

Dynamics of CD4⁺ T cell responses against *Listeria monocytogenes*

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Supplemental Material

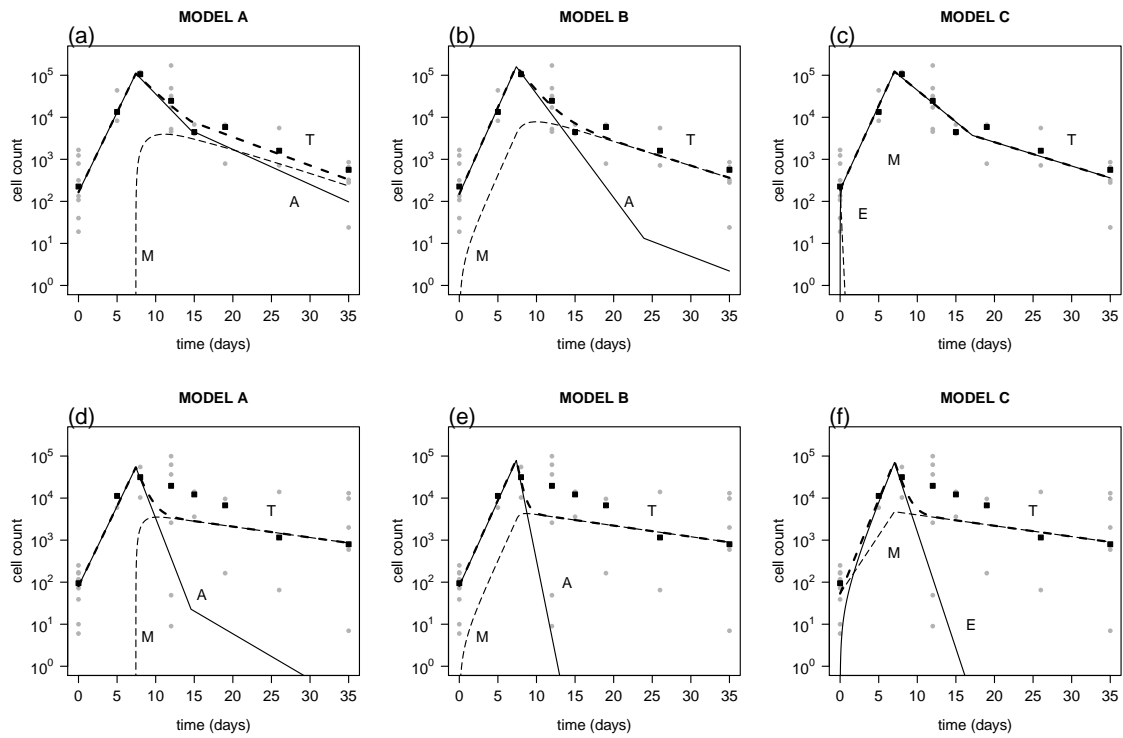


Figure S1: Data and fitted curves for the CD4⁺ T cell count of LLO118 and LLO56 cells. The separate models correspond to the models explained in Figure 1. In this case, a biphasic contraction phase was assumed in each of the models (see *Materials and Methods*). The total number of CD4⁺ T cells (T , long-dashed line), the number of activated and effector CD4⁺ T cells, respectively (A , E solid line) and the number of memory cells (M , dashed line) are shown.

Table S1: Parameter estimates for models with rapid apoptosis phase

parameter	symbol	unit	Model A	Model B	Model C
Proliferation rate	ρ^{LLO118}	day ⁻¹	0.88 [0.85,0.9]	0.97 [0.94,0.99]	0.92 -
	ρ^{LLO56}		0.88 [0.85,0.9]	0.97 [0.94,0.99]	1.03 -
Memory cell formation	r^{LLO118}	day ⁻¹	0.028 [0.017,0.037]	0.024 [0.019,0.027]	9.88 -
	r^{LLO56}		0.084 [0.074,0.093]	0.035 [0.032,0.039]	0.39 -
Activated cells at $t = 0$	$A(0)^{\text{LLO118}}$	cells	165 [156,172]	150 [142,157]	190 -
	$A(0)^{\text{LLO56}}$		80 [75,85]	82 [76,88]	54 -
Death rate of memory cells	δ_M^{LLO118}	day ⁻¹	0.15 [0.14,0.16]	0.13 [0.12,0.14]	0.11 -
	δ_M^{LLO56}		0.06 [0.05,0.06]	0.06 [0.05,0.06]	0.06 -
Death rate of activated cells	δ_A	day ⁻¹	0.16 -	0.14 [0.0,0.35]	0.13 -
Fast apoptosis rate	α^{LLO118}	day ⁻¹	0.24 [0.21,0.27]	0.41 [0.18,0.63]	0.22 -
	α^{LLO56}		0.84 [0.73,0.94]	1.92 [1.36,2.48]	1.15 -
End of proliferation phase	T	day	7.4 [7.3,7.5]	7.4 [7.2,7.5]	7.0
Duration of fast contraction phase	Δ	day	7.15 [6.39,7.91]	16.53 -	10.1 -
residual mean square	MNSQ		3.533	3.524	3.499

Parameter estimates for the basic model ((A), Eqs. (1a) and (1b)), a model with the assumption of a constant memory production during the proliferation phase ((B), Eqs. (4a) and (4b)), and for a model assuming the alternative differentiation pathway ((C), Eqs. (5a) and (5b)). For all models, we assume a biphasic contraction phase for the activated/ effector cells as indicated in Eq. (3). 95% confidence intervals for the estimates are calculated based on the standard error approximated by the Hessian-matrix. MNSQ indicates the residual mean square for each model (see *Materials and Methods* for the calculation).