

Paris, June 17, 2009

Press release

**A major breakthrough in understanding the virulence
of the *Listeria* bacterium in humans**

A study carried out by Institut Pasteur researchers in cooperation with Inserm and INRA reveals how *Listeria monocytogenes*, the bacterium responsible for listeriosis, changes the activity of its entire genome to shift from an inoffensive to a pathogenic state. New types of gene products (RNAs) have been discovered. This research, which appeared in the advanced online edition of the journal *Nature*, will be published in the journal on June 18, 2009.

Listeriosis is a bacterial food-borne infection caused by *Listeria monocytogenes*. This bacterium is widespread in nature (in water, soil, plants and animals) and can contaminate a large number of food products. It can lead to gastro-enteritis, brain infections and in pregnant women to fetal infections and abortions. It is fatal in 20 to 30% of cases.

Institut Pasteur researchers from the Bacteria-Cell Interactions Unit (Inserm Unit 604, INRA USC2020), led by Pascale Cossart, in cooperation with other groups from the Institut Pasteur (Microbes and Host Barriers Group, Inserm Avenir 604; *In Silico* Genetics Unit, Institut Pasteur Genopole) and a Swedish team, have demonstrated how this inoffensive bacterium in the environment becomes a dangerous pathogen in its mammal host.

Using new DNA micro-arrays, which enable the entire genome of the bacterium to be analyzed (genes and inter-gene regions), the scientists compared the activity of the genome in its inoffensive state and its pathogenic state. To do this, they analyzed all the gene products in the bacterium (RNAs) and studied their regulation when the bacterium grows in the environment or in the infected host (in the intestine or blood). The set of all bacterial RNAs in a genome at a given time is known as the transcriptome.

The results of this comprehensive "transcriptomic" analysis firstly showed that when the bacterium reaches the intestine, and then the bloodstream, it radically changes the activity of its genome and successively activates various groups of virulence genes. 50 small RNAs were also identified. Some are absent from the non-pathogenic species *Listeria innocua* and are differentially expressed during infection; at least two of these small RNAs contribute to the virulence of *Listeria*

monocytogenes. The researchers also discovered a series of new types of regulatory RNAs (for example long non coding antisense RNAs) which certainly also exist in other bacteria.

This work paves the way for a full understanding of *Listeria*'s adaptation mechanisms when the bacterium moves from the environment to the infected host. They especially open up new possibilities in the highly competitive field of RNA regulation, in all species of the living world.

For further information

Please read the Institut Pasteur listeriosis fact sheet (in French) at

<http://www.pasteur.fr/ip/easysite/go/03b-00000j-0hk/presse/fiches-sur-les-maladies-infectieuses/listeriose>

Source

The Listeria transcriptional landscape from saprophytism to virulence, **Nature**, June 18, 2009.

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<http://www.nature.com/nature/journal/vaop/ncurrent/abs/nature08080.html>

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