

Variation in *Salmonella* Enteritidis RAPD-PCR Patterns May Not Be Due to Genetic Differences

Demetrius L. Mathis, Roy D. Berghaus, Margie D. Lee, and John J. Maurer
Contact Address: berghaus@uga.edu

Important Findings

Because pulsed-field gel electrophoresis (PFGE) has limited utility in distinguishing between clonal *Salmonella* Enteritidis isolates, random amplified polymorphic DNA (RAPD) polymerase chain reaction (PCR) has been recommended as an alternative molecular fingerprinting tool. This study found that duplicate testing of *Salmonella* Enteritidis isolates produced RAPD DNA patterns that ranged in similarity between 61.5 and 100%. These results indicate that the repeatability of RAPD-PCR is insufficient to distinguish genetic differences among related and unrelated *Salmonella* Enteritidis isolates.

Significance of Findings

Salmonella Enteritidis is a leading cause of gastroenteritis associated with consumption of contaminated poultry meat and eggs. The study objective was to determine whether increasing PCR stringency would improve the repeatability of RAPD DNA patterns based on assessment of target sites within the genome. However, the repeatability of RAPD was poor despite the stringent conditions of the PCR performed in this study.

Additional Information

There are an estimated 9.4 million cases of foodborne illness each year in the United States caused by known pathogens, of which 11% are attributed to *Salmonella*. Retail poultry products account for 17% of salmonellosis outbreaks and, from a public health perspective, this is particularly concerning because poultry consumption has increased globally.

Of the potentially thousands of *Salmonella enterica* serotypes associated with human illnesses, Enteritidis and Typhimurium

account for 64% of all *Salmonella* infections reported worldwide. *Salmonella* Enteritidis was documented as a significant contributor to human illnesses in the 1980s, and the source of infections has been linked to the consumption of grade A table eggs since the 1940s. A recent *Salmonella* Enteritidis outbreak in 2010, associated with 1,939 human illnesses, was also tied to consumption of grade A eggs.

Reducing poultry contamination with *Salmonella* Enteritidis requires an understanding of *Salmonella* transmission within the food production system. Birds can acquire *Salmonella* from their environment, feed, or through contact with other infected birds or animals. However, *Salmonella* Enteritidis can also be vertically transmitted from hen to offspring because the organism can colonize the ovary and reproductive tract of hens, resulting in contamination of the egg interiors. Therefore, the epidemiology of *Salmonella* Enteritidis within the poultry production system can be complex, requiring a subtyping tool that can reliably detect the source of contamination.

Although there are many methods available for subtyping bacterial species that exhibit a range of genome similarities, PFGE, has become the preferred strain-typing tool by the Centers for Disease Control and Prevention for identifying foodborne outbreaks. It has also proven useful in understanding *Salmonella* transmission dynamics within integrated poultry production systems. However, PFGE is unsatisfactory for subtyping *S. Enteritidis* because of its clonal nature; most isolates are indistinguishable in their PFGE profile. Phage typing is currently used in an effort to discriminate strain differences. There are at least 30 different *Salmonella* Enteritidis phage types (PT). The most frequently identified phage types in the United States are PT4, PT8, and PT13; this reduces the usefulness of phage typing in tracing back the source of an outbreak when multiple suppliers are involved. A good molecular subtyping tool is expected to discriminate among isolates that have no epidemiologic link and to confirm isolates belonging to the same source or outbreak.

Copyright © 2011, American Association of Avian Pathologists, Inc. 1933-5334 online

La Variación en los Patrones RAPD-PCR de *Salmonella* Enteritidis Puede que no se Deban a Diferencias Genéticas

Demetrius L. Mathis, Roy D. Berghaus, Margie D. Lee, y John J. Maurer
Dirección para contactar: berghaus@uga.edu

Hallazgos Importantes

Debido a que la electroforesis en gel en campo pulsátil (PFGE, por sus siglas en inglés) tiene una utilidad limitada para distinguir entre aislamientos clonales de *Salmonella* Enteritidis, se ha recomendado como una herramienta alternativa la reacción en cadena de la polimerasa (PCR como por sus siglas en inglés) ADN polimórfico amplificado al azar (RAPD, por sus siglas en inglés) para la toma de huella o perfil molecular. El estudio encontró que pruebas duplicadas de aislamientos de *Salmonella* Enteritidis produjeron patrones de ADN mediante RAPD que tuvieron rangos similares entre 61.5 y

100%. Estos resultados indicaron que la repetibilidad de la RAPD-PCR es insuficiente para distinguir diferencias genéticas entre aislamientos de *Salmonella* Enteritidis relacionados y no relacionados.

Relevancia de los Hallazgos

La *Salmonella* Enteritidis es la causa principal de la gastroenteritis asociada con el consumo de carne de aves y de huevos que están contaminados. El estudio tuvo el objetivo de determinar si el aumento de rigor de la PCR mejoraría la repetibilidad de los patrones de ADN por RAPS con base en la evaluación de sitios blanco dentro del genoma. Sin embargo, la repetibilidad del RAPD fue mala debido a las estrictas condiciones de la PCR realizada en este estudio.

Copyright © 2011, American Association of Avian Pathologists, Inc. 1933-5334 online