

**Doctoral position at Anses Laboratory for Food Safety in Maisons-Alfort (France)  
starting 1<sup>st</sup> November 2013**

**Title**

Detailed characterisation of *Listeria monocytogenes* strains of food origin

**Recruiting unit**

Bacterial Characterization and Epidemiology (CEB) Unit at the ANSES Maisons-Alfort Laboratory for Food Safety .

This unit is made up with 7 technicians, 8 scientists and 1 post PhD student. This unit is specialized in characterization of food-borne pathogens such as *Salmonella*, *Listeria monocytogenes*, *Staphylococcus aureus* and *Bacillus cereus*.

The PhD student will be assigned to the Molecular typing team. This team is one of the research teams that make up the European Union Reference Laboratory (EURL) and the French national reference laboratory (NRL) for *Listeria monocytogenes*.

**Context**

*Listeria monocytogenes* (*Lm*) is a ubiquitous, intracellular bacterium that causes severe foodborne illness. Many studies have revealed the great diversity of *Lm* strains, in terms of genetic make-up as well as virulence level. A small number of epidemiologically important clonal complexes have been described in a recent study conducted on a large collection of strains isolated from human clinical cases. However, there is little data on the distribution of these clones for strains isolated from the basic food production sectors. Given its reference activities, the CEB unit has amassed a large collection of *Lm* food strains collected in France over the past 20 years and has created a molecular database (under BioNumerics software) with detailed epidemiological information and the associated typing data for each isolate. Preliminary results obtained during a previous research project conducted jointly with the Pasteur Institute revealed a clonal complex that appears to be mainly associated with strains that have only been found in food. This clonal complex has been observed in only very few strains isolated from clinical cases.

**Objectives of the project**

In the interest of analysing and managing foodborne health risks, it is important to evaluate the potential of this clonal complex to cause foodborne illness and determine whether the strains in this clonal complex threaten public health. We therefore propose to characterise this clonal complex more precisely — both phenotypically and genotypically. The results will be compared to those obtained for other food strains belonging to the same clonal complexes as the clinical strains that caused actual cases of listeriosis.

In regard to methodology, we will use powerful and innovative molecular typing tools, such as whole genome sequencing. The strains will then be sequenced at the Technical University of Denmark (DTU). The DTU has developed a bioinformatic pipeline associated with the project entitled “Centre of Genomic Epidemiology” (CGE). In addition, DTU is also one of the lead institutes within the “Global Microbial Identifier (GMI)” typing all microorganisms for global surveillance.

The analysis and the comparison of the strains’ genomes in close collaboration between ANSES (Maisons-Alfort, Boulogne sur Mer and Ploufragan) and DTU will help to identify the genetic factors that may explain the observed differences in ecological distribution and virulence. The results of this project will be published in international, peer-reviewed journals and disseminated at national and international conferences.

This multidisciplinary project will be carried out in close collaboration with the various teams of the Laboratory for Food Safety of as well as the French Pork and Pig Institute (IFIP) (France), Anses Ploufragan (France), and INRA Loire Valley Centre (France).

**Keywords:** *Listeria monocytogenes*, food production sectors, public health risks, PFGE, MLST, whole genome sequencing, bioinformatics analysis.

**Activities :**

At ANSES Laboratory for Food Safety(18 months) :

- Phenotypic characterisation tests and virulence tests
- Genotypic characterisation (pulsed field gel electrophoresis (PFGE) and multilocus sequence typing (MLST))
- Use of the CEB Unit molecular database under BioNumerics software

At DTU (18 months) :

- Genomic characterisation of food strains by whole genome sequencing
- Use of the CGE pipelines with new-generation high-throughput sequencers (Miseq or relevant sequence platforms)
- Bioinformatics analysis such as genomic comparison e.g. blast atlas etc..
- Assembly of de novo sequences and exploration of assembled sequences, interpretation of biological sequences and screening for markers of interest

**Applicant :**

Skills in microbiology, molecular biology and bioinformatic are essential. The English speaking level of the applicant will be taken into account. His/her ability to write English will be carefully evaluated. Skills in working under Quality Assurance scheme will be appreciated. The cv has to be written in English.

**Deadline for submission:** 15<sup>th</sup> august 2013

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