Studies on virtual whole-blood infection assays

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Infection dynamics in healthy individuals and patients

Healthy Individuals:

Experiments: We performed whole-blood infection assays, where blood from healthy donors is infected with *C. albicans* or *C. glabrata* cells. With phagocytosis assays and survival plates we determined pathogen populations of alive, killed, extracellular and phagocytosed cells by monocytes and neutrophils.

State-based model: The SBM consists of states and transitions between these states that resemble the biological system. Fitting the SBM to the experimental data allowed quantification of immune reaction rates, such as phagocytosis and killing rates.

Transition rates from SBM



[3]

Agent-based model: To investigate also spatial aspects we build an ABM, where single cells are simulated in a continuous three-dimensional environment. Based on the experimental data and the previously estimated rates we could determine diffusion coefficients of neutrophils (D_N) and monocytes (D_M) .

Virtual Neutropenic Patients (VNP):

We simulated infection dynamics in VNP with different severity degrees of neutropenia by reducing the number of neutrophils in the ABM. We selected five VNP (see Table) and identified patterns to characterize the infection outcome that were based on the fraction of killed (P_K) and immune evaded pathogens (P_{AIE}).

			Severe		Severe	Horman
			Neutropenia	cell count	Neutropenia	cell count
VNP	Severity Degree	Neutrophils/µl				
1	mild	1250	8.0 je		<u>9.0 (in called and in called </u>	
2		1000	ans c	Jan State S	ata c	
3	moderate	750	albic.		la l	i X
4		500			ن م 14	a de la compañía de
5	severe	250		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	itive ne	

Hospital Patients:

We quantified functional parameters of innate immune cells in blood from patients undergoing cardiac surgery. These patients experience a well-characterized inflammatory insult, which results in mitigation of the pathogen-specific response patterns towards *Staphylococcus aureus* and *C. albicans* that are characteristic of healthy people and patients.



[4]

Pathogen immune evasion

Whole-blood experiments with blood from healthy donors and patients revealed that a certain fraction of pathogens remain extracellular. In combination with mathematical modelling we could show that this can only be explained by pathogen immune evasion (IE). However, as of now the underlying mechanism is not understood. Therefore, we compared simulations with various possible immune evasion mechanisms in order to generate hypotheses that allow for targeted **Pathogens:** experimental investigations.

Possible mechanisms of pathogen immune evasion:





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- Model for pre-existing IE could be falsified by automated image-analysis
- Three base models and their combinations
- Least-square error (LSE) to measure agreement with experimental data
- Corrected Akaike Information criterion (AIC_c) as measure for model quality with penalty for number of parameters



- 6.0-**出** 5.0-2.5--5 -3 -1 1 3 5 0 10 20 30 40 AIC_C count spon-alivePre-IE PMNmed-alivePre-IE spon-PMNmed-IE spon-PMNmed-alivePre-IE
 - More complex models could not compensate for their penalized complexity by a better agreement with the experimental data
 - Model-specific patterns could be derived
 - Proposal of new experiments that will contribute to the identification of IE mechanism in the future

[5,6]

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References

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