

PK-PD MODELLING OF AN ANTI-PD-L1 MONOCLONAL ANTIBODY

Ana M Contreras-Sandoval¹, María García-Cremades¹, María Merino¹, Kepa Berraondo², Iñaki F. Trocóniz¹, María J. Garrido¹
¹School of Pharmacy, Department of Pharmacy and Pharmaceutical Technology, University of Navarra, 31008 Pamplona, Spain
²Division of Gene Therapy and Hepatology, Center for Applied Medical Research (CIMA), University of Navarra, 31008, Pamplona, Spain

BACKGROUND AND AIM

Programmed death-1 ligand-1 (PD-L1 or B7-H1) is a co-stimulatory molecule which is expressed at higher levels in tumor cells [1]. PD-L1 and its receptor PD-1 at the activated lymphocytes, play a critical role in T-cell regulation to enhance immune-inhibitory activity, and therefore anti-tumor activity [1]. PD-1/PD-L1 binding is able to enhance lymphocyte apoptosis (effector T cells) and tumor proliferation by inhibition of cytokines production such as interleukin (IL)-2 and interferon gamma (IFN- γ) [1, 2]. Therefore, although overexpression of PD-L1 in tumor cells allows the use of this pathway as a mechanism to escape from immune response [1, 2]. This PDL-1 pathway had been also proposed as a novel anti-tumor strategy, being possible to block the PD-1/PD-L1 interaction by a targeted molecule in order to increase tumor specific T-cell response [1, 2]. Nowadays, the development of anti-PD-L1 monoclonal antibodies (mAbs) arises as an effective approach for specific tumor immunotherapy [3], so that its pharmacokinetics and pharmacodynamics characterizations are essential. Hence, the aim of this work was to develop a mAb targeted to PD-L1 PK/PD model able to characterize its anti-tumor effect based on different initial tumor sizes (Ts).

MATERIALS AND METOHODS

Drug administration: 100 μ g/mouse, I.V. single dose.

Animals and samples: 6 female C57BL/6 mice, were administrated with the drug and serum samples were taken at specific times based on several extraction windows for every animal.

Data analysis: One compartmental model was used to describe plasma concentrations of mAb in mice.

Animal model: B16-OVA melanoma cell line, PD-L1 positive.

Animals: C57BL/6 mice, were randomly divided into four groups (n = 7/group): G1) small Ts, G2) medium Ts, G3) large Ts and G4) control group.

Tumor cells inoculation: 2x10⁵ (CN₁) and 5x10⁵ (CN₂) B16-OVA cells/100 μ L/mouse were S.C. inoculated on day 0 in one flank of every mouse.

Treatment regimen: 100 μ g/mouse, I.V. Q3D x 4 administrations.

Data analysis: Time profiles of tumor volume (mm³) data were fit using the Hahnfeldt's model [4].

For PK/PD modelling, all data were log transformed and the analysis was done using NONMEM 7.2. and R program for graphs.

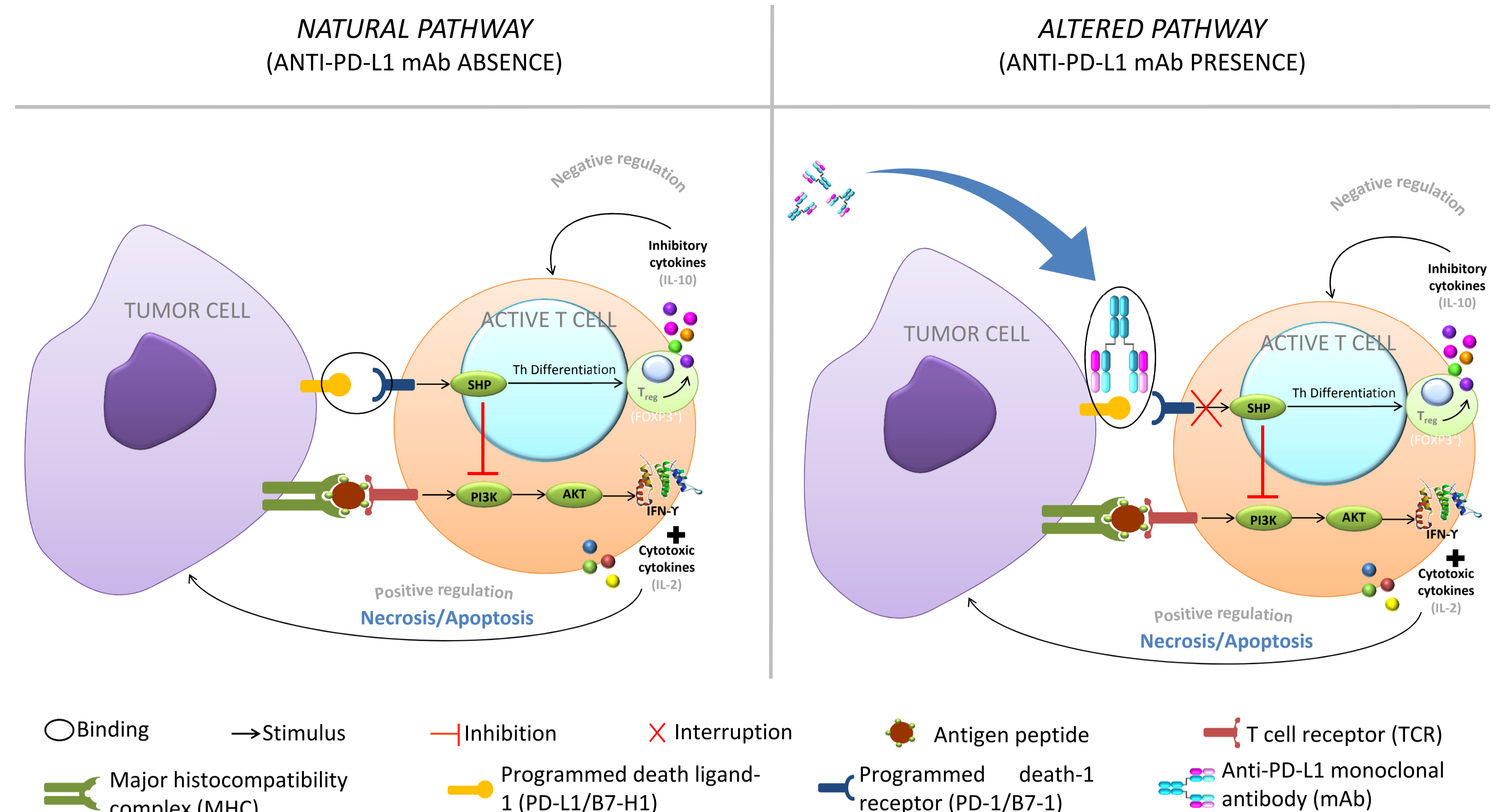


Figure 1. Mechanism of tumor evasion from host immunity and anti-PD-L1 mAb strategy

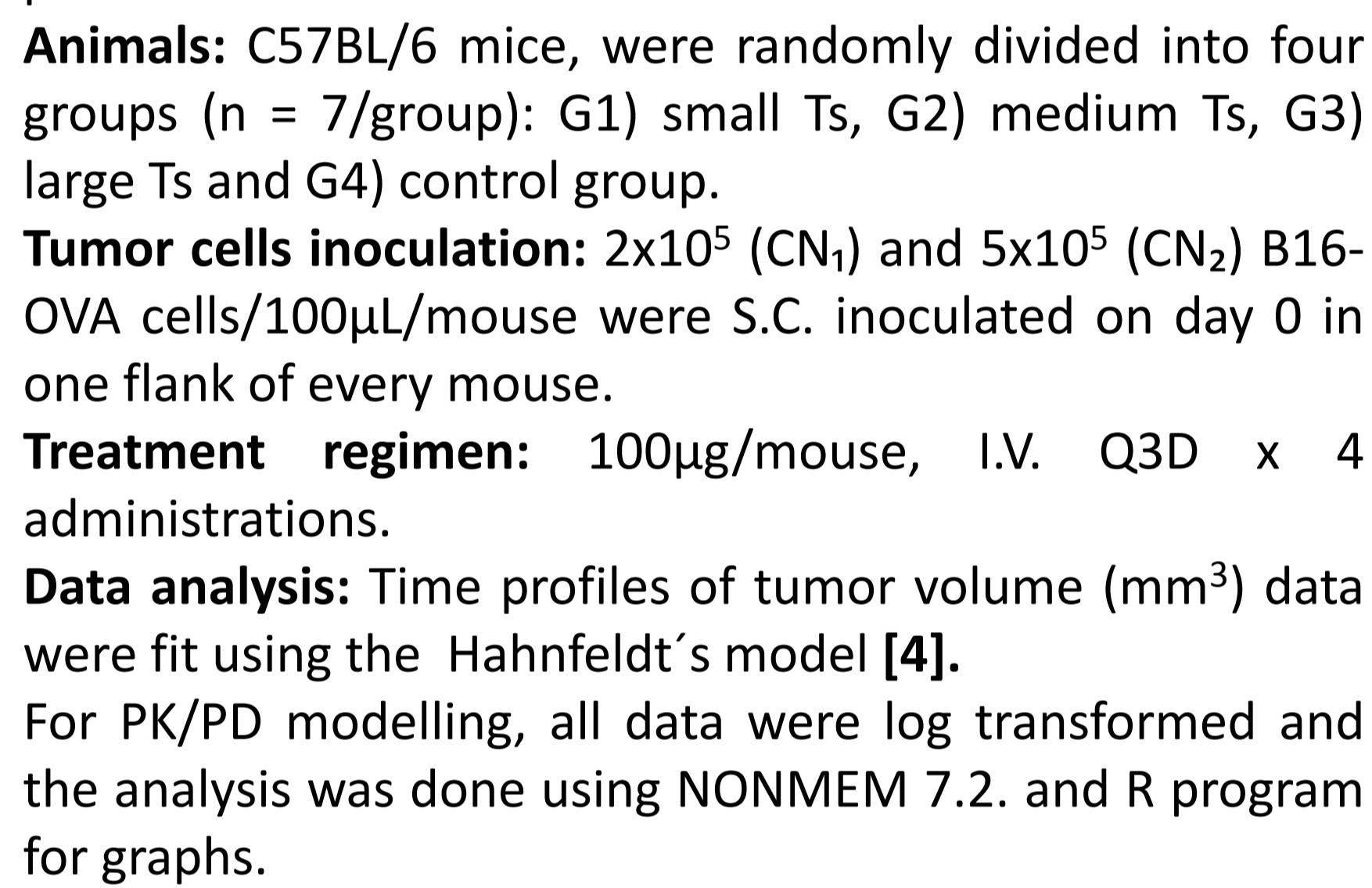


Figure 2. Schematic representation of the experimental design

RESULTS

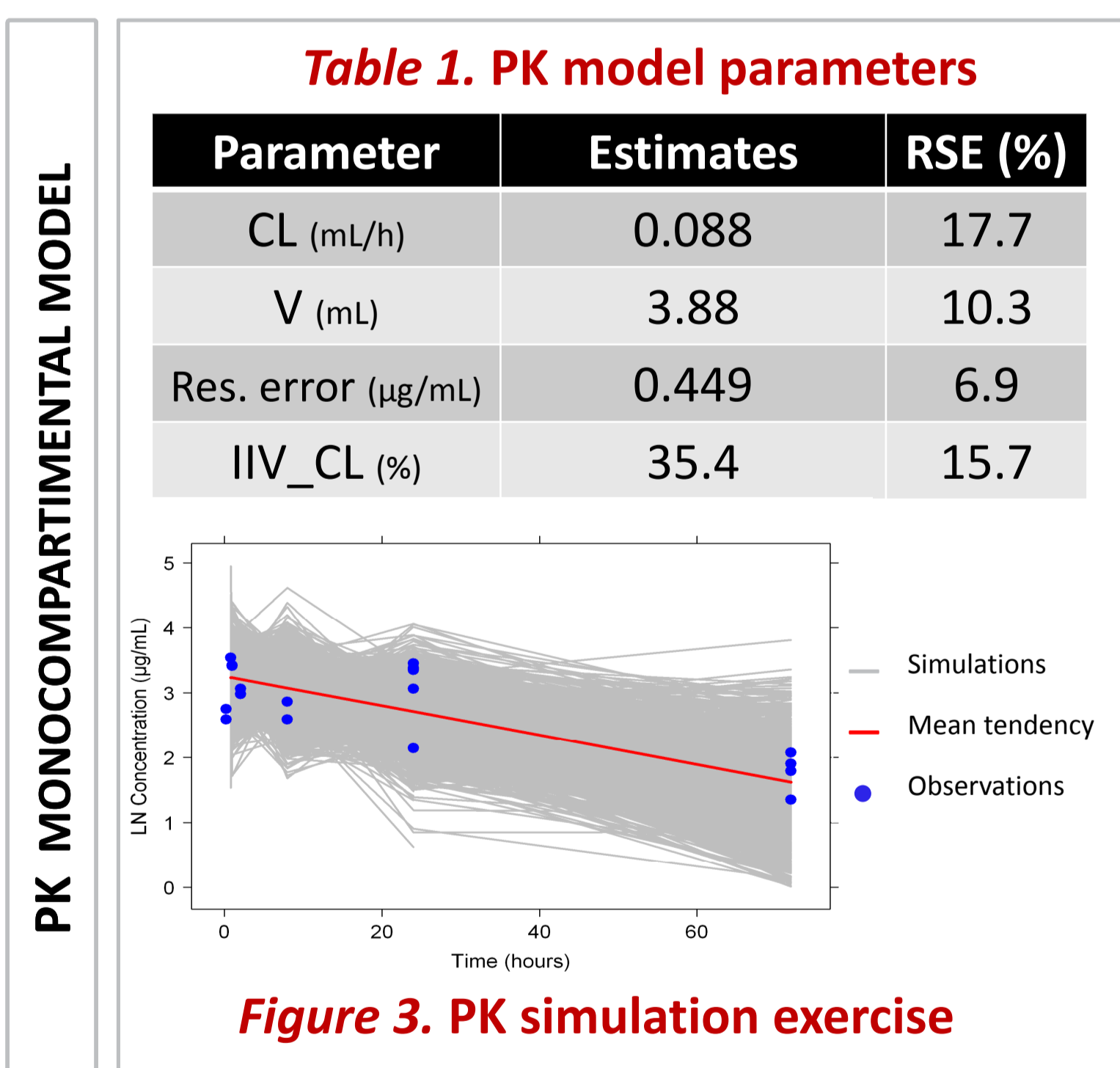


Figure 3. PK simulation exercise

Table 2. PK/PD model parameters

Parameter	Estimates	RSE (%)
α_1 (days ⁻¹)	0.596	48.7
CN ₁ (mm ³)	20.7	30.2
CN ₂ (mm ³)	5.35	49
k (mm ³)	0.504	67.7
b (days ⁻¹)	0.503	8.5
d (days ⁻¹ (mm ³) ^{-2/3})	0.00044	56.4
Res. error (mm ³)	0.416	6.6
SLOPE (μ g/mL)	0.0119	2
γ	0.216	28.7
IIV_ α_1 (%)	80.4	37.6
IIV_CN ₁ (%)	87.4	25.6
IIV_CN ₂ (%)	86.8	96.3

α_1 : tumor proliferation. CN₁: initial tumor size for control population 1. CN₂: initial tumor size for control population 2. k: carrying capacity or vasculature. b: stimulatory capacity of the tumor upon the inducible vasculature. d: endogenous inhibition of previously generated vasculature. w: residual error. SLOPE: drug effect constant. γ : shape parameter

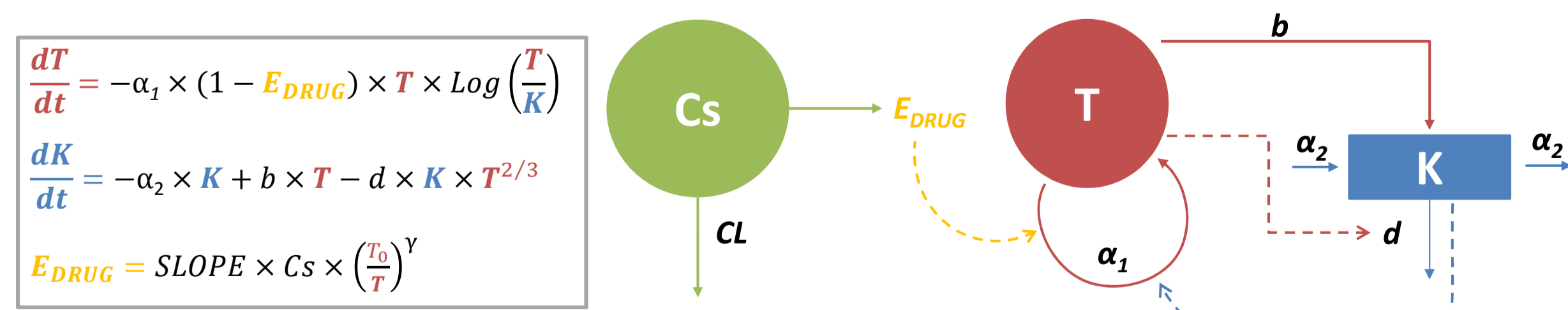


Figure 4. Schematic representation of the PK/PD model for and anti-PD-L1 mAb

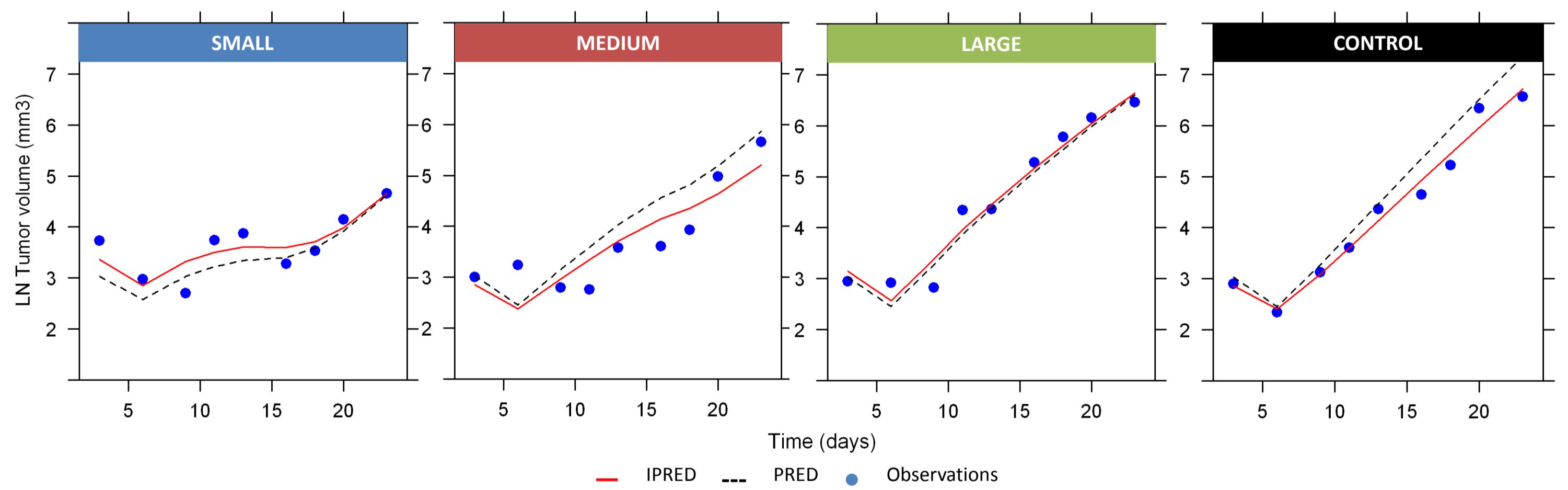


Figure 5. Individual PK/PD predictions of the model for each group

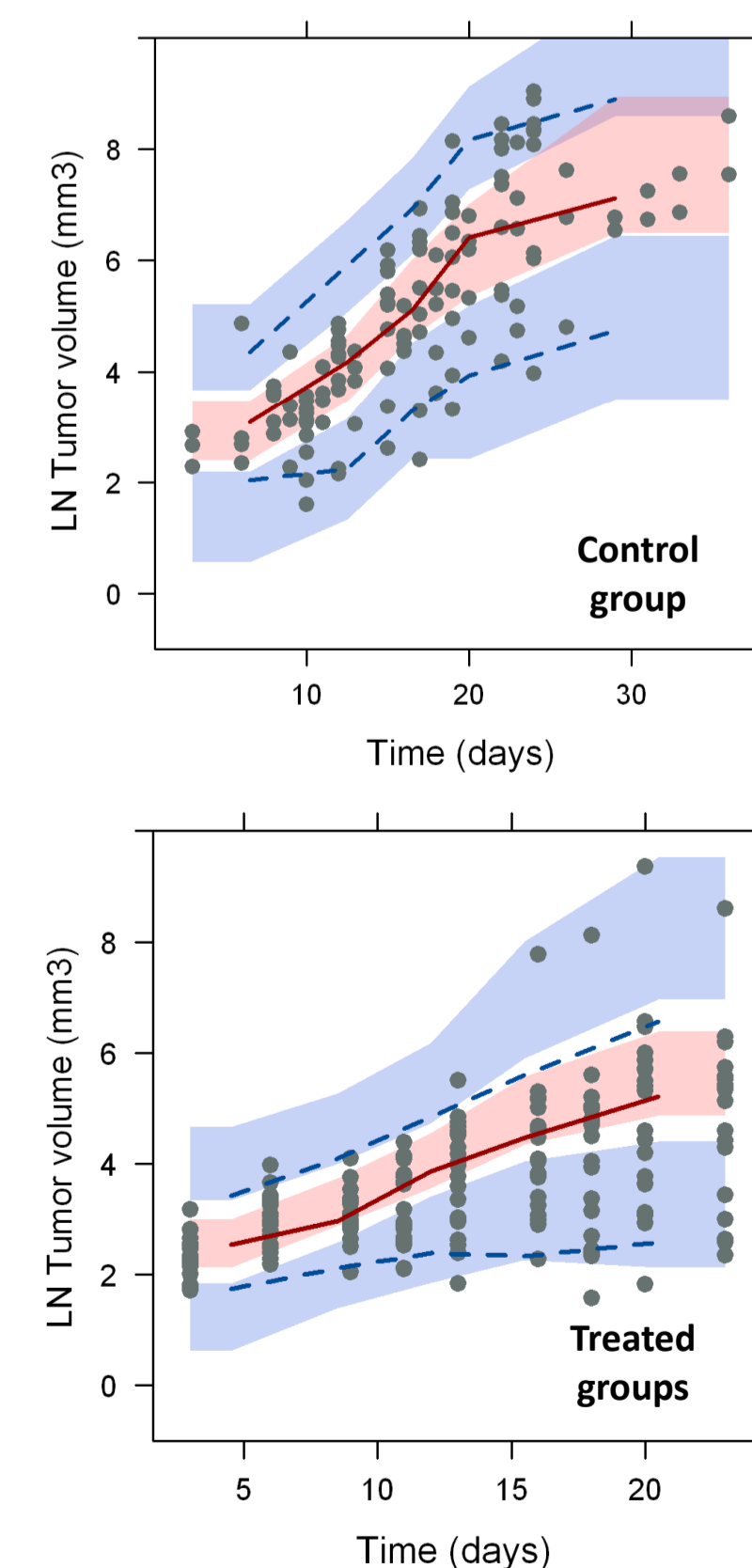


Figure 6. PRED corrected VPC

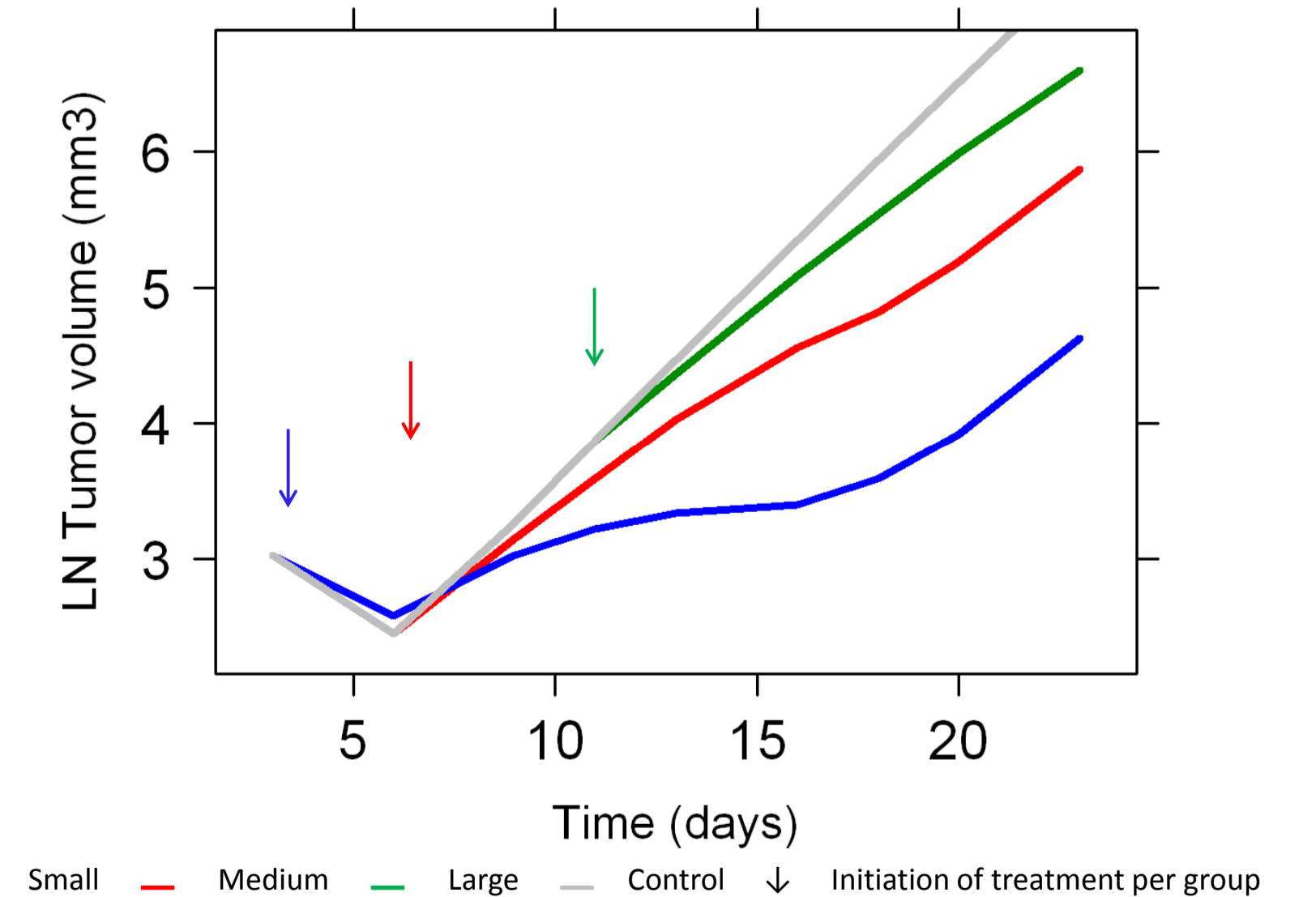


Figure 7. Population PK/PD predictions of the model for each group

CONCLUSIONS

1. The body disposition of the anti-PD-L1 mAb (clone 10F.9.G2) was described by a mono-compartmental model
2. The tumor growth of a B16-OVA mouse model was described by the Hanhfeldt model.
3. The proliferation rate of B16-OVA cells was affected by the anti-PD-L1 mAb (clone 10F.9.G2) inducing a delay on the tumor growth and that effect was dependent on the initial tumor size.

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