J. Math. Anal. Appl. ••• (••••) •••–•••

Contents lists available at ScienceDirect

Journal of Mathematical Analysis and Applications

www.elsevier.com/locate/jmaa

# Boundedness of solutions to a virus infection model with saturated chemotaxis

Bingran Hu [a], Johannes Lankeit [b,*]

[a] School of Information and Technology, Dong Hua University, 200051 Shanghai, PR China
[b] Institut für Mathematik, Universität Paderborn, 33098 Paderborn, Germany

ARTICLE INFO

*Article history:*
Received 29 May 2018
Available online xxxx
Submitted by V. Radulescu

*Keywords:*
Boundedness
Classical solvability
Chemotaxis
Virus infection model

ABSTRACT

We show global existence and boundedness of classical solutions to a virus infection model with chemotaxis in bounded smooth domains of arbitrary dimension and for any sufficiently regular nonnegative initial data and homogeneous Neumann boundary conditions. More precisely, the system considered is

$$\begin{aligned} u_t &= \Delta u - \nabla \cdot \left(\frac{u}{(1+u)^\alpha}\nabla v\right) - uw + \kappa - u, \\ v_t &= \Delta v + uw - v, \\ w_t &= \Delta w - w + v, \end{aligned}$$

with $\kappa \geq 0$, and solvability and boundedness of the solution are shown under the condition that

$$\begin{cases} \alpha > \frac{2}{3}, & \text{if} \quad n = 1 \\ \alpha > \frac{1}{2} + \frac{n^2}{6n+4}, & \text{if} \quad 2 \leq n \leq 4 \\ \alpha > \frac{n}{4}, & \text{if} \quad n \geq 5. \end{cases}$$



## 1. Introduction

In theoretical immunology it is not uncommon to model the evolution of a virus population by a system of ODEs ([18,7]). These models already yield key insights into infections ([18]; for clinical advice based on models of this type, see e.g. [4]), but by their very nature are ill-suited for gaining spatial information concerning the distribution of infected cells. For this reason it makes sense to include spatial dependence

* Corresponding author.
*E-mail addresses:* hubingran@foxmail.com (B. Hu), jlankeit@math.uni-paderborn.de (J. Lankeit).

https://doi.org/10.1016/j.jmaa.2018.08.019
0022-247X/

into the model (for examples of resulting PDEs, like reaction-diffusion systems, in biology and chemistry and related mathematical techniques, see e.g. [6] and references therein) and in an attempt to better understand the formation of patterns on the onset of an HIV infection, in [19] the following model was proposed (where $\kappa$, $\alpha$, $\beta$, $d_\chi$, $d_v$ and $d_w$ are suitable positive constants):

$$\begin{aligned} u_t &= \Delta u - d_\chi \nabla \cdot (u \nabla v) + \kappa - (\kappa - 1) uw - u, \\ v_t &= d_v \Delta v + \alpha(uw - v), \\ w_t &= d_w \Delta w + \beta(v - w). \end{aligned} \tag{1}$$

Herein, $u$ and $v$ stand for the population density of uninfected and infected cells, respectively, and $w$ is used to describe the concentration of virus particles. All three of the populations move around randomly (i.e. diffuse) and decay. The virus is also produced by infected cells and its presence causes healthy cells to be converted into infected cells. Healthy cells are, moreover, produced with a constant rate $\kappa$. In addition, in chemotactic response to cytokines emitted by infected cells healthy cells move toward high concentration of those. The corresponding cross-diffusive term in (1) is the key contributor to mathematical challenges already the global existence analysis of (1) poses.

In contrast to the aggregation phenomena described by the famous classical Keller–Segel type models ([12], see also the surveys [2,9,8]), in the present setting a blow-up of solutions is not to be expected according to the biological observations. Motivated from the desire to hence exclude the possibility of blow-up, in [19, Sec. 8], the chemotaxis term was substituted by a term essentially of the form of $\nabla \cdot (\frac{u}{1+u} \nabla v)$. In line with this reasoning, it is the purpose of this article to investigate whether weaker changes can have a similar consequence: If we employ chemotaxis terms of the form $\nabla \cdot (\frac{u}{(1+u)^\alpha} \nabla v)$, can we still guarantee (global existence and) boundedness of solutions? More accurately: for which values of $\alpha$ is it possible?

It seems appropriate to note that weakening the cross-diffusion is not the only possible change to (1) that can ensure global existence and boundedness of solutions:

In [3], Bellomo and Tao replaced the conversion term $uw$ by the term $\frac{uw}{1+au+bw}$ of Beddington–deAngelis type ([1,5]) with positive parameters $a$, $b$, and succeeded in proving global existence and boundedness of solutions to the resulting model, as well as their stabilization as $t \to \infty$ for small basic reproduction numbers. For a closely related system, see also [21].

From a mathematical perspective, one of the most significant differences between (1) and the well-studied Keller–Segel type models is the presence of a nonlinear production term ($+uw$ in the second equation). While also chemotaxis-consumption models (see e.g. [20,15]), popular in the context of studies concerning the interaction between chemotactically active bacteria and their fluid environment (cf. e.g. [14] and references therein), feature a nonlinear term, that term there only appears as sink, not as source term, thus favourably factoring into boundedness considerations.

The mathematically most inconvenient difference to the spatially homogeneous setting apparently lies in the chemotaxis term. Let us briefly contemplate why in its presence the source term of the second equation seems more troublesome: In the ODE setting, a Lyapunov function has been found (in [13]), essentially solving questions of boundedness and long-time behaviour. Attempts to employ a corresponding functional (or even only a functional involving the same term for the first component) will result in the necessity to deal with a term of the form $\int_\Omega \frac{\nabla u \cdot \nabla v}{u}$, which in part can be estimated by the contribution of the diffusion term, but then requires something to cancel $\int_\Omega |\nabla v|^2$. This we can easily provide by adding $\int_\Omega v^2$ to the functional, whereupon the nonlinear production term raises its head as $\int_\Omega uvw$ (cf. (27)) and can barely be controlled by $-\int_\Omega v^2$ and an analogue stemming from the third equation, if $u$ is replaced by a bounded function, cf. [3] (which basically is what the change to this term in [3] does). If we want to retain the factor $u$, i.e. the true nonlinearity of the term $+uw$, which was originally taken from the standard SIR model (cf. [19, Sec. 2]), however, similar estimates seem no longer possible.

Please cite this article in press as: B. Hu, J. Lankeit, Boundedness of solutions to a virus infection model with saturated chemotaxis, J. Math. Anal. Appl. (2018), https://doi.org/10.1016/j.jmaa.2018.08.019