

Dendritic cell-mediated responses to secreted *Cryptosporidium* effectors promote parasite-specific CD8+ T cell responses

Haskins, Breanne E; Gullicksrud, Jodi A; Wallbank, Bethan A; Dumaine, Jennifer E; Guérin, Amandine; Cohn, Ian S; O'Dea, Keenan M; Pardy, Ryan D; Merolle, Maria I; Shallberg, Lindsey A; Hunter, Emma N; Byerly, Jessica H; Smith, Eleanor J; Buenconsejo, Gracyn Y [**and 4 more**]

This publication URL: Publication DOI:

https://archive-ouverte.unige.ch/unige:178790 10.1016/j.mucimm.2024.03.003

© This document is protected by copyright. Please refer to copyright holders for terms of use.

Supplemental Figure 1.



Supplemental Figure 1. (Refers to Figure 1). Representative flow plots display SIINFEKL:K^{b+} CD8⁺ T cells in mLN and IEL from one uninfected mouse in experiments performed in Fig. 1D.

Supplemental Figure 2.



Supplemental Figure 2. (Refers to Figure 2). Representative flow plots display OT-I cells in mLN and PP from experiments performed in Fig. 2A/B.

Supplemental Figure 3.



Supplemental Figure 3. (Refers to Figure 3). **A-F**. Summary bar graphs of the percentages of OT-I cells that express the given parameter from Fig. 3D-I.

Supplemental Figure 4.



Supplemental Figure 4. (Refers to Figure 4). **A**. Experimental timeline for experiments performed in Fig. 4A created with BioRender.com. **B**. Representative flow plots show CD8⁺ T cellThy1.1 and SIINFEKL:K^b expression in mLN and PP from experiments performed in Fig. 4A.

Supplemental Figure 5.



Supplemental Figure 5. (Refers to Figure 5). **A**. Representative flow plots show OT-I cells in mLN and PP from experiments in Fig. 5C. **B**. Parasite burdens (relative luminescence) over time from mice infected in Fig. 5C. **C**. Representative flow plots show OT-I cells in mLN and PP from experiments in Fig. 5D. **D**. Parasite burdens (relative luminescence) over time from mice infected in Fig. 5D.

Supplemental Figure 6.



Supplemental Figure 6. (Refers to Figure 6). **A**. WT C57BL/6J mice were left untreated or treated with 1 mg/mouse α IFN- γ 2 days prior to infection and 2 days post infection with 10⁴ M2-OVA. mLN, PP, and IEL were harvested 12 dpi for flow cytometry. Representative flow plots show OT-I cells in IEL, gated on Singlets, Live, CD19-, NK1.1-, CD90.2+, CD4-, CD8 α +, CD45.1+ V α 2+. Summary bar graphs from one experiment of percentages of OT-I cells. N=3-4 mice/group for 2 independent experiments. **B**. Parasite burdens from experiments performed in **A**. **C**. Representative flow plots show OT-I cells in mLN and PP from experiments in Fig. 6B.

Supplemental Table 1. List of	Primers for plasmid constru	ction						
Use	Sequence							
Linearizing p3XHA_nLuc-Neo for SIINFEKL insertion	taacccgggatgcatcttca							
	ggcataatctggaacatcgtaagg							
SIINFEKL sequence for Gibson assembly	ccttacgatgttccagattatgccagtataatcaactttgaaaaactg							
	tgaagatgcatcccgggttacagtttttca							
Repair template amplification M2-OVA	aaaaagaaaaagagaagagggggaaaagatgatcttagaggactattaagaggattatccggttcaagtaaagacatactacacgacttagagaaaattggaagtggaggacgggaattc							
	taattatcttgttaataacacatttgaatagtttatacttcacataaccaaattaagataaaaagaaaaacttaatcgatactatcctacacg							
M2 targeting guide	gttgaggattatccggttcaagta							
	aaactacttgaaccggataatcct							
Repair template amplification ROP1-OVA	tataaatcacctgaattccgaaaatggaagtggaggacgggaattc							
	gaatttgggtattttctcgtctcaccgcgtttaaactgattggtacta							
ROP1 targetting guide	gttggactaaaaataattgtttcaa							
	aaacttgaaacaattatttttagtc							
Linearizing p3XHA_nLuc-Neo_M2 for tdTom inserti	aattggttcgtggcgtgtagga							
	gaagaattcgtcaagaagacgatagaa	g						
tdTom amplification for Gibson assembly	gccttctatcgtcttcttgacgaattcttcggtgagggcaggggtagattgttgacttgcggtgacgttgaggagaaccccggcccgatggtgagtaagggcgag							
	tcacttatacagctcatccatgc							
Repair template NS-M2-OVA	tagcttttttgccacagcgacaaatagttttgatttcagtaagtttatcaccatagctgcgccaaattttgc							
	tccagtactatgctatggtttgagaacaga							
TK targetting guide for NS-M2-OVA insertion	gttggaaggaagtaaatacttattagca							
	aaactgctaataagtatttacttc							

NOTE: Please save this file locally before filling in the table, DO NOT work on the file within your internet browser as changes will not be saved. Adobe Acrobat Reader (available free here) is recommended for completion.

ARRIVE The ARRIVE guidelines 2.0: author checklist

The ARRIVE Essential 10

These items are the basic minimum to include in a manuscript. Without this information, readers and reviewers cannot assess the reliability of the findings.

ltem		Recommendation			
Study design	1	For each experiment, provide brief details of study design including:			
		a. The groups being compared, including control groups. If no control group has been used, the rationale should be stated.	Results Figure legends		
		b. The experimental unit (e.g. a single animal, litter, or cage of animals).			
Sample size 2		a. Specify the exact number of experimental units allocated to each group, and the total number in each experiment. Also indicate the total number of animals used.			
		b. Explain how the sample size was decided. Provide details of any <i>a priori</i> sample size calculation, if done.	Figure legends		
Inclusion and 3 exclusion criteria	3	a. Describe any criteria used for including and excluding animals (or experimental units) during the experiment, and data points during the analysis. Specify if these criteria were established <i>a priori</i> . If no criteria were set, state this explicitly.			
		b. For each experimental group, report any animals, experimental units or data points not included in the analysis and explain why. If there were no exclusions, state so.	Figure legends		
		c. For each analysis, report the exact value of <i>n</i> in each experimental group.			
Randomisation 4	4	a. State whether randomisation was used to allocate experimental units to control and treatment groups. If done, provide the method used to generate the randomisation sequence.			
		b. Describe the strategy used to minimise potential confounders such as the order of treatments and measurements, or animal/cage location. If confounders were not controlled, state this explicitly.	Not applicable		
Blinding	5	Describe who was aware of the group allocation at the different stages of the experiment (during the allocation, the conduct of the experiment, the outcome assessment, and the data analysis).	Not applicable		
Outcome 6 measures	6	a. Clearly define all outcome measures assessed (e.g. cell death, molecular markers, or behavioural changes).	Results		
		b. For hypothesis-testing studies, specify the primary outcome measure, i.e. the outcome measure that was used to determine the sample size.			
Statistical 7 methods	7	a. Provide details of the statistical methods used for each analysis, including software used.	Methods		
		b. Describe any methods used to assess whether the data met the assumptions of the statistical approach, and what was done if the assumptions were not met.	Methous		
Experimental animals	8	a. Provide species-appropriate details of the animals used, including species, strain and substrain, sex, age or developmental stage, and, if relevant, weight.			
		b. Provide further relevant information on the provenance of animals, health/immune status, genetic modification status, genotype, and any previous procedures.	Methods		
Experimental 9 procedures	9	For each experimental group, including controls, describe the procedures in enough detail to allow others to replicate them, including:			
		a. What was done, how it was done and what was used.	Methods		
		b. When and how often.	Results		
		c. Where (including detail of any acclimatisation periods).			
		d. Why (provide rationale for procedures).			
Results	10	For each experiment conducted, including independent replications, report:	Desults		
		a. Summary/descriptive statistics for each experimental group, with a measure of variability where applicable (e.g. mean and SD, or median and range).	Results Figure legends		
		b. If applicable, the effect size with a confidence interval.			