Virulence of broad- and narrow-host-range Salmonella enterica serovars in the streptomycin-pretreated mouse model.

Abstract:

Salmonella enterica subspecies I serovars are common bacterial pathogens causing diseases ranging from enterocolitis to systemic infections. Some serovars are adapted to specific hosts, whereas others have a broad host range. The molecular mechanisms defining the virulence characteristics and the host range of a given S. enterica serovar are unknown. Streptomycin pretreated mice provide a surrogate host model for studying molecular aspects of the intestinal inflammation (colitis) caused by serovar Typhimurium (S. Hapfelmeier and W. D. Hardt, Trends Microbiol. 13:497-503, 2005). Here, we studied whether this animal model is also useful for studying other S. enterica subspecies I serovars. All three tested strains of the broad-host-range serovar Enteritidis (125109, 5496/98, and 832/99) caused pronounced colitis and systemic infection in streptomycin pretreated mice. Different levels of virulence were observed among three tested strains of the host-adapted serovar Dublin (SARB13, SD2229, and SD3246). Several strains of host restricted serovars were also studied. Two serovar Pullorum strains (X3543 and 449/87) caused intermediate levels of colitis. No intestinal inflammation was observed upon infection with three different serovar Paratyphi A strains (SARB42, 2804/96, and 5314/98) and one serovar Gallinarum strain (X3796). A
second serovar Gallinarum strain (287/91) was highly virulent and caused severe colitis. This strain awaits future analysis. In conclusion, the streptomycin pretreated mouse model can provide an additional tool to study virulence factors (i.e., those involved in enteropathogenesis) of various S. enterica subspecies I serovars. Five of these strains (125109, 2229, 287/91, 449/87, and SARB42) are subject of Salmonella genome sequencing projects. The streptomycin pretreated mouse model may be useful for testing hypotheses derived from this genomic data.