



# The road of genetics

On a global scale, illness arising from bacteria-contaminated food is a primary threat to humans. Of the causative pathogens, Salmonella bacteria are the most common and are responsible for distinct clinical presentations.

Dr. Andrea Moreno-Switt, Director of the Veterinary Medicine Center of the Faculty of Ecology and Natural Resources at the Universidad Andrés Bello, is working on a research project to characterize genetic markers from distinct strains of Salmonella. This information will facilitate the early identification of outbreak origin, thereby preventing further consumption of contaminated foods and, ultimately, reducing the cases of disease.

This project was awarded “investigator start-up” funding from Fondecyt in 2014 and was ranked first in the Animal Health category. While research data are obtained using available technologies, the proposed methods for data analysis are novel. “It is currently possible to sequence entire genomes for less than US\$100. What is paramount is being able to understand the generated data and apply it to public health,” notes Dr. Moreno-Switt.

Moreover, Dr. Moreno-Switt explains that this study is being carried out under the hypothesis that phages, or viruses that exclusively infect bacteria, are differentially distributed among the animals from which Salmonella have been isolated. For example, Salmonella and its phages isolated from dairy cows would present differences compared to strains from pigs.

Currently, this project has collected more than 100 different bacteriophages that will be sequenced in the near future together with multiple Salmonella strains. “Once this investigation concludes, we will have a collection of data on bacteria and phages that could serve as a starting point for distinct biotechnological applications,” states Dr. Moreno-Switt.

Finally, Dr. Moreno-Switt mentions that, “In parallel, we are performing prevalence and characterization studies on certain bacterial strains that could give rise to new epidemiological studies and risk analyses. The information provided by our project will be a valuable support to health monitoring systems by proposing a method that will avoid infections and restrict future outbreaks.”