

## PORK SAFETY

**Title:** Bioinformatics Based Genome Comparison of Six *Salmonella* spp. to Provide a Foundation for the Development of Reliable Molecular Epidemiological Methods.  
**NPB #03-132**

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### II. Abstract:

*Salmonella* research is the top priority for the industry especially related to pre-harvest reduction of pathogens with potential public health significance. The pre-harvest food safety research for *Salmonella* proposed here falls under the category of control strategy. The research proposed here is highly relevant and applied in nature. Without the groundwork, foundation and benefit of comprehensive genetic and bioinformatic analyses many shotgun approaches to molecular epidemiology based upon methods that are applicable to other microorganisms for instance will ultimately fail when used for *Salmonella* spp. Using the genome of *Salmonella typhimurium* LT2 as a backbone we have successfully aligned the entire genomes of between 6 and 10 additional *Salmonella* spp. strains/serotypes. This data has been made available on the internet <http://199.133.147.108/salmonella/salmonella.html> by clicking on the *Salmonella* multiple alignment viewers. Additional genetic information is still be generated for several of these strains of *Salmonella* and we will continue to curate this information and perform whole genome comparisons, generate publicly available analysis tools, and provide this information over the internet to the research community. In addition during our own analysis we have identified many regions of these genomes that show potential as molecular epidemiology targets. It is this type of region that taken individually or in groups tend to have the strongest potential for use as powerful and sensitive molecular epidemiology tools. Based upon our current analysis we may have identified regions that would allow for molecular serotyping at the very least which would be useful for source tracking. This project makes available to food safety scientists a powerful comparative database that can be used to develop epidemiological methods that are specific to *Salmonella* spp. rather than attempting to adapt used with other organisms. *Salmonella* spp. because of how closely related the serovars tend to be presents a significant challenge to the development and applicability of molecular epidemiological methods. This project is the primary and quite simply the only logical foundation step that will ever result in the development of a method that fulfills all the requirements of a superior molecular epidemiological method for *Salmonella* spp.

*These research results were submitted in fulfillment of checkoff funded research projects. This report is published directly as submitted by the project's principal investigator. This report has not been peer reviewed*

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