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Physiologically-based pharmacokinetic modelling of dendrimer nanoparticles to unravel structure – PK parameters relationship







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METHODS

CONTEXT & OBJECTIVES

Many types of nanoparticles (NPs) developed but no tools to	Dendrimer C18 NOTA chelator	Reduction of alkyl chain and fluorination of C18	 <u>Data</u>: Model: healthy Swiss mice 	Parameter	Source
rationalize NPs development ⇒ Need of tools for rational nanodrugs optimization	$Ga = [68Ga]Gallium$ $= \int Ga = [68Ga]Gallium$	A constraint of the second	 Administration: intravenous mPET/CT imaging for 2h (n=6, except for (C₄F₉)-C11 n=5, and (C₄F₉)-C11 with RGD n=3) gamma counting (blood) for 2h (n=6, except (C₄F₉)-C11 with RGD n=3) Software: R version 4.2.2 Ordinary Differential Equation (ODE) solver: deSolve 	Partition coefficients (Kp)	In vivo data ^[2] Concentration in organs, tissues (%ID/g) Concentration in blood (%ID/g)
Current work on 7 formulations				Physiology Permeability (P)	Brown et al. ^[3] Estimated
of gallium-68 radiolabeled				(mL/h) Renal clearance (CLr. mL/h)	In vivo data (popPK
				Hepatic clearance	In vivo data (popPK

PBPK modeling: quantitative PK estimations and predictions

Development of a computational model describing the distribution of dendrimers in the organism depending on their characteristics

Plots: ggplot and GraphPad Prism 9.5

RESULTS

2. Structure-PK parameters relationships

1. Structure of the nanoPBPK model

Tissue model: permeability-limited tissue distribution



 $\frac{dA_{vascular}}{dt} = Q^*(CA - CV_{tissue}) - P_{ti}$ P_{tissue} * C_{tissue} * CV.



Effect of the alkyl chain length \rightarrow lower affinity for kidneys when chain > 12C

model)^[2]



Effect of the fluorination \rightarrow

(CLh, mL/h)

$$\frac{dA_{interstitial}}{dt} = P_{tissue} * CV_{tissue} - \frac{P_{tissue} * C_{tissue}}{Kp}$$

C: concentration (%ID/g) CA: arterial concentration (%ID/mL) CV: venous concentration (%ID/mL) Q: Blood flow (mL/h)



4. Predictions of dendrimers disposition *in vivo*



Internal evaluation of the model

Comparison of blood PK parameters (Cmax and AUC) calculated from observed data (**obs**) and predicted (**pred**) from the PBPK model for each dendrimer

Dendrimer	Cmax _{obs} (%ID/g)	Cmax _{pred} (%ID/g)	Cmax Fold error	AUC _{obs 0-2h} (%ID/g.h)	AUC _{pred 0-2h} (%ID/g.h)	AUC Fold error
C18	22.29	27.87	1.25	30.19	39.87	1.32
(CF ₃) ₃ -C15	24.57	26.19	1.07	32.84	37.03	1.13
C ₄ F ₉ -C14	30.42	24.39	0.80	42.09	33.69	0.80
(CF ₃) ₃ -C12	30.98	27.66	0.89	35.99	32.55	0.90
C ₄ F ₉ -C11	16.47	13.9	0.84	19.10	17.39	0.91
C₄F ₉ -C11 RGD 1:3	24.91	24.04	0.97	23.35	29.79	1.28
C₄F ₉ -C11 RGD 3:1	25.67	22.67	0.88	28.05	26.84	0.96
			Fold error	< 2		

CONCLUSION

Space for improvement (overprediction in liver, underprediction in heart for C_4F_9 -C11)

- PBPK model accurately predicted the distribution of dendrimers
- Relationships between dendrimer structure and PK parameters established \rightarrow tool to guide the development of dendrimers

PERSPECTIVES

- Collection of *in vitro* parameters to add NP-specific processes in the model (cellular uptake (endocytosis), opsonization)
- Expand the PBPK model to other types of NPs
- Apply this approach to design new optimal NPs

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[1] Garrigue P. et al., Proc. Natl. Acad. Sci. 115, 11454–11459 (2018) [2] Ou J. et al., hal-03930671 (2022) [3] Brown RP et al., Toxicol Ind Health. 13: 407 (1997)

Abbreviations

AUC: Area under the curve C: carbon ID: injected dose MPS: Mononuclear Phagocyte System RGD: Arginyl-glycyl-aspartic acid