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Establishing and characterizing a Brazilian collection of newborn meningitis-causing *Escherichia coli*

Simone Iahnig Jacques¹, Tobias Weber Martins¹, Raul Simon Batista¹, Luís Fernando dos Santos², Joice Reis Pedreira³, Christian de Alencar Siebra⁴, Rita de Cássia Silveira⁵, Caroline Pissetti⁶, and Fabiana Horn¹

(monijac@gmail.com)

1 – Universidade Federal do Rio Grande do Sul, Departamento de Biofísica, Porto Alegre, RS.

2 – Centro de Bacteriologia, Instituto Adolfo Lutz, SP.

3 – Laboratório de Microbiologia Clínica, Faculdade de Farmácia, Universidade Federal da Bahia, Salvador, BA.

4 – Setor de Bacteriologia, Laboratório Central do Estado do Paraná, São José dos Pinhais, PR.

5 – Hospital de Clínicas de Porto Alegre, Serviço de Neonatologia, Porto Alegre, RS.

6 – Centro de Diagnóstico de Sanidade Animal, BR153, km 110, Concórdia, SC.

Extraintestinal pathogenic *Escherichia coli* (ExPEC) are responsible for various infections outside the gastrointestinal tract in humans, farm animals, and pets. Newborn meningitis-causing *E. coli* (NMEC), one of the ExPEC sub-pathotypes, has in the last 30 years emerged as the major cause of neonatal meningitis among premature neonates with very low birth weight (<1.5 kg). Because all we know about NMEC epidemiology comes from North America and Europe, the aim of this work is to establish the first collection of genomically characterized NMEC strains from Brazil. Until now, we gathered 59 NMEC isolated from the cerebrospinal fluid of ill patients: 12 isolates from São Paulo (Instituto Adolfo Lutz), 38 from Bahia (UFBA), eight from Paraná (LACEN), and a recent one from Porto Alegre (HCPA). The phylogenetic analysis by pulsed-field gel electrophoresis (PFGE) of the isolates (excluding the one from HCPA) revealed five pairs of clones, four among the UFBA and one among the IAL, and a varied profile of the remaining isolates. DNA of the isolates were extracted using a ThermoFisher kit and sent to Illumina sequencing. The genomes of the 12 isolates from São Paulo have already been characterized (manuscript in preparation), and sequencing of the isolates from Bahia and Paraná ($n = 46$) is under way at INTA – CIMMYT (Argentina-Mexico). The resulting Illumina NovaSeq 6000 files will be assembled by the *de novo* approach, the genomes will be annotated using Prokka, and the core and the pangenome will be identified with the Roary software. Genomes will be analysed *in silico* for their phylogenetic status, serotype, multilocus sequence type (MLST) and ExPEC-associated virulence genes, and will be compared to the genomes of ExPEC model strains. Meanwhile, we used the yeast agglutination assay to test the production of type 1 fimbriae, a key ExPEC virulence factor: among the 12 IAL isolates, six agglutinated; among the UFBA, 20; and among LACEN-PR, five. The phenotype of yeast agglutination will be confronted with the presence (or absence) of the *fim* operon in the genomes of the isolates. Accordingly, production of siderophores, tested in Chrome Azurol S agar plates, will be confronted with the presence of known siderophore-encoding genes in their genomes. This will be the first collection of characterized NMEC strains in Brazil. Because of our similar social-economical conditions, our data may serve as a parameter for future studies on NMEC also in other South American and African countries.

Palavras-chave: *E. coli* K1, Neonatal Meningitis, Neonatal Meningitis-causing *E. coli*, NMEC, PFGE, Whole Genome Sequence

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