Mathematical Modeling of the Dynamics of *Salmonella* Cerro Infection in a US Dairy Herd PREM CHAPAGAIN, Department of Population Medicine and Diagnostic Sciences, Cornell University, Ithaca, NY 14853, USA, JO ANN VAN KESSEL, JEFFREY KARNS, Environmental Microbial Safety Laboratory, Agricultural Research Service, USDA, Beltsville, MD 20705, USA, DAVID WOLFGANG, Animal Diagnostic Laboratory, Pennsylvania State University, PA 16802, USA, YNTE SCHUKKEN, YRJO GROHN, Department of Population Medicine and Diagnostic Sciences, Cornell University, Ithaca, NY 14853, USA — Salmonellosis has been one of the major causes of human foodborne illness in the US. The high prevalence of infections makes transmission dynamics of *Salmonella* in a farm environment of interest both from animal and human health perspectives. Mathematical modeling approaches are increasingly being applied to understand the dynamics of various infectious diseases in dairy herds. Here, we describe the transmission dynamics of *Salmonella* infection in a dairy herd with a set of nonlinear differential equations. Although the infection dynamics of different serotypes of *Salmonella* in cattle are likely to be different, we find that a relatively simple SIR-type model can describe the observed dynamics of the *Salmonella enterica* serotype Cerro infection in the herd.

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