

Research program IZS VE 02/16

Insight into factors influencing the ecological success of zoonotic *Salmonella enterica* by coupling genomic data with in vitro phenotypic assays

Project coordinator: Lisa Barco

Salmonella spp. are the second most frequent zoonotic agents responsible of human cases in the European Union (EU) and represent a major challenge for food safety. There is much evidence suggesting that only a few *Salmonella* serovars among those commonly isolated from animal and food samples are responsible for the vast majority of human infection cases, but, at the same time, it is unclear why these common serovars might have greater ecological success. A combination of different factors specific to each serovar, such as the presence of virulence plasmids, the cell surface structure, the presence of flagellin genes and the *Salmonella* pathogenicity islands can be associated with human *Salmonella* infections.

The main objective of the present proposal is to deeply unravel the eco-evolutionary mechanisms enabling some *Salmonella* serovars to be the most common in human infections. This will lead to a better understanding of the epidemiology of *Salmonella* virulence and eventually to the design of more efficient control actions at animal level.