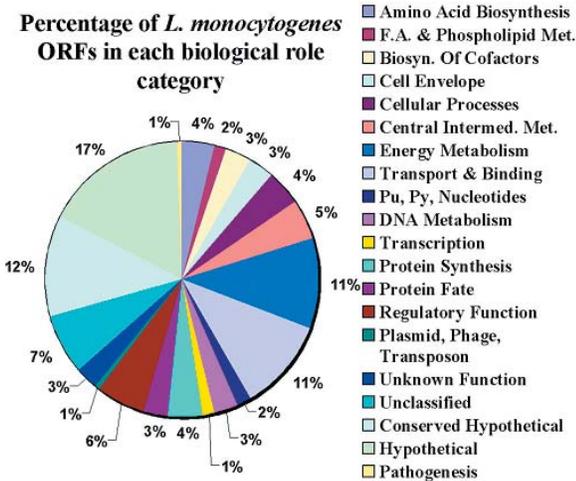
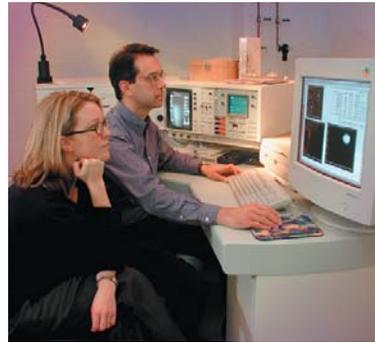


## Genomic Analyses of Foodborne Pathogens: Focus on *Listeria monocytogenes*

### Program Background

Our programmatic focus is to study the genes and proteins that support the viability, persistence, and virulence of *L. monocytogenes* associated with animals, food processing environments, foods, and humans.

*L. monocytogenes* is a considerable health threat to humans and an appreciable economic burden to consumers and the food industry.



To gain insight on how this bacterium persists and causes illness, the complete genome of a serotype 4b strain was sequenced. The genomic sequence is currently being annotated to localize known genes.

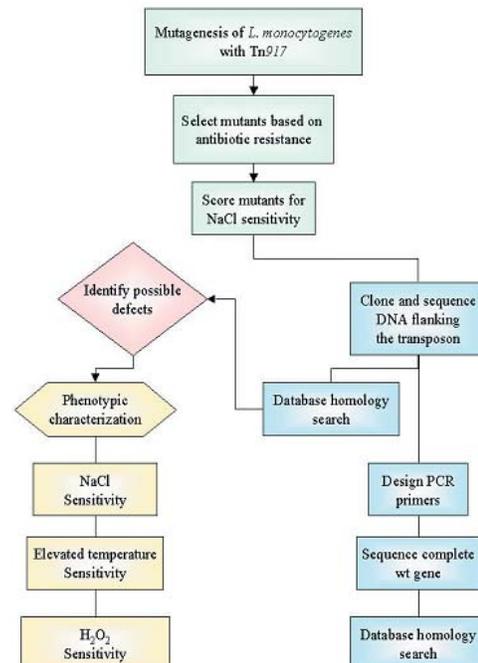
The results from this program will be useful to our stakeholders in industry, academia, and regulatory agencies.

### Research Objectives

The *L. monocytogenes* sequence information will be used to study global gene expression. Incorporating sequence information into the design and optimization of nucleic acid arrays and chips will facilitate studies to identify genes expressed or repressed in response to external cues such as those likely to be encountered by this bacterium in the environment, foods, and humans.

The information generated will also be useful for studying the population genetics of this bacterium in various substrates, including foods, and for molecular tracking and epidemiological studies of this bacterium throughout the food chain.

It is also anticipated that the information gained will promote the development of more rapid and less costly diagnostic methods. It will also assist investigators studying microbial systematics, vaccine development, and analyses of resistance to antimicrobial, toxins and/or disinfectants.



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## Impact

The benefits of this initiative will be many and far reaching. The results will allow the food industry and regulators to better utilize science-based decision-making regarding *L. monocytogenes* and other microbes of food safety concern.

In a broader context, this program will allow us to construct a working library of bioinformatic tools and resources, to enhance our existing capabilities, interests, and expertise.

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