

Research Project Proposal
Academic year 2017-2018

Project Nº 25
Title: Molecular characterization of <i>Listeria monocytogenes</i> strains from clinical isolates.
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<p>Summary</p> <p><i>Listeria monocytogenes</i> is a food borne pathogen that can cause invasive diseases in humans and farm animals, including meningitis, fetal loss, sepsis, and febrile gastroenteritis. Although <i>L. monocytogenes</i> is an uncommon human pathogen, it has a disproportionate share of the food borne disease burden. <i>L. monocytogenes</i> is a diverse species and has been typed using several procedures to examine the epidemiology and population genetics. Serotyping is a classic subtyping method with limited discriminatory power (thirteen serotypes of <i>L. monocytogenes</i> are recognized). Pulsed Field Gel Electrophoresis (PFGE) provides higher discrimination than serotyping and is often considered the standard subtyping method. Multi-locus sequence typing (MLST) based on nucleotide sequences of housekeeping genes has also been shown to be highly discriminatory for <i>L. monocytogenes</i>, with an added advantage that it provides unambiguous results. Over the last ten years, our team has compiled a collection of 70 strains of <i>L. monocytogenes</i> (clinical origin). The main objective of this study is the development of the MLST technique, to characterize the collection of <i>Listeria</i> strains that we have, which will allow us to know if these strains are related to each other, thus establishing the existence of outbreaks of infection.</p> <p>References</p> <p>Schlech WF 3rd: Foodborne listeriosis. <i>Clin Infect Dis</i> 2000, 31:770–775</p> <p>Ragon M, Wirth T, Hollandt F, Lavenir R, Lecuit M, Le Monnier A, Brisse S: A new perspective on <i>Listeria monocytogenes</i> evolution. <i>PLoS Pathog</i> 2008, 4:e1000146.</p>