**HELICOBACTER PYLORI** is a species of bacterium that was discovered in the 1980s, and was quickly shown to be associated with gastritis – inflammation of the stomach lining. It infects a high proportion of the global population, somewhere between 20 and 70 per cent, and causes disease in around 10 per cent of those it infects. About 1 per cent of individuals who suffer from disease caused by *H. pylori* will go on to develop cancer because of the infection – which is why the World Health Organization has classified it as a class 1 carcinogen.

But *H. pylori* really a human pathogen? This intriguing question is at the heart of an extensive research programme being pursued by Dr Luisa F Jiménez-Soto and her colleagues at Ludwig Maximilian University of Munich in Germany. Jiménez-Soto hypothesises that the bacterium is simply part of the benign microflora of the stomach. Under this theory, the medical symptoms that are associated with *H. pylori* infection are caused when imbalances in the stomach environment cause the bacteria to alter their behaviour, and induce an immune response.

It has long been known that there are many different strains of *H. pylori* that are associated with different effects on the human system. In the late 1980s, clinical studies had already demonstrated that strains with the *cagA* gene were associated with severe forms of gastric disease – and, for the past 20 years or so, most research on this species has focused on the *cagA* and *vacA* genes and the toxins they produce.

**THE MORE, THE MERRIER**

Some studies, however, have indicated that when a patient has more than one strain of *H. pylori* in their stomach, the disease they are affected by is less severe – and this is where Jiménez-Soto and her colleagues come in. In their own tests, the Munich scientists have shown that the infection of a cell culture with multiple bacterial strains blocks or reduces the toxic damage caused by *CagA*.

To gain a greater insight into this phenomenon, they are now collaborating with the Fundacion Santa Fe de Bogotá and the Universidad de los Andes in Colombia to investigate how often the Colombian population is infected with different types of the bacteria. Finally, the researchers are also conducting *in vitro* experiments in their lab at the Max von Pettenkofer Institute to discover the molecular mechanisms behind the patterns they are observing in human health.