS patients, patients who had detectable mutant  $KRAS$  in ctDNA pre-treatment.

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