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A REACTION-DIFFUSION SYSTEM OF A PREY WITH THREE GENOTYPES AND A PREDATOR*

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Abstract The global existence and the asymptotic behavior of solutions to a reaction-diffusion system of a prey with three genotypes and a predator are considered. We establish the evolvement of a pure strain. Here an assumption concerning the diffusion is needed.

Key Words Reaction-diffusion system; predator-prey model; genotype; asymptotic behavior.

Classifications 35K57, 92D10, 92D40.

We consider a reaction-diffusion system of a prey with three genotypes and a predator

$$\begin{cases} \dfrac{\partial u_1}{\partial t} = d_1\Delta u_1 + \dfrac{\left(u_1+\frac{1}{2}u_2\right)^2}{u^2}B(u) - (D(u)+vP_1(u,v))\dfrac{u_1}{u} \\ \dfrac{\partial u_2}{\partial t} = d_2\Delta u_2 + \dfrac{\left(u_1+\frac{1}{2}u_2\right)\left(u_3+\frac{1}{2}u_2\right)}{u^2}B(u) - (D(u)+vP_2(u,v))\dfrac{u_2}{u} \\ \dfrac{\partial u_3}{\partial t} = d_3\Delta u_3 + \dfrac{\left(u_3+\frac{1}{2}u_2\right)^2}{u^2}B(u) - (D(u)+vP_3(u,v))\dfrac{u_3}{u}, \quad (x,t)\in\Omega\times R^+ \\ \dfrac{\partial v}{\partial t} = d_4\Delta v + v\Big(-S+k\displaystyle\sum_{i=1}^{3}\frac{u_i}{u}P_i(u,v)\Big) \end{cases} \tag{1}$$

with initial data and homogeneous Neumann boundary value condition

$$u_i(x,0)=u_{i0}(x),\quad i=1,2,3;\quad v(x,0)=v_0(x),\quad x\in\Omega \tag{2}$$

$$\frac{\partial u_i}{\partial n}\Big|_{\partial\Omega\times R^+}=0,\quad i=1,2,3;\quad \frac{\partial v}{\partial n}\Big|_{\partial\Omega\times R^+}=0 \tag{3}$$

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Here the population densities of the predator and the prey with three genotypes AA, Aa, and aa are denoted by $v(x,t)$, $u_1(x,t)$, $u_2(x,t)$ and $u_3(x,t)$, $u = \sum_{i=1}^{3} u_i$, with diffusion constants d_i, $i = 1,2,3,4$. Ω is a bounded domain in R^n. $B(u)/u$ and $D(u)/u$ are the intrinsic birth and death rates of the entire population of the prey. The coefficients of $D(u)$ show the principle that the three genotypes share the same death rate in proportion to their relative numbers. $\frac{u_i}{u} P_i(u,v)$, $i = 1,2,3$, are three predator functional responses. Gene a is recessive while gene A is dominant, and hence $P_1(u,v) = P_2(u,v)$. The original ODE model was studied by H.I. Freedman and Paul Waltman in [1, 2], where the following assumptions were made

(H-1) $B(u) \geq 0, \quad D(u) \geq 0, \quad B(0) = D(0) = 0, \quad B'(0) > D'(0) \geq 0,$

$$v > 0, \quad P_i(u,v) = 0 \Leftrightarrow u = 0, \quad P_{iu}(u,v) > 0, \quad i = 1,2,3$$

There exists a unique positive number K such that

(H-2)
$$B(K) = D(K) > 0 \qquad \text{and} \qquad B'(K) < D'(K)$$

(H-3)
$$0 < \sum_{i=1}^{3} u_{i0} < K$$

(H-4)
$$P_1(u,v) = P_2(u,v) \geq 0, \quad \inf_{\substack{0<u\leq K \\ 0<v\leq M}} \frac{P_1(u,v) - P_3(u,v)}{u} \geq \delta(M) > 0$$

(H-5)
$$\begin{cases} u'(t) = B(u) - D(u) - vP_3(u,v) \\ v'(t) = v(-S + kP_3(u,v)) \end{cases} \tag{4}$$

has a globally (in the first quadrant) asymptotically

stable critical point (u^*, v^*)

or

(H-4)$'$
$$P_1(u,v) = P_2(u,v) \geq 0, \quad \inf_{\substack{0<u\leq K \\ v^*\leq v\leq M}} \frac{P_3(u,v) - P_1(u,v)}{u} \geq \delta(M) > 0$$

(H-5)$'$
$$\begin{cases} u'(t) = B(u) - D(u) - vP_1(u,v) \\ v'(t) = v(-S + kP_1(u,v)) \end{cases} \tag{5}$$

has a globally asymptotically stable critical point (u^*, v^*)

in the first quadrant

The assumption (H–4) (or (H–4)$'$)shows that u_3 (or u_1 and u_2) has an advantage in its susceptibility to the predator.