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Strain Differentiation Among Listeria Monocytogenes Isolates Gregory Thomas Jeffers, 1998

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Development of Molecular Subtyping Databases to Improve Control of Listeria Monocytogenes Eric Brandon Fugett, 2006 Listeria monocytogenes is a foodborne pathogen that can cause a serious foodborne disease, listeriosis, which may result in abortion, meningitis, and septicemia. The high hospitalization and mortality rates of listeriosis warrant continued research efforts to reduce the transmission of L. monocytogenes to humans. Molecular subtyping techniques, which can be used to differentiate bacteria beyond the species level, facilitate the identification and tracking of L. monocytogenes subtypes throughout the food chain. Pulsed-field gel electrophoresis is a rapid and highly discriminatory molecular subtyping method currently used by public health and regulatory agencies to identify and track outbreaks of foodborne disease and link outbreak related cases to suspected vehicles. Although PFGE facilitated outbreak recognition and response has been successful in reducing the number of listeriosis associated fatalities, additional large-scale analysis of subtype data is needed to develop a better understanding of L. monocytogenes ecology and further reduce the incidence of foodborne listeriosis. To this end, we subtyped 495 L. monocytogenes isolates

from human clinical cases, foods, ruminant farms, and urban and natural environments using two-enzyme (AscI and ApaI) PFGE to better understand L. monocytogenes PFGE type diversity and distribution. We found that while L. monocytogenes is a genetically diverse organism, nine PFGE types were significantly associated with certain sources, and two PFGE types were specific to a single processing facility each. Conversely, nine PFGE types were geographically widespread and isolated from multiple sources, indicating that large molecular subtyping databases are necessary to facilitate epidemiological investigations by identifying the distribution patterns of PFGE types that cause outbreaks. To meet this need, we developed PathogenTracker, a publicly available molecular subtyping database that will facilitate storage and large-scale analysis of different L. monocytogenes subtype data. Data in PathogenTracker can be gueried through a variety of options, including DNA sequence and banding pattern-based searches (e.g., ribotype, PFGE type). This database also allows for the creation of individualized summary tables and permits simple statistical analysis of summary table data. Currently populated with subtype data for over 6,000 L. monocytogenes isolates, PathogenTracker will facilitate more rapid listeriosis outbreak detection and source tracking, development of a better understanding of L. monocytogenes transmission and ecology, and definition of specific characteristics for L. monocytogenes subtypes isolated from different sources populations. We also developed a freely available standard L. monocytogenes reference strain collection, organized into a diversity set (25 isolates representing 25 PFGE types) and an outbreak set (21 isolates representing nine listeriosis outbreaks), which has not been previously available. In combination with inclusion of these isolates in

PathogenTracker, which includes continuously updated information on strain characteristics and peer-reviewed references that utilized specific isolates, this strain collection provides a unique resource that will aid efforts to further improve our ability to reduce human foodborne listeriosis through development of improved diagnostic procedures and intervention strategies. In addition, this strain collection provides a unique resource for basic and applied studies on the physiology, ecology, evolution, and pathogenesis of L. monocytogenes. (Abstract).

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- Advantages of eBooks Over Traditional Books
- 2. Identifying FSL
 - Exploring Different Genres
 - Considering Fiction vs. Non-Fiction
 - Determining Your Reading Goals
- 3. Choosing the Right eBook Platform
 - Popular eBook Platforms
 - Features to Look for in an FSL
 - User-Friendly Interface
- 4. Exploring eBook Recommendations from FSI.
 - Personalized Recommendations
 - FSL User Reviews and Ratings
 - FSL and Bestseller Lists
- Accessing FSL Free and Paid eBooks
 - ∘ FSL Public Domain eBooks
 - FSL eBook Subscription Services
 - FSL Budget-Friendly Options
- 6. Navigating FSL eBook Formats
 - ∘ ePub, PDF, MOBI, and More

- FSL Compatibility with Devices
- FSL Enhanced eBook Features
- 7. Enhancing Your Reading Experience
 - Adjustable Fonts and Text
 Sizes of FSL
 - Highlighting and Note-Taking FSL
 - Interactive Elements FSL
- 8. Staying Engaged with FSL
 - Joining Online Reading Communities
 - Participating in Virtual Book Clubs
 - Following Authors and Publishers FSL
- 9. Balancing eBooks and Physical Books FSL
 - Benefits of a Digital Library
 - Creating a Diverse Reading Collection FSL
- 10. Overcoming Reading Challenges
 - Dealing with Digital Eye Strain
 - Minimizing Distractions

- o Managing Screen Time
- 11. Cultivating a Reading Routine FSL
 - o Setting Reading Goals FSL
 - Carving Out Dedicated Reading Time
- 12. Sourcing Reliable Information of FSL
 - Fact-Checking eBook Content of FSI.
 - Distinguishing Credible Sources
- 13. Promoting Lifelong Learning
 - Utilizing eBooks for Skill Development
 - Exploring Educational eBooks
- 14. Embracing eBook Trends
 - Integration of Multimedia Elements
 - Interactive and Gamified eBooks

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