GLOBAL DYNAMICS OF A PLANT-HERBIVORE MODEL WITH TOXIN-DETERMINED FUNCTIONAL RESPONSE*

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Abstract. Studies of the dynamics of plant-herbivore interactions that explicitly address model robustness are important in assessing uncertainty. Hence, identifying conditions that guarantee the global stability of plant-herbivore systems can be used to assess the rationale involved in, for example, the selection of management and/or control decisions. The model used here to illustrate these issues is naturally capable of supporting complex dynamics; the result of the explicit incorporation of plant toxicity in the functional response. Unlike the traditional Holling Type 2 functional response, the selected toxin-determined functional response loses its monotonicity at high levels of plant toxicity. Systems with nonmonotone functional responses are capable of supporting multiple interior equilibria and bistable attractors. Therefore, identifying conditions that guarantee global stability is not only mathematically challenging but important to scientists. We are able to find necessary and sufficient condition on the nonexistence of a closed orbit via the transformation of the model to a new equivalent system. The Poincaré–Bendixson theorem is used to show that the existence of a unique interior equilibrium point guarantees its global asymptotical stability *whenever* it is locally asymptotically stable. It is shown that, whenever there are multiple interior equilibria, the local stability of the "first interior equilibrium" implies model bistability. In other words, the phase space is characterized by two subregions: the basins of attraction of two stable equilibria, the interior and the boundary equilibria.

Key words. plant-herbivore interaction, toxin-determined functional response, global stability, bistability

1. Introduction. Plant-herbivore interactions can be complex, and the source of this complexity in ordinary differential equation (ODE) models is traced to the nature of the nonlinearity used to model the herbivore's functional response [9, 10]. It is known that ODE models of prey-predator or consumer-resource dynamics using the Holling Type 2 response can generate a Hopf bifurcation, and therefore the system may exhibit oscillatory behaviors. Most existing models for mammalian browsing involving traditional functional response models (e.g., Lundberg [13, 14], Augustine, Frelich, and Jordan [1], Spalinger and Hobbs [19], Cohen, Pastor, and Moen [3], Pastor et al. [16], Hobbs et al. [8]) tend not to explicitly include the effect of plant toxicity on plant-herbivore interactions. Many plant species "defend" themselves against maximal herbivory through the release of secondary chemicals (toxins) that, for example, in some mammal-plant systems determine satiation [7, 2, 15, 18, 4]. We have introduced toxin-determined functional response models (acronym TDFRM) in order to establish a modeling framework where the effect of plant toxicity on the dynamics of plant-herbivore interactions can be assessed.

Our previous results show that the TDFRM can support more complex dynamics, including Hopf and homoclinic bifurcations, than the Holling Type 2 functional re-

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