Chronic *Staphylococcus aureus* infection is cured by theory-driven therapy

Lito A. Papaxenopoulou,[1]* Gang Zhao,[1] Sahamoddin Khailaie,[1] Konstantinos Katsoulis-

Dimitriou,[2] Ingo Schmitz,[2,3,4] Eva Medina,[5] Haralampos Hatzikirou,[1,6,7]* Michael Meyer-

Hermann[1,8,9]*

[1] Department of Systems Immunology and Braunschweig Integrated Centre of Systems Biology,

Helmholtz Centre for Infection Research, 38106, Braunschweig, Germany.

[2] Institute for Molecular and Clinical Immunology, Medical Faculty, Otto-von-Guericke-

University, 39120, Magdeburg, Germany.

[3] Systems-oriented Immunology and Inflammation Research Group, Department of Experimental

Immunology, Helmholtz Centre for Infection Research, 38124, Braunschweig, Germany.

[4] Department of Molecular Immunology, ZKF2, Medical Faculty, Ruhr-University Bochum,

44780, Bochum, Germany

[5] Department of Infection Immunology, Helmholtz Centre for Infection Research, 38124,

Braunschweig, Germany.

[6] Technische Univesität Dresden, Center for Information Services and High Performance

Computing, 01062, Dresden, Germany.

[7] Mathematics Department, Khalifa University, P.O. Box: 127788, Abu Dhabi, UAE.

[8] Institute for Biochemistry, Biotechnology and Bioinformatics, Technische Universität

Braunschweig, 38106, Braunschweig, Germany.

[9] Centre for Individualised Infection Medicine (CiiM), 30625, Hannover, Germany.

*Correspondence: papaxenopoulou.lito@gmail.com (LP); haralampos.hatzikirou@ku.ac.ae
(HH); mmh@theoretical-biology.de (MMH).

SUMMARY

Staphylococcus aureus is considered a dangerous pathogen due to its ability to evade the immune system and resist multiple antibiotics. These evasive strategies lead to difficult-to-treat chronic infections and abscesses in internal organs including kidneys, which are associated with the expansion of myeloid-derived suppressor cells (MDSCs) and their suppressive effect on T cells. Here, we developed a mathematical model of chronic *S. aureus* infection that incorporates the T-cell suppression by MDSCs and suggests therapeutic strategies to eradicate *S. aureus*. We quantified *in silico* a therapeutic protocol with heat-killed *S. aureus* (HKSA), which we tested *in vivo*. Contrary to conventional administration of heat-killed bacteria as vaccination prior to infection, we administered HKSA as treatment, when the hosts were already chronically infected. Our treatment cured all chronically *S. aureus*-infected mice, reduced MDSCs, and reversed T-cell dysfunction by inducing acute inflammation during ongoing, chronic infection without any use of standard treatments that involve antibiotics, MDSC-targeting drugs (chemotherapy), or procedures such as abscess drainage. This study is a proof-of-principle for a treatment protocol against chronic *S. aureus* infection and renal abscesses by repurposing heat-killed treatments, guided and quantified by mathematical modelling. Our mathematical model further explains why previous treatment with inactivated *S. aureus* administered to long-term infected human patients has not led to cure. Overall, our results can have direct relevance to the design of human therapeutics against chronic *S. aureus* infections.

In brief: A theory-driven treatment protocol with heat-killed *S. aureus* eradicates *S. aureus*, reduces MDSCs, and reverses T-cell dysfunction *in vivo*.

Graphical abstract

Chronic *Staphylococcus aureus* infection

Infection → **Chronic inflammation** → **Immunosuppression**

Difficult-to-treat infections

Abscesses in kidneys and accumulation of myeloid-derived suppressor cells (MDSCs) in spleen

MDSCs suppress T cells causing T-cell dysfunction

Staphylococcus aureus

no prophylactic vaccine

increasing antibiotic resistance

Kidneys | **Spleen**

Abscesses

M-MDSC

PMN-MDSC

Eo-MDSC

MDSCs

T cells

Mathematical modelling

In silico treatment protocols suggest bacterial clearance using heat-killed (inactivated) *S. aureus* during chronic *S. aureus* infection

In silico quantification for experiments: heat-killed treatment dose, administration time of heat-killed treatment, sampling time for verification of bacterial clearance

Experiments *in vivo*

1. C57BL/6 mice with chronic *S. aureus* infection

VALIDATION of model-driven heat-killed treatment protocol

2. heat-killed *S. aureus* treatment <u>during</u> chronic *S. aureus* infection

3.

MDSC populations diminished naturally

S. aureus was completely cleared in <u>all</u> heat-killed treated mice.

Chronic *S. aureus* infection was fully resolved.

T-cell dysfunction was reversed

45
46

Keywords

Chronic *Staphylococcus aureus* infection, mathematical model, myeloid-derived suppressor cells (MDSCs), chronic bacterial infection, model-driven experiments, heat-killed treatment, *S. aureus* infection cured, sterilizing immunity.

INTRODUCTION

Staphylococcus aureus is a bacterial human pathogen colonizing 20%-30% of the world population and is responsible for nosocomial-acquired and community-acquired infections. Colonization by *S. aureus* as a commensal bacterium is non-problematic. However, after a skin cut, surgery or implantation of medical devices, *S. aureus* can reach deeper tissues and cause life-threatening conditions like pneumonia, endocarditis, osteomyelitis and abscesses in internal organs (*1*, *2*).

The pathogen is of substantial medical concern because it can infect any organ in the body (*1*, *2*), even without being disseminated via the bloodstream (*3*). Moreover, its multiple mechanisms to manipulate and evade immune defenses along with its increasing antibiotic-resistance lead to its persistence in the host and cause chronic, difficult-to-treat infections (*4*). The urgency for new treatments aiming at curing *S. aureus* infections is also emphasized by the WHO, which, on its global priority list of infectious agents, identified *S. aureus* as a "high-priority" pathogen.

Chronic *S. aureus* infections such as chronic osteomyelitis, recurrent furunculosis, and abscesses are hard to eliminate. We have previously shown that during the *chronic phase* of *S. aureus* infection, effectors of innate immunity, such as macrophages (MΦ) and neutrophils, as well as B cells are dispensable for bacterial containment, unlike T cells, which are critical for bacterial control (*5*). However, T cells fail to eradicate the pathogen because prolonged antigenic

stimulation (confluent with chronic infection) causes them to enter an anergic state that seems to

be irreversible (*5*). As we demonstrated, T-cell dysfunction (also known as T-cell anergy, T-cell

suppression, or T-cell hyporesponsiveness) during chronic *S. aureus* infection is attributed to

myeloid-derived suppressor cells (MDSCs) rather than other immunosuppressive cells such as

regulatory T and B cells, or tolerogenic dendritic cells (*6*).

MDSCs constitute a heterogeneous population of immature myeloid cells that expand in

long-lasting pathological conditions, such as chronic bacterial and viral infections (*7*, *8*)

including severe SARS-CoV-2 infection (*9*), cancer (*10*), and autoimmunity (*11*). Expansion of

MDSCs serves as a natural, anti-inflammatory response to mitigate the detrimental effect of

prolonged inflammation (*12*). Often pathogens exploit the immunosuppressive effect by MDSCs

to persist within the host, thus establishing chronic infections (*12*). MDSCs are distinguished in

three subsets that share the capacity to suppress T cells during chronic *S. aureus* infection:

monocytic $CD11b^+Ly6C^+Ly6G^{low}$, granulocytic/neutrophilic

$CD11b^+Ly6C^{low}Ly6G^+$ and eosinophilic $CD11b^+Ly6C^{low}Ly6G^{low}$ MDSCs, known as M-

MDSC, PMN-MDSC and Eo-MDSC respectively (*6*, *8*, *13*).

Despite much research, there is no *S. aureus* vaccine to confer prophylaxis against *S.*

aureus infections and along with antibiotic-resistance, *S. aureus* is becoming increasingly

dangerous every year. It has been estimated that in 2001 *S. aureus* infections afflicted 292045

US hospital inpatients, caused almost 12000 inpatient deaths and cost $9.5 billion in excess

charges in US hospitals alone (*14*). By 2014, the number of US inpatients afflicted with

methicillin-susceptible and methicillin-resistant *S. aureus* alone has risen dramatically to 616070

individuals and associated costs were estimated to be around $14.6 billion (*15*). Abscesses

caused by antibiotic-resistant *S. aureus* have also been increasing. Current treatments rely on

simultaneous use of various antibiotics (which promote antibiotic resistance), MDSC-targeting

drugs (which are cytotoxic and can have side-effects), and surgery to drain abscesses. Renal

abscesses in particular are highly destructive and when multiple antibiotics and abscess drainage

fail, immediate nephrectomy is required to save a patient's life (*16*). Consequently, finding new

treatments against *S*. *aureus* infections is absolutely essential.

Experimental investigations have offered important information on mechanisms of

bacterial persistence or MDSC-mediated immunosuppression, however, how to intervene in the

complex balance between bacteria, T cells and MDSCs during chronic *S*. *aureus* infections in

order to cure, remains obscure. In this study we constructed a mathematical model to understand

the balance between immunity and *S*. *aureus* during chronic infection and to explore strategies

that could cure the infection. Modelling the chronic infection mathematically could bestow a

broader observation of possible treatments that would be challenging to discover only by

experimental means, whereas *in silico* they could expeditiously and cost-effectively be tested for

rendering sterilizing immunity. Mathematical models have been used to shed light on *S*. *aureus*

transmission in community and hospitals (*17*, *18*), staphylococcal growth on foods (*19*),

interactions of the pathogen and immune cells during the acute phase of infection (*20*), but also

to suggest the optimal sequence of antibiotic administration that could reduce the virulence of *S*.

aureus (*21*). However, there are still large gaps on chronic *S*. *aureus* infections and how to cure

them. To our knowledge, this is the first mathematical model that investigates the dynamics of

chronic S. *aureus* infection between bacteria and T cells, in the presence of MDSCs, and

suggests curative treatments.

Our *in silico* analysis suggested various strategies that could perturb the dynamics of the

chronic infection system and cure the infection. For experimental testing *in vivo*, we quantified *in*

silico a dose-day treatment protocol using heat-killed (HK), namely inactivated, bacteria. Unlike

prior vaccination with HK *S. aureus* (HKSA), which is meant as prophylaxis but instead fails to

eradicate the pathogen and exacerbates the infection (*22*), we administered HKSA as treatment,

when the hosts were already chronically *S. aureus*-infected. Our *in silico* therapeutic protocol

was validated *in vivo*. We here report for the first time reversion of T-cell dysfunction, MDSC-

reduction and eradication of *S. aureus* in all HKSA-treated mice without any use of antibiotics,

MDSC-targeting drugs, or procedures such as abscess drainage. Our experiments further verified

that our HKSA protocol triggered acute inflammation during the already established chronic *S.*

aureus infection, which served as the perturbation of the system dynamics and cured the

infection. The therapeutic effect of heat-killed treatment is not limited to HKSA, because

treatment with heat-killed *Streptococcus pyogenes* (HKSP) also cured a portion of treated

animals, reverted T-cell dysfunction and induced acute inflammation during ongoing chronic *S.*

aureus infection. Our study is a proof-of-principle for a treatment protocol against chronic *S.*

aureus infection and renal abscesses by repurposing heat-killed administration, guided and

quantified by mathematical modelling that can have direct relevance to the design of human

therapeutics against chronic *S. aureus* infections and abscesses in internal organs.

RESULTS

Dynamics of chronic infection

We have previously shown that intravenous inoculation with *S. aureus* results in chronic infection and abscesses in kidneys (*5, 6*). Bacterial containment in the chronic phase of infection is not attributed to innate immune cells but mainly to effector CD4$^+$ T cells, which gradually lose functionality due to suppression by MDSCs (*5, 6*). Here, we constructed a mathematical model that includes the above-mentioned interactions between bacteria B(t), T cells T(t), and T-cell suppression by MDSCs (Θ) during *chronic S. aureus* infection. In the following the term T cells will refer to CD4$^+$ T cells unless otherwise stated.

The ordinary differential equation (ODE) system reads

$$\dot{B}(t) = r_b B(t)\left(1 - \frac{B(t)}{\kappa}\right) - c_b T(t) B(t), \qquad (1)$$

$$\dot{T}(t) = r_t T^2(t)\left(1 - \frac{T(t)}{K_T}\right) + k_b B(t) - c_T B(t) T(t) - \Theta\, T(t), \qquad (2)$$

where a dot represents differentiation with respect to time.

During infection, *S. aureus* uses various mechanisms to persist within the host (*23*). This is represented with the term $r_b B(t)(1-B(t)/\kappa)$ capturing bacterial expansion by logistic growth. Staphylococcal presence stimulates T cells (term $k_b B(t)$), which proliferate (term $r_t T^2(t)$). T-cell proliferation is represented with the term $r_t T^2(t)$ because activated T cells secrete Interleukin-2 (IL-2), which induces cell cycle progression of T cells. In return, it creates a positive feedback loop for T-cell proliferation, and hence the term $r_t T^2(t)$ as we reported previously (*24*). The term $(1-T(t)/K_T)$ describes the carrying capacity of T cells. As infection becomes chronic, T cells

contain bacteria (term $c_b T(t) B(t)$) (*5*). However, bacterial persistence causes chronic (long-

lasting) inflammation, which is harmful to the host. To protect from the adverse effect of

prolonged inflammatory signal, MDSCs gradually expand to suppress T-cell activity (*6*). T-cell

suppression by MDSCs can happen *systemically,* namely distantly from the site of infection such

as in the spleen (*6, 13*), where T cells increase substantially during chronic *S. aureus* infection

(*5*). This is represented with the term $\Theta\ T(t)$, since MDSC-mediated immunosuppression on T

cells requires direct cell–cell contact or cell–cell proximity (*6*). *Locally*, namely at the site of

infection, the pathogen can exploit MDSCs towards T-cell suppression to promote its persistence

(term $c_T B(t) T(t)$) (*12*). A schematic representation of the model is illustrated in Fig. 1A. It is

important to note that although innate immune responses do not explicitly appear in the

equations, they were not ignored but were rather indirectly incorporated into the term describing

bacterial growth, $r_b B(t)(1-B(t)/\varkappa)$ (Eq. (1)). In particular, model parameters were identified with

the use of our previously reported experimental results from T and B cells-deficient RAG2$^{-/-}$

mice (only innate immunity present) and immunocompetent mice with chronic *S. aureus*

infection and renal abscesses (*5*) (full description in Supplementary Materials). We previously

reported major T-cell suppression by MDSCs in spleens of mice with local, chronic *S. aureus*

infection in kidneys (*6, 13*). This phenomenon is known as extramedullar haematopoiesis,

happens during chronic inflammation and involves haematopoiesis mostly in spleen, which

further induces accumulation of MDSCs in the organ (*25*). In accordance, our fitting revealed

that parameter c_T describing local T-cell suppression by MDSCs in kidneys (the site of

infection), was negligible compared to parameter Θ describing systemic T-cell suppression by

MDSCs, such as in spleens (Supplementary Materials).

We previously demonstrated experimentally that during chronic *S. aureus* infection there

is substantial negative correlation between MDSC populations and activated T cells, which are

not suppressed (dysfunctional) and hence maintain their ability to proliferate (*6*). To validate the

accuracy and consistency of our mathematical model, we reproduced the inverse proportional

behaviour between T cells and T-cell suppression by MDSCs (Fig. 1B). Further *in silico* analysis

showed how chronic *S. aureus* infection is established naturally, without any treatment

intervention (Fig. 1C). Infection induces strong inflammation, which activates T cells.

Competition for dominance between bacteria and T cells creates oscillations in the population

dynamics (Fig. 1C). To protect from the damaging effect of prolonged inflammation, MDSCs

expand gradually to suppress T cells. Increasing accumulation of MDSCs leads to increasing

suppression on T cells (Θ). Upon a critical threshold, T-cell suppression by MDSCs is so strong

that T cells become dysfunctional and cannot promote sterilizing immunity anymore (Fig. 1D,

pink line). This *in silico* result agrees with our previous experimental observations, showing that

gradual expansion of MDSCs leads to gradual loss of T-cell function, which in turn promotes

chronic *S. aureus* infection and failure of sterilizing immunity (*5, 6*). At this point the immune

system finds the balance between maximal bacterial clearance and minimal collateral tissue

damage, whereas bacteria persist in the host organism but are simultaneously unable to further

grow due to their containment by T cells (*5*) (mathematically known as equilibrium of the

system). This equilibrium is found to be stable by our mathematical model (Fig. 1E) and

biologically refers to chronic *S. aureus* infection. Once at this stage (Fig. 1D, *pink line;* 1E),

sterilizing immunity can be attained only by using treatment-interventions that can destabilize

(i.e. perturb) this stable steady state of chronic infection.

Fig. 1. Dynamics of chronic *Staphylococcus aureus* infection. (**A**) Schematic representation of

chronic *S. aureus* infection model. (**B**) Correlation between T cells and T-cell suppression by

MDSCs (Θ) is inversely proportional. The correlation was plotted using the analytical solutions of

the T-cell differential equation in steady state (Supplementary Materials, Eq. (S5)) for increasing

values of parameter Θ. (**C**) Dynamics of bacteria (B) and activated T cells (T) in time are shown as

numerical solutions of the ODE system. Infection was induced by setting the bacterial population

equal to 5×10^7 cells at day 0 in Eq. (1) to be consistent with experimental bacterial inoculation

causing chronic *S. aureus* infection (*6*). Model parameters are as shown in table S1. (**D**) Infection

was initiated as in (**C**). Numerical calculation of bacteria for changing values of parameter Θ (T-cell

suppression by MDSCs) in the range [0, 0.2]. For bacterial numbers <0.000001, the infection is

considered cured (blue), else persisting (pink) and the corresponding day of bacterial clearance is

shown or set to zero, respectively. The blue star represents a scenario of MDSC-absence and hence

non-existent T-cell suppression (Θ=0). As Θ gradually increases, the infection progresses towards

chronic phase and bacterial clearance becomes more difficult. The blue line represents when, despite

MDSC-mediated suppression, the infection can be cured by the immune response alone. The white

star represents the critical value of Θ, when T cells become anergic by MDSC-mediated suppression,

the infection persists and external treatment-intervention is required for cure. Table S1 shows the

values for the rest of the model parameters. (**E**) Stable steady state of ODE system between bacteria

and T cells. For changing initial numbers of bacteria in the range $[10^5, 6 \times 10^7)$ at day 0, the system

always terminates in stable equilibrium, which biologically corresponds to the chronic infection.

Black arrows illustrate the flow of the system. Model parameters are shown in table S1.

Model-driven therapeutic strategies

To explore perturbation strategies (treatments) that would destabilize the equilibrium between

bacteria, T cells and MDSCs, we varied values of k_b and Θ. These parameters, representing T-

cell activation and recruitment by bacterial presence, and T-cell suppression by MDSCs,

respectively, were specifically chosen because they play a key role in the establishment of

chronic infection (5, 6). Different values of k_b and Θ gave different eigenvalues for the ODE

system (Eqs. (1)-(2)), which were used to characterize the steady states (equilibria) of the

mathematical model as unstable or stable (analytical forms are found in Supplementary

Materials). Combining *in silico* all steady states in one separatrix (phase diagram) led to the

distinguished areas of cure and chronic infection (Fig. 2A).

To gain more understanding of the dynamical system and suggest strategies for bacterial

clearance, we next estimated the average position of an infected host on the separatrix of cure

and chronic infection (Fig. 2A, *white star*), using the values of parameters k_b and Θ as fitted

previously (table S1). We found that it lay in the region of chronic infection, yet close to the

basin of attraction (region) of cure. According to the separatrix, we concluded that the resolution

of chronic infection is achieved via either (a) relocation of the infected host from the chronic

infection area towards the area of cure (Fig. 2A) by (i) increasing T-cell activation and

recruitment (k_b) and/or by (ii) decreasing T-cell suppression by MDSCs (Θ) or (b) via expansion

of the cure zone itself (Fig. 2B) by counter-intuitively (iii) increasing the proliferation rate of

bacteria (r_b) and/or (iv) by reducing bacterial containment by T cells (c_b). These *in silico* results

accord with previous experimental studies reporting that brief suppression of immunity (namely

c_b reduction) with cyclophosphamide (*3*) or targeting MDSCs (namely Θ decrease) (*26*) during

S. aureus infection reduce bacterial burden. Altogether the model indicates that all four

aforementioned perturbation categories (each of which can be implemented *in vivo* in various

ways) can destabilize the dynamics of chronic infection so that eradication of *S. aureus* and

sterilizing immunity is achieved (fig. S1).

Design of quantitative, model-driven experiments

Our *in silico* analysis suggested treatment strategies that were MDSC-targeting (Θ decrease),

pathogen-targeting (r_b increase or c_b decrease), or host-directed (k_b increase). Experimental

testing was essential to validate the model predictions. Since validation of bacterial eradication

would have immense importance for human therapeutics, we sought to test experimentally a

treatment that would be safe and easy to apply.

MDSC-targeting drugs, such as gemcitabine chemotherapeutic agent, usually bear

adverse side-effects because of their cytotoxicity. They simultaneously deplete mature immune

cells (*26*), which are indispensable components of immunity. Furthermore, available MDSC-

targeting drugs fail to eliminate MDSCs in many organs (*27*). Lastly, the heterogeneity of

MDSCs makes it particularly difficult to identify a single drug that would deplete all distinct

MDSC subsets, each of which is linked to different bacterial infections and even distinct tumors

(*8*, *28*).

Contrary to conventional bacteria-targeting drugs, such as antibiotics, that aim at fighting

bacteria and whose use should be limited because they promote development of drug-resistance,

the bacteria-targeting strategies suggested by our *in silico* analysis counterintuitively promote

bacterial   growth.   However,   these   strategies   would   involve   treatments,   such   as

immunosuppression (c_b decrease), that would be difficult to implement in reality because,

besides cytotoxicity and side-effects that immunosuppressive agents (e.g. cyclophosphamide)

cause, patients would be at risk of becoming susceptible to other infections.

Despite ample research focusing on the development of antimicrobial drugs, there is

surprisingly a large gap on the development of therapeutics that promote host defense during

infection (*29*). Such host-directed therapeutics are safer than pathogen-targeting drugs because

they promote the health of the host rather than attack the pathogen (*29*). Therefore, for our

experimental testing we singled out the category of k_b increase (namely T-cell activation and

recruitment). One of the most conventional and safe ways to boost k_b *in vivo*, which is also an

established, widely-used method for vaccine development, is via administration of inactivated

bacteria, namely antigens. Such treatment would be extremely practical in human therapeutics,

since pathogens causing renal abscesses in humans can be isolated from urine samples without

involving any invasive processes (*30*) and easily get inactivated. We chose inactivation of

bacteria with heat over toxic chemicals, such as formalin. Furthermore, heat-killed cells are more

effective, quicker to prepare and provide enhanced survival in treated animals than other

inactivation options (*31*). While inactivated bacteria in vaccines serve as prophylaxis from

infection, their use as treatment for ongoing chronic infections is limited. Here we explored

whether HK treatment during infection leads to cure, as our *in silico* results suggested.

Since our aim was to cure chronic *S. aureus* infection, the experimental perturbation (HK

treatment) had to be carried out when infection enters its chronic phase. As we have previously

shown, inoculation with $3–7\times10^7$ colony-forming units (CFU) of *S. aureus* results in chronic

infection and renal abscesses, and by day 14 of infection T cells are already strongly suppressed

by MDSCs (*5, 6*). Therefore, the perturbation with HKSA was scheduled at day 14 after initial

infection with 5×10^7 CFU of *S. aureus*. The physiological k_b increase via HK treatment was

incorporated into the model with the addition of term $k_b B_d$ to the T cells' ODE on the day of

treatment (*Materials and Methods*), where B_d the dose of HKSA and k_b the activation and

recruitment of T cells via HKSA assumed the same as for live bacteria during initial inoculation

(table S1). This assumption was based on the fact that, although live cells produce virulence

factors that stimulate the immune system, implying a greater value of k_b, heat-killed cells cannot

hijack or evade immunity as live *S. aureus* does. The only consequence of their existence in the

host is the stimulation of immune cells. Additionally, HKSA cells are injected when the host is

already chronically infected and had already encountered staphylococcal antigens during initial

inoculation. Secondary exposure to pathogens always initiates much stronger (and quicker)

immune response than the initial exposure to the same pathogen.

Numerical simulations for initial inoculation with 5×10^7 *S. aureus* cells and HK

treatment at day 14 of infection suggested that the minimum HKSA-dose required for cure would

be 4×10^7 HKSA (Fig. 2C). For our experiments, we opted for the amount of 10^8 HKSA. To

identify, on which day the infected mice would recover from infection to perform the

experimental sampling, we followed the *in silico* results, which predicted sterilizing immunity at

day 34.5 of infection (Fig. 2D). Because biological systems involve extrinsic and intrinsic

stochasticity and therefore not all infected mice are synchronized in the same infection phase, the

experimental sampling was set at day 37 of infection (Fig. 2D). As a result of secondary

exposure to *S. aureus*, HKSA-treatment initiates a cascade of inflammatory events, providing a

concomitant, rapid boost in T-cell population (Fig. 2E, *brown*), which is followed by further,

gradual increase of activated T cells as illustrated in our simulations (Fig. 2E). Consequently,

HKSA-treatment destabilizes to a sufficient extent the system dynamics of chronic infection and

leads to cure (Fig. 2D-2E).

Fig. 2. Model-driven insights for cure. (**A-B**) Based on the eigenvalues of the ODE system, the

phase diagram was divided into stable states (pink) and unstable states (blue), which represent the

physiological chronic infection and cure, respectively. The white star represents the average position

of an infected host during a chronic staphylococcal infection and was determined by the fitted values

of parameters k_b and Θ (table S1). Given the position of the infected host (white star), cure is

achieved (**A**) by increase of T-cell activation and recruitment (k_b) and/or decrease of T-cell

suppression by MDSCs (Θ) (shown as blue stars) or (**B**) by increasing the proliferation rate of

bacteria (r_b) and/or reducing the bacterial containment by T cells (c_b). (**C-E**) *In silico* treatment with

HKSA. Initial infection was induced by setting the bacterial population equal to 5×10^7 cells at day 0

in Eq. (1). T cells were set to 10^3 at day 0 in Eq. (2). HKSA-treatment was administered *in silico* at

day 14 of infection (shown as white bullet) by adding the term $k_b B_d$ to the T-cell ODE at time

t=perturbation day, for a 12-hour perturbation window as explained in Eq. (3) (*Materials and*

Methods). (**C**) A minimum dose of HKSA for curing chronic *S. aureus* infection was estimated to be

$B_d = 4\times10^7$ HKSA. *In silico* administration of 10^8 HKSA, namely staphylococcal antigens, at day 14

of infection provides (**E**) quick boost of T cells (increase of parameter k_b), as shown in brown, and

(**D**) bacterial numbers are diminished to zero. Chronic *S. aureus* infection is cured.

In vivo cure after model-driven perturbation treatment with HKSA

Our next step was to provide proof-of-concept by validating our *in silico* predictions of cure *in*

vivo. For this purpose, C57BL/6 mice were infected intravenously with *S. aureus* strain SH1000.

At day 14 of infection mice were treated intraperitoneally with HKSA, strain SH1000. Control

mice received phosphate-buffered saline (PBS) (Fig. 3A).

Our previous study in chronically *S. aureus* SH1000-infected C57BL/6 mice has shown

that *S. aureus* is progressively depleted from multiple organs and persists only in the kidneys (5).

Therefore, at day 37 of infection, bacterial load quantification was performed in mice's kidneys.

The mathematical model's predictions *in silico* (Fig. 2D) were validated by our experiments *in*

vivo: mice treated with HKSA were cured with success percentage of 100% and no *S. aureus* at

all was found in their kidneys (Fig. 3B). In contrast, the majority of untreated animals remained

infected with high bacterial burden (Fig. 3B).

Progression of *S. aureus* infection from acute to chronic drives spleen T cells into T-cell

dysfunction, which we previously found irreversible (*5*). T-cell dysfunction during chronic *S.*

aureus infection is caused by the expansion and suppressive effect of all three MDSC subsets in

spleen (*6, 13*). Therefore, at day 37 of infection, we next investigated the effect of the HKSA-

treatment on the proliferative response of T cells and on the MDSC populations. We found that

HKSA-treatment restored the function of spleen T cells. Stimulation with anti-CD3/anti-CD28

antibodies showed that T cells were hyperresponsive and actively proliferated (Fig. 3C). In

contrast, spleen T cells of infected untreated animals remained hyporesponsive to TCR re-

stimulation (Fig. 3C). We further observed significant reduction of all MDSC subsets in spleens

of HKSA-treated mice, whereas MDSC populations remained high in spleens of infected,

untreated (control) animals, which had received PBS (Fig. 3D). Together, these findings reveal

that HKSA-treatment during chronic *S. aureus* infection not only boosts T-cell function (namely

in vivo k_b increase) but also has a previously unidentified potential to indirectly target the

MDSCs (namely *in vivo* Θ decrease). Because MDSC-expansion and MDSC-mediated

suppression on T cells are associated with the chronic but not acute phase of the infection (*5, 6,*

8), these results suggest that acute inflammation caused by administration of HKSA (see below)

disrupts the balance of chronic infection, which sustains MDSCs, leading to natural MDSC-

depletion.

HKSA-treatment during chronic *S. aureus* infection induces strong acute inflammation

Our *in silico* analysis suggested that destabilizing the system of chronic *S. aureus* infection by administering a sufficient amount of HKSA would lead to cure. It was natural to expect that the insertion of staphylococcal antigens into the hosts via HKSA-injection would trigger acute inflammation. To verify *in vivo* that the HKSA-injection initiated acute inflammation during chronic *S. aureus* infection, we sampled peritoneal exudates 12 hours after intraperitoneal HKSA-treatment and assessed differences in populations of macrophages, as well as infiltrating monocytes and granulocytes compared to untreated mice. It has been previously shown that two distinct subsets of macrophages exist in mouse peritoneal cavity (PerC), the $CD11b^{hi}F4/80^{hi}$ large peritoneal macrophages (LPMs) and the $CD11b^{+}F4/80^{low}$ small peritoneal macrophages (SPMs), and together are responsible for most of phagocytosis happening in PerC (*32*, *33*). Under normal physiological conditions, LPMs are the predominant macrophage subset in PerC (*32*). However, under inflammatory conditions, the PerC environment changes drastically: LPMs disappear and SPMs become the major subset along with substantial recruitment of SPM-precursors, the $CD11b^{+}Ly6C^{+}$ monocytes (*32*) and of $CD11b^{+}Ly6G^{+}$ granulocytes (neutrophils). In accordance, we observed massive increase in amounts of $CD11b^{+}Ly6C^{+}$ monocytes and $CD11b^{+}Ly6G^{+}$ granulocytes (neutrophils) in PerC of HKSA-treated mice compared to untreated (control) mice (Fig. 3E). LPMs were the predominant macrophage subset in chronically *S. aureus*-infected, untreated mice, indicating homeostatic conditions in PerC, whereas treatment of chronically *S. aureus*-infected mice with HKSA resulted in disappearance of LPMs and predominance of SPMs, indicating acute inflammation (Fig. 3E). Total number of MΦ (LPMs plus SPMs) was increased in PerC of HKSA-treated mice (Fig. 3E). These results

383   suggest that treatment with HKSA during chronic *S. aureus* infection induced strong acute

384   inflammatory responses.

Fig. 3. Bacterial burden and immune cells after treatment with heat-killed *S. aureus*.

A) Experimental schema. C57BL/6 mice were intravenously inoculated with $5×10^7$ CFU of *S.*

aureus and intraperitoneally treated with 10^8 HKSA at day 14 of infection. Untreated (control) mice

received PBS. Sampling was conducted at day 37 of infection.

(**B**) Treatment with HKSA at day 14 of infection cures all chronically *S. aureus*-infected mice.

Bacterial loads were determined in kidneys of untreated (control) and HKSA-treated mice at day 37

of infection. n=4-5 mice per group, two independent experiments. Data represent mean±SD.

**p=0.0018, Student's t-test. Right: Representative images of ten-fold serial dilutions on blood agar

plates for enumeration of viable *S. aureus* (golden-yellow colonies) in kidney homogenates from

control (untreated) or HKSA-treated mice, showing high bacterial burden (bacterial persistence) or

absence of bacteria (bacterial eradication), respectively.

(**C**) Proliferative response of spleen T cells at day 37 of infection from chronically *S. aureus*-infected

mice which received PBS or HKSA to *in vitro* stimulation with anti-CD3/anti-CD28. T-cell

proliferation was measured by ^{3}H-thymidine incorporation. n=4-5 mice per group, two independent

experiments. Data represent mean counts per minute (cpm) ± SD. ****p<0.0001, Student's t-test.

(**D**) HKSA-treatment reduces MDSCs. (left) Representative fluorescence-activated cell sorting

(FACS) illustrating monocytic $CD11b^+Ly6C^+Ly6G^{low}$, neutrophilic $CD11b^+Ly6C^{low}Ly6G^+$ and

eosinophilic $CD11b^+Ly6C^{low}Ly6G^{low}$ MDSCs, and (right) percentage of each MDSC subset

within the total spleen cell population of untreated (control) or HKSA-treated mice at day 37 of

infection. n=4-5 mice per group, two independent experiments. Data represent mean±SD. *p<0.05

and **p<0.01, Student's t-test.

(**E**) Intraperitoneal HKSA-treatment at day 14 of infection induces acute inflammation. Peritoneal

exudate cells were collected from chronically *S. aureus*-infected mice 12 hours after administration

of PBS (control) or HKSA. Percentage of $CD11b^+Ly6C^+$ monocytes, $CD11b^+Ly6G^+$ granulocytes,

$CD11b^{hi}F4/80^{hi}$ LPMs, $CD11b^+F4/80^{low}$ SPMs along with total MΦ population (LPMs plus

SPMs) within the total peritoneal cell population is shown. n=5-10 mice per group, two independent

experiments. Data represent mean±SD. **p<0.01, ****p<0.0001, Student's t-test.

Non-antigen-specific HK treatment

The mathematical model suggested that treatment with HK *S. aureus* would cure chronic *S. aureus* infection. Because MDSCs during chronic *S. aureus* suppress T cells, including antigen-specific T cells, we proceeded to assess experimentally whether the HK treatment (perturbation strategy) works in an antigen-specific manner. For reliable comparison with the experiments using HKSA, we maintained the experimental design of the aforementioned quantified HKSA-protocols (namely same CFU of *S. aureus* for inoculation, HK-dose, routes of administration, times of treatment and sampling) and only replaced HKSA with HK cells of a different bacterium. Therefore mice were inoculated with 5×10^7 *S. aureus*, however, they were treated intraperitoneally with 10^8 HK *Streptococcus pyogenes* at day 14 of infection. Sampling was performed at day 37 of infection (Fig. 4A). HKSP-treatment successfully cured 50% of chronically *S. aureus*-infected mice (Fig. 4B), whereas the majority of control mice remained infected. Similarly to experiments with HKSA-treatment, we explored how HKSP-treatment affected T-cell proliferation and MDSC populations. Spleen T cells of HKSP-treated mice responded to stimulation with anti-CD3 plus anti-CD28 antibodies and proliferated significantly more than spleen T cells of untreated mice, which remained hyporesponsive (Fig. 4C). In contrast to HKSA-treatment that led to considerable MDSC-depletion, the reduction of MDSCs in HKSP-treated mice was insignificant compared to MDSCs in untreated mice (Fig. 4D).

As in the case of HKSA-treatment, peritoneal exudates were sampled 12 hours after HKSP-treatment and confirmed acute inflammation. CD11b$^+$Ly6C$^+$ monocytes and CD11b$^+$Ly6G$^+$ granulocytes (neutrophils) increased massively in PerC of HKSP-treated mice compared to untreated mice (Fig. 4E). LPM-disappearance further confirmed acute inflammation induced by HKSP-treatment along with significant increase of SPMs (Fig. 4E). It is important to

note that after HKSA-treatment, which cured all infected hosts, $CD11b^+Ly6C^+$ monocytes

increased massively, whereas after HKSP-treatment, which cured half of the infected hosts,

$CD11b^+ Ly6G^+$ granulocytes (neutrophils) increased massively (Fig. 4E).

These results confirmed that HK treatment with either *S. aureus* or *S. pyogenes* induces

acute inflammation during chronic *S. aureus* infection. However, it was expected that HKSA-

treatment would initiate stronger acute inflammation than HKSP-treatment, because HKSA was

a re-exposure to *S. aureus*, while HKSP-treatment was a first-time exposure to *S. pyogenes*

antigens. This is reflected by a significant increase of total MΦ (LPMs plus SPMs) in PerC after

HKSA but not after HKSP-treatment compared to control, untreated mice (Fig. 4E). Weaker

acute inflammation after HKSP- than HKSA-treatment was also indicated by less reduction of

MDSCs in spleens (Fig. 3D, 4D), which are sustained in conditions of chronic (but not acute)

inflammation (*8*) in addition to almost twofold lower proliferative response of spleen T cells in

HKSP-treated compared to HKSA-treated mice (Fig. 3C, 4C). These results combined can

explain cure in 50% of HKSP-treated animals in comparison to cure in 100% of HKSA-treated

animals and accord with previous studies, suggesting that monocytes and macrophages promote

S. aureus clearance (*26*) and that after antigen immunization in PerC, SPMs migrate to lymph

nodes where they activate T cells (*33, 34*).

Because treatment with 10^8 HKSP induced weaker acute inflammation and T-cell

stimulation than treatment with 10^8 HKSA, we hypothesized that treatment with higher HKSP-

dose (more antigens) would naturally induce stronger acute inflammation (including more

$CD11b^+Ly6C^+$ monocytes and SPMs), hence more indirect depletion of MDSCs and more

activated T cells, leading to cure of all HKSP-treated mice. For this purpose, we reduced the

value of parameter k_b in the treatment term $k_b B_d$ by two or three times to reflect the weaker T-cell

stimulation by HKSP compared to HKSA and estimated day of clearance for varying HKSP-

doses B_d administered at day 14 of infection. Our simulations suggested that if higher HKSP-

dose ($>10^8$) is administered, all HKSP-treated mice could be cured (namely 100% success) by

sampling day, day 37 of infection (fig. S2).

As commonly known, secondary exposure to antigens elicits a faster immune response,

meaning that HKSA-treatment, which was a re-exposure to staphylococcal antigens, triggered a

much faster immune response compared to HKSP-treatment, which was a first-time exposure to

streptococcal antigens. Therefore, for HKSP-dose the same as HKSA-dose, HKSP-treatment

would require longer time to induce immune response relatively as strong as that induced by

HKSA. Consequently, although the cure of 50% of HKSP-treated mice at day 37 of infection,

when experimental sampling was conducted, was not statistically significant (Fig. 4B), we

hypothesized that at a later time-point HKSP-treatment could eventually cure all hosts. For this

purpose, we reduced the value of parameter k_b in the treatment term $k_b B_d$ by two or three times to

reflect the weaker T-cell stimulation by HKSP compared to HKSA and we estimated the day of

clearance for 10^8 HKSP (B_d) administered at day 14 of infection. Indeed, our simulations

suggested that if sampling is conducted approximately 10 days or later than day 37 of infection,

all HKSP-treated mice may be cured, namely 100% success (fig. S2).

Figure 4. Bacterial burden and immune cells after treatment with heat-killed *S. pyogenes*.

(**A**) Experimental schema. C57BL/6 mice were intravenously inoculated with 5×10^7 CFU of *S. aureus* and intraperitoneally treated with 10^8 HKSP at day 14 of infection. Untreated (control) mice received PBS. Sampling was conducted at day 37 of infection.

(**B**) Treatment with HKSP at day 14 of infection cures 50% of chronically *S. aureus*-infected mice. Bacterial loads were determined in kidneys of untreated (control) and HKSP-treated mice at day 37 of infection. n=5 mice per group, two independent experiments. Data represent mean±SD, Student's t-test.

(**C**) Proliferative response of spleen T cells at day 37 of infection from chronically *S. aureus*-infected

mice which received PBS or HKSP to *in vitro* stimulation with anti-CD3/anti-CD28. T-cell

proliferation was measured by ^{3}H-thymidine incorporation. n=5 mice per group, two independent

experiments. Data represent mean counts per minute (cpm) ± SD. **p=0.0024, Student's t-test.

(**D**) HKSP-treatment slightly reduces MDSCs in spleen. Representative fluorescence-activated cell

sorting   (FACS)   illustrating   monocytic $CD11b^+Ly6C^+Ly6G^{low}$,   neutrophilic

$CD11b^+Ly6C^{low}Ly6G^+$ and eosinophilic $CD11b^+Ly6C^{low}Ly6G^{low}$ MDSCs (left), and percentage

of each MDSC subset within the total spleen cell population of untreated (control) or HKSP-treated

mice (right) at day 37 of infection. n=5 mice per group, two independent experiments. Data represent

mean±SD, Student's t-test.

(**E**) Intraperitoneal injection with HKSP at day 14 of infection induces acute inflammation.

Peritoneal exudate cells were collected from chronically *S. aureus*-infected mice 12 hours after

administration of PBS (control) or HKSP. Percentage of $CD11b^+Ly6C^+$ monocytes, $CD11b^+Ly6G^+$

granulocytes, $CD11b^{hi}F4/80^{hi}$ LPMs, $CD11b^+F4/80^{low}$ SPMs along with total MΦ population

(LPMs plus SPMs) within the total peritoneal cell population is shown. n=5-10 mice per group, two

independent experiments. Data represent mean±SD. *p<0.05, **p<0.01, ****p<0.0001, one-way

ANOVA with Tukey's multiple comparisons test. Peritoneal exudate cells collected 12 hours after

HKSA-treatment at day 14 of infection are included for comparison.

Reasoning for past unsuccessful applications of the treatment

Our model-driven protocol suggesting sufficient HKSA-dose, its administration day, and day of complete bacterial clearance has proved reliable and effective for all HKSA-treated animals. Although administration of inactivated cells as treatment for infections has been used in the past, this kind of therapy is narrowly established. This is due to lacking information regarding the sufficient dose(s) required and day(s) of administration that could resolve *S. aureus* infections successfully. Until now, treatments with inactivated bacteria against *S. aureus* infections have been based on vague experimental experience.

Here, we explain *in silico* why heat- or formalin-killed bacteria treatments used so far have not been successful in yielding clearance. We base our arguments on a previous study (*35*), in which scientists administered at least 19 injections with increased dose of formalin-killed *S. aureus* over the period of 3 months in human patients with *S. aureus* infection (furunculosis).

In the study none of the chronically infected patients was reported to have attained sterilizing immunity, even though they experienced moderate to strong clinical improvement. The injecting scheme in the study consisted of increasing killed *S. aureus* doses (B_d) given in intervals of 3-5 days as follows:

– Suspension I:$(0.1,0.2,0.3,0.4,0.5) \times 5 \times 10^8$

– Suspension II: $(0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1) \times 10^9$

– Suspension III:$(0.5,0.6,0.7,0.8,0.9,1) \times 2.5 \times 10^9$.

We assumed that the bacterial capacity in humans is 1000 times greater than the bacterial capacity in mice (based on the kidney weight ratio between mice and humans), created the corresponding murine suspensions:

– Suspension IV:$(0.1,0.2,0.3,0.4,0.5) \times 5 \times 10^5$

– Suspension V: $(0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1) \times 10^6$

– Suspension VI: $(0.5, 0.6, 0.7, 0.8, 0.9, 1) \times 2.5 \times 10^6$,

and applied them in our mouse model *in silico* every 4 days, starting from day 14, when chronic

infection is established in mice.

The conventional administration of injections with inactivated bacteria is based on the

belief that repeated vaccination could work more efficiently. Here, we employed *in silico* the

analogous protocol that has been administered in humans (suspensions IV-VI, 19 injections) and

showed that repeated injections with increasing doses of killed *S. aureus* cannot render

eradication of *S. aureus* (Fig. 5A). We also explored the case when not only more injections are

given (25 in total) but also with high fixed dose (almost fivefold higher than the highest dose of

suspensions IV-VI) and found that such treatments still fail to eliminate the infection (Fig. 5A).

Our results explicitly negate the current belief by showing that challenging the system of chronic

infection repeatedly with insufficient killed *S. aureus* dose and in high-frequency intervals does

not result in cure (Fig. 5A).

To gain a broader perspective on curative protocols, we simulated varying doses from

10^6 to 10^7 inactivated *S. aureus*, number of injections from 1-20 and time intervals between

injections from 0 up to 14 days (Fig. 5B-5D). Our *in silico* results suggested that for doses of 10^6

to 10^7 inactivated *S. aureus,* only treatment protocols involving HK injections with time

intervals from 1-3 days could cure (Fig. 5B, *blue*), with the maximum time interval of 3 days

requiring a minimum dose of 10^7 inactivated *S. aureus* to be effective (Fig. 5C). Therefore, both

the time intervals of 3-5 days and doses (suspensions IV-VI) analogous to as administered to

furunculosis patients (*35*) were fruitless attempts towards bacterial clearance, since the

administered doses in those time intervals were low to sufficiently stimulate the immune system

and lead to cure (Fig. 5B-5D). We next postulated that higher doses could have cured chronically

S. aureus-infected patients. For this purpose, we simulated curative and non-curative protocols

for varying number of injections, time intervals between injections and doses from 8×10^6 up to

10^8 inactivated *S. aureus*. Our results clearly indicated that higher doses could lead to cure (Fig.

6A-6C). Furthermore, our results showed that in case time intervals between injections need to

increase, (e.g. schedules of doctors), then higher HK-doses are required for cure (Fig. 6B).

560   Even though treatments with insufficient-for-cure doses of inactivated *S. aureus*, such as

the doses given to furunculosis patients, cannot confer complete clearance of bacteria,

furunculosis patients still reported improvement. In accordance, *in silico* administration of low

HK-doses showed that although they do not cure the hosts, they alleviate chronic infection by

providing remission (Fig. 6D). In fact, administration of HK treatment as early as possible leads

to longer remission of the infection (Fig. 6D). Lastly, we investigated how the administration

time of a HK-injection affects the clinical outcome. For middle-sized doses the day of

administration is crucial for the outcome of chronic infection, since it can provide cure if given

as early as possible or only provide temporary remission without clearing the infection (Fig. 6E).

These results highlight the urgency of treating chronic *S. aureus* infections as early as possible,

which is often compromised in cases of *S. aureus*-caused renal abscesses by improper and/or

time-consuming treatments (*16*, *30*).

Fig. 5. Simulations explain why previous treatments with inactivated *S. aureus* in humans were unsuccessful and suggest curative treatment protocols. At each injection day starting from day 14

of infection (when infection is chronic), treatment was incorporated into the T-cell ODE (Eq. (2)) as

$k_b B_d$, where k_b as defined in table S1 and B_d the varying, administered HKSA-dose. (**A**) Repeated

administration of inactivated *S. aureus* cannot render clearance. 19 HKSA-injections with increasing

dose in an analogous way to as administered in humans (suspensions IV-VI, purple) or 25 injections

with high fixed dose (yellow) were administered every four days. Chronic *S. aureus* infection

persists. (**B-D**) *In silico* predictions for cure plotted for 1 up to 20 HKSA-injections, HKSA-doses

ranging from 10^6 to 10^7, and time intervals between HKSA-injections from 0-7 days, or 2 weeks.

Time interval of 0 days means that only one HKSA-injection is administered. (**B**) Possibility of cure

declines when time intervals between HK-injections increase, even if many injections with high

HKSA-dose are administered. Each blue circle represents a unique, curative treatment protocol and

shows that cure is achieved only when time intervals between injections are 1-3 days with minimum

HKSA-dose needed for cure as in (**C**). (**D**) Interconnection between HKSA-doses 10^6 to 10^7,

HKSA-injections and time intervals between injections in three-dimensional plot.

Fig. 6. *In silico* correlation between HKSA-doses from 8×10^6 to 10^8, number of HKSA-injections and time intervals between injections for curative treatment protocols or remission. (**A-C**) Same as in Fig. 5B-5D for HKSA-doses ranging from 8×10^6 to 10^8. Each blue circle represents a unique, curative treatment protocol, for which the minimum dose required for successful treatment is indicated in (**B**). Black square in (**A**) and (**C**) represents the treatment protocol of 10^8 HKSA in a single injection that was tested experimentally in this study and cured all hosts *in vivo*. (**D-E**) Influence of administration time of HKSA-injection on the chronic infection. The HKSA-treatment *in silico* was added as term $k_b B_d$ to the T-cell ODE (Eq. (2)) at day 14 or 20 for a 12-hour perturbation window, where k_b as in table S1 and B_d the HKSA-dose. Critical HKSA-dose required for cure when administered at day 14 (early chronic infection) was estimated to be 4×10^7 (Fig. 2C). Although lower HKSA-dose (**D**) for example $B_d = 3\times10^7$ HKSA cannot cure, it provides remission. Higher HKSA-dose (**E**), such as $B_d = 5\times10^7$, confers sterilizing immunity when administered at early timepoints of chronic infection but fails to cure when administered later, although it provides remission temporarily.

DISCUSSION

At present, no treatment has proved to be completely effective in resolving chronic *S*. *aureus* infections. There is no vaccine against *S*. *aureus* infections because all clinical trials have failed (*36*). The development of new antibiotics would only be a temporary solution, until the bacterium develops antibiotic resistance. Recent reports warn on the alarming increase of antibiotic-resistant *S*. *aureus* infections in organs that have not been conventionally infected before, including kidneys (*16*, *37*). Such reports highlight that treating infections in organs,

where the medical community is not traditionally used to encountering, is very challenging and

often misdiagnosed, therefore requiring prompt intervention once identified (*30*). Furthermore,

the current medical arsenal of antibiotics, MDSC-targeting drugs or surgery, is insufficient,

ineffective or inadvisable due to bacteria-resistance mechanisms, cytotoxicity of drugs, inability

to drain abscesses because of their location in internal organs or the high-risk medical status of

patients. Consequently, new, less complicated ways of treatment against *S. aureus* infections are

absolutely essential to find. We here reported cure of all chronically *S. aureus*-infected mice with

renal abscesses, using heat-killed *S. aureus* treatment, as quantified by our mathematical model.

Although inactivated *S. aureus* has been used to treat soft skin infections *(35)* this is, to our

knowledge, the first time heat-killed *S. aureus* is used to treat renal abscesses.

Conventional vaccination with inactivated microorganisms always requires multiple

doses to ensure prophylaxis. Hence, it is believed that inactivated microorganisms, when used as

treatment, should also be administered in multiple doses to be efficient (*35*). Here we provided

evidence that treatment with one HK-injection alone can cure chronic *S. aureus* infection (Fig.

2D, 3B). This is an important finding, because it means that a single injection with the right HK-

dose, besides being extremely practical to implement in human therapeutics, can suffice to break

the chronic phase of infection and lead to bacterial clearance, without the need for antibiotics,

that multidrug-resistant *S. aureus* can evade, or surgery for abscess drainage, or cytotoxic

MDSC-targeting drugs. Most importantly, pathogens causing renal abscesses in humans are

easily obtained without any invasive methods from urine samples from patients (*30*), which can

then be easily cultured and heat-killed. Regarding safety, the administration of inactivated *S.*

aureus as treatment of staphylococcal skin infection in human patients had only minor side-

effects, such as temporary pain at the site of injection (*35*). In accordance, our treatments with

HKSA or HKSP were well-tolerated. Treated animals did not exhibit any signs of side-effects or

discomfort. They were active, alert, observant of their environment, with eyes wide open, fur

laying flat and maintained normal body weight and appetite. Consequently, HK treatments bear

the potential to become easily produced, easily stored, cost-effective, and safe treatments in

medicine.

The recently identified Eo-MDSC inhibit, as other MDSCs, T-cell proliferation during

chronic *S. aureus* infection (*13*). Our results agree with previous results on the suppressive effect

of Eo-MDSC on T cells, since high Eo-MDSC numbers in control (untreated) mice contributed

to high T-cell suppression that was reduced as a result of reduced Eo-MDSC after HKSA-

treatment (Fig. 3C-3D). More Eo-MDSC have been directly linked with more CFU of *S. aureus*

(*13*). In accordance, our results showed that significant decrease of Eo-MDSC contributed to

bacterial clearance (Fig. 3B, 3D). Additionally, we here revealed a previously unidentified

approach for depletion of Eo-MDSC that was achieved in an indirect way, in contrast to

cytotoxic agents, which directly target MDSC-populations and bear side-effects.

Our mathematical model aimed to predict variables that could transition a chronic *S.*

aureus infection to an active inflammatory state to promote bacterial clearance. Our experiments

in vivo verified that perturbation with HKSA initiates acute inflammation during the chronic

establishment of *S. aureus* infection, showing massive increase in amounts of $CD11b^+Ly6C^+$

monocytes, $CD11b^+Ly6G^+$ granulocytes (neutrophils) and $CD11b^+F4/80^{low}$ SPMs in HKSA-

treated mice (Fig. 3E). Our previous study has shown that T cells from chronically *S. aureus*-

infected mice remained hyporesponsive after *in vitro* stimulation with either heat-killed *S. aureus*

or anti-CD3 plus anti-CD28 (*5*). This indicates that it is not the heat-killed treatment per se that

cured the infection, but rather the mathematically-driven concept of sufficiently destabilizing the

system dynamics *in vivo*. One of the strategies for destabilization of the chronic infection system,

as shown in this study, was achieved via administration of HKSA that caused acute inflammation

and subsequently created a new cascade of inflammatory events (including T-cell boost),

resulting in sterilizing immunity.

For the experiments regarding antigen-specificity of the treatment, *S. pyogenes* was

chosen because together with *S. aureus* they are the two most common gram-positive cocci of

medical significance (*38*). Delivery of 10^8 HKSP cleared *S. aureus* in 50% of animals,

suggesting that a portion of the effects of the HK treatment are antigen-independent and that a

non-antigen specific HK treatment may be completely effective if combined with other

perturbation strategies (antigen-specific or not). Even a higher HKSP-dose alone could have

potentially resolved the chronic infection in all HKSP-treated animals (fig. S2). Interestingly, we

found that other studies have used a similar approach to treat chronic *Mycobacterium*

tuberculosis infections with heat-killed *Mycobacterium vaccae*, especially in patients, in whom

previous treatment with antibiotics and/or chemotherapy had failed. Consistent with our results,

they also reported a therapeutic effect that cures patients (success percentages varying), along

with increase of T cells and an exemplary safety record even in patients co-infected with human

immunodeficiency virus (HIV). The copious advantages of heat-killed *M. vaccae* treatments led

to extensive Phase III clinical trials in patients in a plethora of countries around the globe (*39,*

40). Taking all the above into account, our results with *S. pyogenes* could be pioneer for chronic

S. aureus infections because they suggest that chronic *S. aureus* infections may be successfully

treated with other *S. aureus* strains or even other bacteria, for example *S. pyogenes*. If the

presented results are corroborated by further evidence and hold in human, a standardized cocktail

of the most frequent organisms causing renal abscesses can be added to hospital stocks for

immediate treatment of patients afflicted with renal abscesses. In addition, these results could

also help current efforts towards vaccine development for protection against *S. aureus*, since

antigens from other cocci/bacteria could be incorporated for vaccine testing.

Some diversity in the bacterial loads of control mice in all experiments *in vivo* was

observed (Fig. 3B, 4B). All control mice were infected with *S. aureus* but did not receive heat-

killed treatment. It was observed that in some of them *S. aureus* was cleared. Such variability can

be occasionally observed since (i) individual immune responses of mice can vary greatly and (ii)

biological systems are inherently stochastic. However, chronic infection and associated renal

abscesses caused by the same *S. aureus* strain as used here have been amply studied and the

dynamics of chronicity *in vivo* were published already years ago (*5*, *6*). Even though these

controls would be typically discarded, we included them for reasons of scientific transparency

and because this observed behaviour is explained mathematically in Fig. 2A: The average

position of an infected animal in the separatrix (*white star*) lies in the basin of attraction of

chronic infection (Fig. 2A, *pink area*) but is very close to the basin of attraction of cure (Fig. 2A,

blue area), indicating that a small portion of infected mice could spontaneously get cured.

Mathematically, points that lie close to the boundary separating two basins of attraction could

end up in the other attractor domain, namely the cure region, after stochastic perturbations

(possibly happening during the acute phase of the infection). Most essential is, however, the

effectiveness of the treatment because renal abscesses are often misdiagnosed, hence associated

with high risk of mortality (*30*), and once correct diagnosis takes place, the patients might

already experience organ damage and be in life-threatening conditions, whose lives could be

saved because of this treatment.

Our mathematical model is not limited to our proof-of-concept presented here. The

potential, novelty and usefulness of our mathematical model are further depicted in Fig. 6,

showing a plethora of unique, curative HKSA-treatment protocols with varying HK-doses,

number of HK-injections and time intervals between HK-injections (each blue bullet point). This

variety of quantified protocols can offer important flexibility for future treatments or clinical

trials because they can comply with the scientific and social circumstances, for instance working

hours of doctors, sensitivity of individuals to high HK-doses, or restrictions in animal permits.

We have started designing a graphical user interface for all these protocols, so that scientists can

choose HK-dose(s) or time intervals between treatment(s) and easily design their research and

treatments.

The results of this study are specified to C57BL/6 female mice; however, new *in silico*

curative protocols can be obtained when fitting the parameters of the mouse line or human of

interest. Most importantly, the simple structure of our model allows its easy adjustment for

chronic infections caused by other bacteria or staphylococcal strains, which could suggest

curative protocols against other strain- or bacteria-specific infections, including *S. aureus*

biofilms on medical implants that are devastating the clinics, renal abscesses caused by other

bacteria such as *Escherichia coli*, or infections in other internal organs. Future studies could be

such adjustment of model parameters for other bacteria or staphylococcal strains and subsequent

experiments based on model-driven treatment protocols for verification.

We here report cure of chronic *S. aureus* infection and renal abscesses without any use of

antibiotics, cytotoxic MDSC-targeting drugs, or surgical procedures for abscess drainage. Our

study provides proof-of-principle for a novel treatment protocol of chronic *S. aureus* infection by

repurposing heat-killed treatments, guided and quantified by our mathematical model. Unlike

conventional heat-killed administration, which is used as prophylaxis against infections in

humans and sometimes animals, we used this method as a treatment during ongoing chronic

infection. Treatments that are directed to promoting the immune response during an ongoing

infection are lacking. Our work could pave the way and provide a new scientific perspective

towards treatments that do not aim at targeting the infective agent (such as antibiotics), but rather

boost the host's own immune defense to resolve the infection.

METHODS

Mathematical model

The mathematical model was implemented and simulated in MATLAB, see

www.mathworks.com.

Simulating the perturbation treatment

To simulate the perturbation strategy, we incorporated, for a perturbation window of 12 hours,

the extra term $k_b B_d$ into the ODE describing T cells (Eq. (2)), where $B_d = 10^8$ cells is the dose of

heat-killed *S. aureus* and $k_b = 0.001509$ [days^{-1}] the parameter of T-cell activation and

recruitment as estimated during the fitting process (full description in Supplementary Materials;

table S1). The term of heat-killed treatment was incorporated into the ODE of T cells, because

heat-killed cells, as it happens when administered via conventional vaccines, deliver antigens

into the body that enhance the adaptive immunity. On each day (timepoint) of administration of

heat-killed treatment, such as day 14 of infection, the treatment term $k_b B_d$ was added, and the

equations became:

$$\dot{B}(t) = r_b B(t)\left(1 - \frac{B(t)}{\kappa}\right) - c_b T(t)B(t),$$

$$\dot{T}(t) = r_t T^2(t)\left(1 - \frac{T(t)}{K_T}\right) + k_b B(t) - c_T B(t) T(t) - \Theta\, T(t) + k_b B_d. \qquad (3)$$

Since heat-killed bacteria are not present continuously *in vivo*, the treatment term (that

simulates the *in vivo* conditions) was removed after the perturbation window and the equations

returned to their initial form as in equations (1)-(2). For treatment with heat-killed *Streptococcus*

pyogenes or varying HK-dose, the HK-dose B_d and value of k_b in the treatment term $k_b B_d$ were as

stated in the main text.

Experimental protocols

Bacteria

S. aureus strain SH1000 *(41)* was grown to Mid-Log phase in brain heart infusion medium (BHI,

Roth, Karlsruhe, Germany) at 37°C with shaking (120 rpm), collected by centrifugation, washed

with sterile PBS, and diluted to the required concentration. The number of viable bacteria was

determined after serial diluting and plating on BHI-agar.

Mice and infection

A previously described chronic renal abscess infection model *(5)* has been used in this study. It is

known that *S. aureus* strain SH1000 produces renal abscesses after intravenous inoculation *(5)*.

Pathogen-free, 10 weeks-old C57BL/6 female mice were purchased from Harlan-Winkelmann

(Envigo, Netherlands). All animals were provided with food and water ad libitum, and housed in

groups of up to 5 mice per cage in individually ventilated cages. Statistical power analysis with

anticipated incidence of 10% and 90% for control and treated mice, respectively, indicated a

sample size of five mice per group. Mice were infected with 5×10^7 CFU of *S. aureus* in 100 µl of

PBS via a tail vein and monitored on a daily basis for weight loss and sign of pain or distress. At

specified times of infection, mice were sacrificed by CO_2 asphyxiation and the bacterial load was

enumerated in kidney homogenates by plating 10-fold serial dilutions on blood agar plates.

Spleens were removed, transformed in a single cell suspension and further processed for FACS

and proliferation assays.

In vaccination experiments, infected mice were injected intraperitoneally at day 14 of

infection with 10^8 heat-killed bacteria of *S. aureus* strain SH1000 or *S. pyogenes* strain A20 in

200 μl of PBS that were prepared by heating a bacterial suspension at $60°C$ for 1 h. At 12 h

postchallenge, mice were sacrificed and peritoneal exudate cells (PEC) were isolated from

infected mice by lavage of the peritoneal cavity with 2 ml sterile PBS. The lavage fluid was

centrifuged, supernatants stored at $-20°C$ for subsequent cytokine analysis, and PEC resuspended

in complete RPMI, stained and analyzed by flow cytometry (see below).

Animal experiments were performed in strict accordance with the German regulations of

the Society for Laboratory Animal Science (GV-SOLAS) and the European Health Law of the

Federation of Laboratory Animal Science Associations (FELASA). All experiments were

approved by the ethical board Niedersächsisches Landesamt für Verbraucherschutz und

Lebensmittelsicherheit, Oldenburg, Germany (LAVES; permit N. 18/2798).

Flow cytometry analysis

Cells were incubated with purified rat anti-mouse CD16/CD32 (BD Biosciences) for 5 min to

block Fc receptors and then stained with antibodies against CD11b (BioLegend), Ly6C

(BioLegend), Ly6G (Miltenyi Biotec), F4/80 (BD Biosciences) for 20 min at $4°C$. Labeled cells

were measured by flow cytometry using a BDTM LSR II flow cytometer (BD Biosciences) and

analyzed by FlowJo software.

Proliferation assay

Spleen cells were seeded into 96-well flat-bottom plates at 5×10^5 cells/well in 100 µl of

complete RPMI medium and stimulated with 2 µg/ml of anti-CD3/anti-CD28 antibodies (Sigma-

Aldrich) at 37°C and 5% CO_2. After 3 days of incubation, the cells were pulsed with 1 µCi ^{3}H-

thymidine (Amersham) and harvested 18 h later on Filtermats A (Wallac) using a cell harvester

(Inotech). The amount of ^{3}H-thymidine incorporation was measured in a gamma scintillation

counter (Wallac 1450; MicroTrilux).

Statistical analyses

All data were analyzed with GraphPad Prism Software. Comparisons between several groups

were made using a parametric ANOVA test with Tukey's multiple comparisons test. Comparison

between two groups was performed using a Student's t-test. P values <0.05 were considered

significant.

Supplementary Materials for

Chronic *Staphylococcus aureus* infection is cured by theory-driven therapy

Lito A. Papaxenopoulou,* Gang Zhao, Sahamoddin Khailaie, Konstantinos Katsoulis-Dimitriou,
Ingo Schmitz, Eva Medina, Haralampos Hatzikirou,* Michael Meyer-Hermann*

*Corresponding author. Email: papaxenopoulou.lito@gmail.com;
haralampos.hatzikirou@ku.ac.ae; mmh@theoretical-biology.de

The PDF file includes:
816
817 Supplementary Methods
818 Fig. S1. Perturbation strategies suggest eradication of *S. aureus in silico*.
819 Fig. S2. Time of bacterial clearance for varying HK-doses and three values of T-cell
820 stimulatory parameter *in silico*.
821 Table S1. Model parameter values as used for model analysis.
822

823 **Other Supplementary Material for this manuscript includes the following:**

824 Table S2 (Microsoft Excel format). Raw experimental data.
825 MATLAB codes (zip file).

Supplementary Methods

Mathematical model

The mathematical model was implemented and simulated in MATLAB, see *www.mathworks.com*.

Fitting curves and standard deviation of parameters

The unknown parameters in the model were estimated in three steps. First, the carrying capacity of bacteria $\varkappa$ was estimated based on our previously reported experimental results from B and T cells-deficient $RAG2^{-/-}$ mice (only innate immunity present), which were initially infected with 7×10^7 CFU of *S. aureus* strain SH1000 (same strain as used in the study here) and showed a nearly constant level of *S. aureus* in kidneys from day 7 till day 56 (5). The mean of these data points was taken as the bacterial carrying capacity. The carrying capacity of T cells (parameter K_T) was assumed to be of the same order of magnitude as the bacterial carrying capacity. Secondly, the growth rate of bacteria was estimated by solving the logistic growth equation $\frac{dP}{dt} = rP\left(1 - \frac{P}{\varkappa}\right)$ for r

$$r = \frac{ln\left(\frac{P(\varkappa - P_0)}{P_0(\varkappa - P)}\right)}{t}$$

where $\varkappa$ is the bacterial carrying capacity, P_0 is the initial inoculation number of bacteria and P is the bacterial CFU at time t. Our previous experimental data showed that the bacterial loads in B and T cells-deficient $RAG2^{-/-}$ mice reached 75% of the carrying capacity on day 2 and fluctuated afterwards, after intravenous inoculation with 7×10^7 CFU of *S. aureus*. Assuming that

the bacterial load reached 75% of the carrying capacity by day 1 or day 2, we determined the

high and low boundary of r to be 0.636 and 0.318, respectively. The average of the low and high

boundary was taken as the bacterial growth rate r_b of the model. Finally, our previously reported

data of bacterial loads and absolute numbers of T cells in time from immunocompetent mice

with chronic *S. aureus* SH1000-infection and renal abscesses (*5*) were used to fit the rest of

unknown parameters. The fitting process used a Markov Chain Monte Carlo version of

Differential Evolution algorithm *(42)*. Parameter c_T, representing T-cell suppression locally (at

the site of infection which is the kidneys for the chronic infection here) appeared much smaller

than other parameters, in particular parameter Θ (representing T-cell suppression by MDSCs

systemically, namely distant from the site of infection, such as in spleen). We tested, in a second

study, the possibility of fitting the same data with $c_T = 0$. The fit quality remained the same;

therefore we concluded that c_T is zero and that the main T-cell suppression by MDSCs is exerted

systemically. This deduction accords with our previous experimental reports which showed

major T-cell suppression by MDSCs in spleens of mice that had chronic *S. aureus* infection in

kidneys (*6, 13*). Fitted parameter values are shown in table S1.

Scaling the model

For the analytical solutions and analytical stability analysis the calculations were made feasible

by using an analytically amenable ODE model, which approximates the original ODE as

described in Eq. (1)-(2).

With the following change of variables we non-dimensionalize the ODE model (1)-(2):

$B = \beta_0 \xi, \qquad T = c_0 \psi, \qquad t = t_0 \tau.$

$$\implies \frac{dB(t)}{dt} = \frac{\beta_0 d\xi}{t_0 d\tau} = r_b \beta_0 \xi - \frac{r_b}{\kappa} \beta_0^2 \xi^2 - c_b c_0 \psi \beta_0 \xi$$

$$\implies \frac{d\xi}{d\tau} = r_b t_0 \xi - \frac{r_b}{\kappa} t_0 \beta_0 \xi^2 - c_b t_0 c_0 \xi \psi.$$

We impose that the coefficients of ξ, ξ^2 and $\xi\psi$ are equal 1. Then

$$t_0 = \frac{1}{r_b}, \quad \beta_0 = \kappa, \quad c_0 = \frac{r_b}{c_b}. \tag{S1}$$

Therefore the new, non-dimensionalized equation for bacteria is

$$\frac{d\xi}{d\tau} = \xi - \xi^2 - \xi\psi \tag{S2}$$

For the equation $\dot{T}(t)$ we have the non-dimensionalized calculations:

$$\frac{dT(t)}{dt} = \frac{c_0 d\psi}{t_0 d\tau} = r_t c_0^2 \psi^2 + k_b \beta_0 \xi - c_T \beta_0 \xi c_0 \psi - \Theta c_0 \psi$$

$$\implies \frac{d\psi}{d\tau} = r_t t_0 c_0 \psi^2 - \Theta t_0 \psi - c_T \beta_0 t_0 \xi \psi + \frac{k_b \beta_0 t_0}{c_0} \xi$$

Substitution of the t_0, β_0 and c_0 (found in Eq. (S1)) gives the scaled equation for T:

$$\frac{d\psi}{d\tau} = \alpha \psi^2 + \beta \xi - \gamma \xi \psi - \delta \psi \tag{S3}$$

where $\quad \alpha = \frac{r_t}{c_b}, \beta = \frac{\kappa k_b c_b}{r_b^2}, \gamma = \frac{\kappa c_T}{r_b}, \delta = \frac{\Theta}{r_b}. \tag{S4}$

Calculation of equilibrium points

From Eq. (S2) we have:

$\xi - \xi^2 - \xi\psi = 0 \Longrightarrow \xi = 0,\ and\ \xi = 1 - \psi$

• For $\xi = 0$ in Eq. (S3) we have:

891
$$\frac{d\psi}{d\tau} = 0 \Longrightarrow \alpha\psi^2 - \delta\psi = 0 \Longrightarrow \psi_1 = 0,\ and\ \psi_2 = \frac{\delta}{\alpha}$$

893   • For $\xi = 1 - \psi$ in Eq. (S3) in steady state we conclude that:

894
$$\psi_{3,4} = \frac{\beta + \gamma + \delta \pm \sqrt{[-(\beta + \gamma + \delta)]^2 - 4\beta(\alpha + \gamma)}}{2(\alpha + \gamma)} \qquad\qquad \text{(S5)}$$

Consequently the system has four equilibrium points in total:

• $(\xi_1, \psi_1) = (0,0)$

• $(\xi_2, \psi_2) = (0, \frac{\delta}{\alpha})$

• $(\xi_{3,4}, \psi_{3,4}) = (1 - \psi_{3,4}, \psi_{3,4})$ where $\psi_{3,4}$ is as shown above.

Existence of $\psi_{3,4}$

Equilibrium points $\psi_{3,4}$ exist only when $\Delta = (\beta + \gamma + \delta)^2 - 4\beta(\alpha + \gamma) \geq 0$, i.e. only when

$\psi_{3,4}$ have no imaginary part. Equivalently

$(\beta + \gamma + \delta)^2 - 4\beta(\alpha + \gamma) \geq 0$

$\beta^2 + \gamma^2 + \delta^2 + 2\beta\gamma + 2\beta\delta + 2\gamma\delta - 4\alpha\beta - 4\beta\gamma \geq 0$ $(\pm 4\beta\delta)$

$\beta^2 + \gamma^2 + \delta^2 - 2\beta\gamma - 2\beta\delta + 2\gamma\delta - 4\beta(\alpha - \delta) \geq 0$

$(-\beta + \gamma + \delta)^2 - 4\beta(\alpha - \delta) \geq 0$ (S6)

According to the sign of the term $(\alpha - \delta)$ in condition (S6), we investigate when the equilibrium

points $\psi_{3,4}$ exist.

• If $\alpha - \delta \leq 0 \Longrightarrow \delta \geq a$ then the equilibria $\psi_{3,4}$ exist.

• If $0 < \delta < \alpha$ then we reformulate Δ as follows:

913
$$\Delta = (-\beta + \gamma + \delta - 2\sqrt{\beta}\sqrt{\alpha - \delta}) \cdot (-\beta + \gamma + \delta + 2\sqrt{\beta}\sqrt{\alpha - \delta})$$

914   a) If $-\beta + \gamma + \delta \geq 0$ then for existence of $\psi_{3,4}$ we require

915      $-\beta + \gamma + \delta - 2\sqrt{\beta}\sqrt{\alpha - \delta} \geq 0$. Then:

917
$$-\beta + \gamma + \delta - 2\sqrt{\beta}\sqrt{\alpha - \delta} \geq 0 \Longrightarrow \beta - (\gamma + \delta) + 2\sqrt{\beta}\sqrt{\alpha - \delta} \leq 0$$

918
$$\sqrt{\beta}^2 + 2\sqrt{\beta}\sqrt{\alpha - \delta} - (\gamma + \delta) \leq 0$$

919
$$\Longrightarrow \sqrt{\beta} \leq \frac{-2\sqrt{\alpha - \delta} \pm \sqrt{4(\alpha - \delta) - 4[-(\gamma + \delta)]}}{2}$$

920
$$\sqrt{\beta} \leq -\sqrt{\alpha - \delta} + \sqrt{\alpha + \gamma}$$

921   **Note:** The solution $\sqrt{\beta} \leq -\sqrt{\alpha - \delta} - \sqrt{\alpha + \gamma}$ is exempt because by definition $\sqrt{\beta} \geq 0$.

923   b) If $-\beta + \gamma + \delta \leq 0$ then for existence of $\psi_{3,4}$ we require $-\beta + \gamma + \delta +$

924      $2\sqrt{\beta}\sqrt{\alpha - \delta} \leq 0$. Then:

925
$$-\beta + \gamma + \delta + 2\sqrt{\beta}\sqrt{\alpha - \delta} \leq 0 \Longrightarrow \beta - (\gamma + \delta) - 2\sqrt{\beta}\sqrt{\alpha - \delta} \geq 0$$

926
$$\sqrt{\beta}^2 - 2\sqrt{\beta}\sqrt{\alpha - \delta} - (\gamma + \delta) \geq 0$$

927
$$\Longrightarrow \sqrt{\beta} \geq \frac{2\sqrt{\alpha - \delta} \pm \sqrt{4(\alpha - \delta) - 4[-(\gamma + \delta)]}}{2}$$

928
$$\sqrt{\beta} \geq \sqrt{\alpha - \delta} + \sqrt{\alpha + \gamma}$$

Note: The solution $\sqrt{\beta} \geq \sqrt{\alpha - \delta} - \sqrt{\alpha + \gamma}$ is trivially exempt.

Local stability analysis of equilibrium points

Jacobian Matrix $J = \begin{bmatrix} \frac{\partial \dot{\xi}}{\partial \xi} & \frac{\partial \dot{\xi}}{\partial \psi} \\ \frac{\partial \dot{\psi}}{\partial \xi} & \frac{\partial \dot{\psi}}{\partial \psi} \end{bmatrix} = \begin{bmatrix} 1 - 2\xi - \psi & -\xi \\ \beta - \gamma\psi & 2\alpha\psi - \gamma\xi - \delta \end{bmatrix}$

Evaluation of Jacobian matrix in the trivial equilibrium point (ξ_1, ψ_1):

$J(0,0) = \begin{bmatrix} 1 & 0 \\ \beta & -\delta \end{bmatrix} \Rightarrow |J(0,0)| = -\delta < 0$ (S7)

From linear algebra, it is known that if J is a 2×2 matrix and λ_1, λ_2 its eigenvalues, then the

determinant of J, $|J| = \lambda_1 \times \lambda_2$. Since the determinant of the Jacobian matrix in Eq. (S7) is

negative (i.e. det = $-\delta$ <0), it means that the eigenvalues are of a different sign, and hence the

trivial equilibrium point is unstable (i.e. saddle point, which is always unstable).

For the equilibrium point $(\xi_2, \psi_2) = (0, \frac{\delta}{\alpha})$ we have:

$J(\xi_2, \psi_2) = \begin{bmatrix} 1 - \frac{\delta}{\alpha} & 0 \\ \beta - \gamma\frac{\delta}{\alpha} & 2\alpha\frac{\delta}{\alpha} - \delta \end{bmatrix} = \begin{bmatrix} 1 - \frac{\delta}{\alpha} & 0 \\ \beta - \frac{\gamma\delta}{\alpha} & \delta \end{bmatrix} \Rightarrow |J| = \delta \cdot \left(1 - \frac{\delta}{\alpha}\right)$ for the equilibrium

point (ξ_2, ψ_2). The sign of the determinant depends on the term $\left(1 - \frac{\delta}{\alpha}\right)$. When $\delta > \alpha$, then

$|J| < 0$ (hence one positive and one negative eigenvalue), meaning that the equilibrium point is

saddle. This becomes unstable when $\delta < \alpha$. Next, we evaluate the Jacobian matrix in the

equilibrium points $(\xi_{3,4}, \psi_{3,4})$, by using $\xi = 1 - \psi \geq 0$,

$$|J(1 - \psi, \psi)| = \begin{vmatrix} -1 + \psi & -1 + \psi \\ \beta - \gamma\psi & (2\alpha + \gamma)\psi - (\gamma + \delta) \end{vmatrix}$$

$$= -(-1 + \psi)(\beta + \delta + \gamma - 2(\alpha + \gamma)\psi)$$

$$= -(1-\psi)(2(\alpha+\gamma)\psi - (\beta+\delta+\gamma)).$$

We obtain the trace of the Jacobian matrix, tr(J), to determine the type of stability of equilibrium

points $(\xi_{3,4}, \psi_{3,4})$,

$$tr(J) = -1 - \delta + \gamma(-1+\psi) + \psi + 2\alpha\psi = (1+2\alpha+\gamma)\psi - (1+\gamma+\delta).$$

We first need to find some critical values for ψ:

• If $|J(1-\psi,\psi)| = 0$, then

$$\psi_1^* = \frac{\beta+\gamma+\delta}{2(\alpha+\gamma)}. \tag{S8}$$

We know that the term $(1-\psi)$ equals ξ, which represents the bacteria, and hence $\xi = 1 - \psi \geq$

0.

• If $tr(J) = 0$, then

$$\psi_2^* = \frac{1+\gamma+\delta}{1+2\alpha+\gamma} \tag{S9}$$

From the critical points found in Eqs. (S8) and (S9), the stability of the equilibrium points

$(\xi_{3,4}, \psi_{3,4}) = (1-\psi_{3,4}, \psi_{3,4})$ can be classified as follows:

Stable node or spiral (Represents the chronic phase):

▪ $|J| \geq 0 \Rightarrow \psi_1^* \leq (\beta+\gamma+\delta)/(2(\alpha+\gamma))$

▪ $tr(J) \leq 0 \Rightarrow \psi_2^* \leq (1+\gamma+\delta)/(1+2\alpha+\gamma)$

$$\Rightarrow \psi^* \leq \min\{\psi_1^*, \psi_2^*\}$$

Saddle equilibrium point:

971
$$|J| < 0 \Rightarrow \psi_1^* > \frac{\beta + \gamma + \delta}{2(\alpha + \gamma)} \Rightarrow \psi^* > \frac{\beta + \gamma + \delta}{2(\alpha + \gamma)}$$

973   *Unstable node or spiral:*

974   ▪ $|J| \geq 0 \Rightarrow \psi_1^* \leq \frac{\beta + \gamma + \delta}{2(\alpha + \gamma)} \Rightarrow \psi^* \leq \psi_1^*$

975   ▪ $tr(J) \geq 0 \Rightarrow \psi_2^* \geq \frac{1 + \gamma + \delta}{1 + 2\alpha + \gamma} \Rightarrow \psi^* \geq \psi_2^*$

976
$$\Rightarrow \frac{\beta + \gamma + \delta}{2(\alpha + \gamma)} \geq \psi^* \geq \frac{1 + \gamma + \delta}{1 + 2\alpha + \gamma}.$$

977   However, since from fitting results (table S1) $c_T = 0$, we conclude that

978    $\psi_1^* = \frac{\beta + \delta}{2\alpha}$ and $\psi_2^* = \frac{1 + \delta}{1 + 2\alpha}$.

979   Assuming $\Theta^* = \frac{r_t r_b}{c_b}$ and substituting $\alpha, \beta,$ and δ from Eqs. (S4),

980
$$\psi_2^* = \frac{1 + \frac{\Theta}{r_b}}{1 + \frac{2r_t}{c_b}} = \frac{r_b + \Theta}{r_b + 2\Theta^*}.$$

981   Since ξ and ψ are normalized, $\xi, \psi \geq 0$ and therefore $0 \leq \psi_1^*, \psi_2^* \leq 1$. Hence $\psi_2^* \leq 1$ resulting

982   in

983        $\Theta \leq 2\Theta^*.$ (S10)

984   Now, $\psi_1^* = \frac{\frac{\kappa\, k_b\, c_b}{r_b^2} + \frac{\Theta}{r_b}}{2\frac{r_t}{c_b}} = \frac{1}{2\Theta^*}\left(\frac{\kappa k_b r_t}{\Theta^*} + \Theta\right).$

985   From Eq. (S10)

986
$$\psi_1^* \leq \frac{1}{2\Theta^*}\left(\frac{\kappa k_b r_t}{\Theta^*} + 2\Theta^*\right) = 1 + \frac{\kappa k_b r_t}{2(\Theta^*)^2} > 1.$$

987   As a consequence, ψ_1^* is rejected and the stability analysis for the equilibrium points

988     $(\xi_{3,4}, \psi_{3,4}) = (1 - \psi_{3,4}, \psi_{3,4})$ can be updated as follows:

990   • *Stable node or spiral (Represents the chronic phase):*

991
$$\psi^* \leq \psi_2^* \Rightarrow \psi^* \leq \frac{1 + \gamma + \delta}{1 + 2\alpha + \gamma}.$$

992   • *Unstable node or spiral:*

993
$$\psi^* \geq \psi_2^* \Rightarrow \psi^* \geq \frac{1 + \gamma + \delta}{1 + 2\alpha + \gamma}.$$

995　**Supplementary figures**

CORRECTED

Fig. S1. ...ession of *S.*

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bacteria... al and T-cell

dynamics in time are the numerical solutions of the ODE system (Eqs. (1)-(2)). Treatments were

applied *in silico* at day 14 of infection (white bullet), namely when infection was already

chronic, by decreasing or increasing the fitted value of the parameter of interest (table S1) for a

perturbation window of 12 hours up to two days.

1010

1011

Fig. S2. Time of bacterial clearance for varying HK-doses and three values of T-cell

stimulatory parameter k_b *in silico*. Stimulation of T cells by HK *S. aureus* cells at day 14

happens with rate $k_b = 0.001509$ as defined during the fitting process (table S1). Since primary

exposure to *S. aureus* already occurs upon inoculation at day 0, HK *Streptococcus pyogenes* at

day 14 of infection stimulates the immune system at a weaker and slower rate compared to HK *S.*

aureus, assumed as $k_{b2} = k_b/2 = 0.0007545$ or $k_{b3} = k_b/3 = 0.000503$. Simulation of HK treatments

was done by adding the term $k_b B_d$ to the T-cell ODE at day 14 of infection for a perturbation

window of half day (*Materials and Methods*), where k_b the immunostimulatory parameter

varying for three different values (k_b, $k_b/2$, $k_b/3$) and B_d the HK-doses varying in the range

$[4 \times 10^7, 10^9]$. The estimated day of clearance was defined as the first time-point when bacterial

numbers <0.000001.

1023

1024 **Supplementary table**

1025

1026

1027 **Table S1. Model parameter values as used for model analysis.**

Parameter	Description	Value, [Confidence Interval]*	Unit
r_b	Bacterial growth rate (in the presence of innate immunity)	0.477	days^{-1}
$\varkappa$	Carrying capacity of bacteria	1.132×10^{8}	cells
c_b	Rate of bacterial containment by T cells (per cell)	$9.937 \times 10^{-7}, [8.65\times10^{-7}, 1.25\times10^{-6}]$	days^{-1}
r_t	T-cell proliferation rate (per cell)	$2.0955 \times 10^{-7}, [1.04\times10^{-7}, 2.94\times10^{-7}]$	days^{-1}
k_b	T-cell activation and recruitment rate	$0.001509, [0.0011, 0.0017]$	days^{-1}
c_T	Local T-cell suppression rate (per cell)	0	days^{-1}
Θ	Systemic MDSC-mediated suppression rate on T cells	$0.14393, [0.072, 0.18]$	days^{-1}
K_T	Carrying capacity of T cells	10^{8}	cells

1028 * In square brackets is the 95% confidence interval of the parameters as derived by a Markov Chain Monte Carlo

1029 version of Differential Evolution algorithm *(42)*.

1030

REFERENCES

1. L. Thomer, O. Schneewind, D. Missiakas, Pathogenesis of *Staphylococcus aureus* bloodstream infections. *Annu. Rev. Pathol. Mech. Dis.* **11**, 343-364 (2016).

2. S. D. Kobayashi, N. Malachowa, F. R. DeLeo, Pathogenesis of *Staphylococcus aureus* abscesses. *Am. J. Pathol.* **185**, 1518-1527 (2015).

3. B. L. Hahn, P. G. Sohnle, Direct translocation of staphylococci from the skin surface to deep organs. *Microb. Pathog.* **63**, 24-29 (2013).

4. S. V. Kazakova, J. C. Hageman, M. Matava, A. Srinivasan, L. Phelan, B. Garfinkel, T. Boo, S. McAllister, J. Anderson, B. Jensen, D. Dodson, D. Lonsway, L. K. McDougal, M. Arduino, V. J. Fraser, G. Killgore, F. C. Tenover, S. Cody, A clone of methicillin resistant *Staphylococcus aureus* among professional football players. *N. Engl. J. Med.* **352**, 468-475 (2005).

5. C. Ziegler, O. Goldmann, E. Hobeika, R. Geffers, G. Peters, E. Medina, The dynamics of T cells during persistent *Staphylococcus aureus* infection: from antigen-reactivity to in vivo anergy. *EMBO Mol. Med.* **3**, 652-666 (2011).

6. C. Tebartz, S. A. Horst, T. Sparwasser, J. Huehn, A. Beineke, G. Peters, E. Medina, A major role for myeloid-derived suppressor cells and a minor role for regulatory T cells in immunosuppression during *Staphylococcus aureus* infection. *J. Immunol.* **194**, 1100-1111 (2015).

7. M. Ost, A. Singh, A. Peschel, R. Mehling, N. Rieber, D. Hartl, Myeloid-derived suppressor cells in bacterial infections. *Front. Cell. Infect. Microbiol.* **6** (2016).

8. E. Medina, D. Hartl, Myeloid-derived suppressor cells in infection: a general overview. *J. Innate Immun.* **10**, 407-413 (2018).

1054   9. C. Agrati, A. Sacchi, V. Bordoni, E. Cimini, S. Notari, G. Grassi, R. Casetti, E. Tartaglia, E. Lalle, D'Abramo, C. Castilletti, L. Marchioni, Y. Shi, A. Mariano, J.-W. Song, J.-Y. Zhang, F.-S. Wang, C. Zhang, G. M. Fimia, M. R. Capobianchi, M. Piacentini, A. Antinori, E. Nicastri, M. Maeurer, A. Zumla, Expansion of myeloid-derived suppressor cells in patients with severe coronavirus disease (COVID-19). *Cell Death Differ.* **27**, 3196-3207 (2020).

10. E.-K. Vetsika, A. Koukos, A. Kotsakis, Myeloid-derived suppressor cells: major figures that shape the immunosuppressive and angiogenic network in cancer. *Cells* **8**, 1647 (2019).

11. C. Guo, F. Hu, H. Yi, Z. Feng, C. Li, L. Shi, Y. Li, H. Liu, X. Yu, H. Wang, J. Li, Z. Li, X.-Y. Wang, Myeloid-derived suppressor cells have a proinflammatory role in the pathogenesis of autoimmune arthritis. *Ann. Rheum. Dis.* **75**, 278-285 (2016).

12. O. Goldmann, E. Medina, *Staphylococcus aureus* strategies to evade the host acquired immune response. *Int. J. Med. Microbiol.* **308**, 625-630 (2018).

13. O. Goldmann, A. Beineke, E. Medina, Identification of a novel subset of myeloid-derived suppressor cells during chronic staphylococcal infection that resembles immature eosinophils. *J. Infect. Dis.* **216**, 1444-1451 (2017).

14. G. A. Noskin, R. J. Rubin, J. J. Schentag, J. Kluytmans, E. C. Hedblom, M. Smulders, E. Lapetina, E. Gemmen, The burden of *Staphylococcus aureus* infections on hospitals in the United States: an analysis of the 2000 and 2001 Nationwide Inpatient Sample Database. *Arch. Intern. Med.* **165**, 1756-1761 (2005).

15. E. Y. Klein, W. Jiang, N. Mojica, K. K. Tseng, R. McNeill, S. E. Cosgrove, T. M. Perl, National costs associated with methicillin-susceptible and methicillin-resistant *Staphylococcus aureus* hospitalizations in the United States, 2010–2014. *Clin. Infect. Dis.*

68, 22-28 (2018).

16. F. Cedeira, F. Cedeira, E. M. Pagano, G. Castañeda, R. Rivadera, Bilateral nephrectomy as

an extreme measure management for methicillin-resistant *Staphylococcus aureus* (MRSA):

a case report. *Urol. Case Rep.* **33**, 101373 (2020).

17. C. Hogea, T. Van Effelterre, C. J. Acosta, A basic dynamic transmission model of

Staphylococcus aureus in the US population. *Epidemiol. Infect.* **142**, 468-478 (2014).

18. E. McBryde, A. Pettitt, D.L.S. McElwain, A stochastic mathematical model of methicillin

resistant *Staphylococcus aureus* transmission in an intensive care unit: predicting the

impact of interventions. *J. Theor. Biol.* **245**, 470-481 (2007).

19. W.-S. Choi, N. Son, J.-I. Cho, I.-S. Joo, J.-A. Han, H.-S. Kwak, J.-H. Hong, S. H. Suh,

Predictive model of *Staphylococcus aureus* growth on egg products. *Food Sci. Biotechnol.*

28, 913-922 (2019).

20. A. Best, J. Jubrail, M. Boots, D. Dockrell, H. Marriott, A mathematical model shows

macrophages delay *Staphylococcus aureus* replication, but limitations in microbicidal

capacity restrict bacterial clearance. *J. Theor. Biol.* **497**, 110256 (2020).

21. S. K. Shukla, T. C. Carter, Z. Ye, M. Pantrangi, W. E. Rose, Modeling of effective

antimicrobials to reduce *Staphylococcus aureus* virulence gene expression using a two-

compartment hollow fiber infection model. *Toxins* **12**, 69 (2020).

22. M. Schmaler, N. J. Jann, F. Ferracin, R. Landmann, T and B cells are not required for

clearing *Staphylococcus aureus* in systemic infection despite a strong TLR2–MyD88-

dependent T cell activation. *J. Immunol.* **186**, 443-452 (2011).

23. H. K. Kim, V. Thammavongsa, O. Schneewind, D. Missiakas, Recurrent infections and

immune evasion strategies of *Staphylococcus aureus*. *Curr. Opin. Microbiol.* **15**, 92-99

(2012).

24. S. Khailaie, F. Bahrami, M. Janahmadi, P. Milanez-Almeida, J. Huehn, M. Meyer-Hermann, A mathematical model of immune activation with a unified self-nonself concept. *Front. Immunol.* **4**, 474 (2013).

25. C. H. Kim, Homeostatic and pathogenic extramedullary hematopoiesis. *J. Blood Med.* **1**, 13 (2010).

26. C. E. Heim, D. Vidlak, T. D. Scherr, J. A. Kozel, M. Holzapfel, D. E. Muirhead, T. Kielian, Myeloid-derived suppressor cells contribute to *Staphylococcus aureus* orthopedic biofilm infection. *J. Immunol.* **192**, 3778-3792 (2014).

27. C. Ma, T. Kapanadze, J. Gamrekelashvili, M. P. Manns, F. Korangy, T. F. Greten, Anti-Gr-1 antibody depletion fails to eliminate hepatic myeloid-derived suppressor cells in tumor-bearing mice. *J. Leukoc. Biol.* **92**, 1199-1206 (2012).

28. S. Ostrand-Rosenberg, P. Sinha, Myeloid-derived suppressor cells: linking inflammation and cancer. *J. Immunol.* **182**, 4499-4506 (2009).

29. J. S. Ayres, Surviving COVID-19: a disease tolerance perspective. *Sci. Adv.* **6**, eabc1518 (2020).

30. K. A. Anderson, J. W. McAninch, Renal abscesses: classification and review of 40 cases. *Urology* **16**, 333-338 (1980).

31. T. J. Yoon, J. Y. Kim, H. Kim, C. Hong, H. Lee, C.-K. Lee, K. H. Lee, S. Hong, S.-H. Park, Anti-tumor immunostimulatory effect of heat-killed tumor cells. *Exp. Mol. Med.* **40**, 130-144 (2008).

32. A. d. A. Cassado, M. R. D'Império Lima, K. R. Bortoluci, Revisiting mouse peritoneal macrophages: heterogeneity, development, and function. *Front. Immunol.* **6**, 225 (2015).

33. E. E. B. Ghosn, A. A. Cassado, G. R. Govoni, T. Fukuhara, Y. Yang, D. M. Monack, K. R.

Bortoluci, S. R. Almeida, L. A. Herzenberg, L. A. Herzenberg, Two physically,

functionally, and developmentally distinct peritoneal macrophage subsets. *Proc. Natl.*

Acad. Sci. U.S.A **107**, 2568-2573 (2010).

34. E. Takenaka, A. Van Vo, Y. Yamashita-Kanemaru, A. Shibuya, K. Shibuya, Selective

DNAM-1 expression on small peritoneal macrophages contributes to CD4+ T cell

costimulation. *Sci. Rep.* **8**, 1-8 (2018).

35. S. Holtfreter, J. Jursa-Kulesza, H. Masiuk, N. Verkaik, C. de Vogel, J. Kolata, M. Nowosiad,

L. Steil, W. van Wamel, A. van Belkum, U. Völker, S. Giedrys-Kalemba, B. M. Broker,

Antibody responses in furunculosis patients vaccinated with autologous formalin-killed

Staphylococcus aureus. Eur. J. Clin. Microbiol. Infect. Dis. **30**, 707 (2011).

36. D. Missiakas, O. Schneewind, *Staphylococcus aureus* vaccines: deviating from the carol.

J. Exp. Med. **213**, 1645-1653 (2016).

37. V. Vyas, T. Endy, A Rare case of prostatic and bilateral renal abscesses caused by

community-acquired methicillin-resistant *Staphylococcus aureus* infection. *Cureus* **12**

(2020).

38. T. Fiedler, T. Köller, B. Kreikemeyer, *Streptococcus pyogenes* biofilms—formation,

biology, and clinical relevance. *Front. Cell. Infect. Microbiol.* **5**, 15 (2015).

39. J. Stanford, C. Stanford, J. Grange, Immunotherapy with *Mycobacterium vaccae* in the

treatment of tuberculosis. *Front Biosci.* **9**, 1701–1719 (2004).

40. M. I. Gröschel, S. A Prabowo, P.-J. Cardona, J. L. Stanford, T. S. Van der Werf.

Therapeutic vaccines for tuberculosis—a systematic review. *Vaccine.* **32**, 3162–3168

(2014).

41. M. Jonsson, S. Arvidson, S. Foster, A. Tarkowski, Sigma factor B and RsbU are required

for virulence in *Staphylococcus aureus*-induced arthritis and sepsis. *Infect. Immun.* **72**,

6106-6111 (2004).

42. C. J. Ter Braak, A markov chain monte carlo version of the genetic algorithm differential

evolution: easy bayesian computing for real parameter spaces. *Stat. Comput.* **16**, 239-249

(2006).

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