TITLE: MICROBIAL ECOLOGY IDENTIFICATION AND CHARACTERIZATION RELATED TO THE PRESENCE OR ABSENCE OF *Listeria monocytogenes* AND *Salmonella* sp. FROM DAIRY INDUSTRY – A CASE STUDY

AUTHORS: TADIELO, L.E.¹; SANTOS, E.A.R.²; SCHMIEDT, J.A.²; BRUGEFF, E.C.L.²; CERQUEIRA-CÉZAR, C.K.¹; PANTOJA, J.C.F.¹; PEREIRA, M.O.³; PEREIRA, J.G.¹; PINTO, J.P.A.N.¹; BERSOT, L.S.²

INSTITUTIONS: ¹UNIVERSIDADE ESTADUAL PAULISTA, *CAMPUS* DE BOTUCATU (UNESP), FACULDADE DE MEDICINA VETERINÁRIA E ZOOTECNIA (FMVZ), BOTUCATU, SP (DISTRITO DE RUBIÃO JR, S/N, CEP 18618-970, BOTUCATU - SÃO PAULO, BRASIL); ²UNIVERSIDADE FEDERAL DO PARANÁ, DEPARTAMENTO DE CIÊNCIAS VETERINÁRIAS, SETOR PALOTINA, PALOTINA, PR (RUA PIONEIRO, 2153, JARDIM DALLAS, CEP 85950-000, PALOTINA - PARANÁ, BRASIL). ³UNIVERSIDADE DO MINHO. *CAMPUS* DE GUALTAR. CENTRO DE ENGENHARIA

"UNIVERSIDADE DO MINHO, *CAMPOS* DE GUALTAR, CENTRO DE ENGENHA BIOLÓGICA (CEB), BRAGA, PORTUGAL (CEP 4710–057, BRAGA - PORTUGAL).

ABSTRACT:

There is limited information about microbial ecology as responsible for tolerance to cleaning processes and its relationship with pathogenic microorganisms in food industry. The objective of this case study was to identify the presence of Listeria monocytogenes and Salmonella sp. on different surfaces of a dairy industry and comment the relationship between the microbiota and the presence of these pathogens. A hundred and sixty samples were collected from surfaces of equipment and utensils after the pre-operational cleaning process for detection of L. monocytogenes and Salmonella sp., through ISO 11.290-1 (ISO, 2017) and ISO 6579 (ISO, 2017) standard methods, respectively. Of these samples, 12.5% (n=20) were submitted to DNA extraction, sequencing and bioinformatics analysis based on the taxonomic classification of V3-V4 region in 16S RNA gene for identification and characterization of their microbial ecology. L. monocytogenes was detected on the surface of cheese vat (0.6%) and Salmonella sp. on the plastic maturing surface of Parmesan cheese (0.6%). Assessing the accompanying microbial ecology of these pathogens, 33 bacterial genera composed by Kocuria sp. (48%), Staphylococcus sp. (33.5%), Enterococcus sp. (9.6%), Moraxella sp. (3.1%) and Rothia sp. (2.3%) were detected. Moreover, 58 bacterial species were characterized, being Kocuria kristinae (48%), Staphylococcus equorum (17.9%), S. aureus (15.6%), Enterococcus faecalis (9.6%), Moraxella osloensis (3.1%) and Rothia endophytica (2.3%) the main ones. In the absence of pathogens, 44 genera were identified, with a greater predominance of Pseudomonas sp. (78.2%), Enterobacter sp. (15.2%) and Cobetia sp. (3%). Among the 81 characterized species, the main ones were Pseudomonas putida (77.4%), Enterobacter cloacae (13.4%) and Cobetia marina (2.9%). The results presented in this study indicate the existence of pathogens on essential surfaces inside the dairy industry, as well as the identification of bacterial genera and species that are able to interfere not only in the formation and maintenance of biofilms but also in the persistence of these microorganisms. Additionally, we presented relevant information regarding the control of pathogenic microorganisms on surfaces in the dairy industry, which can be used to improve hygiene protocols.

Keywords: food industry; foodborne pathogens; microbiome; 16S RNA gene

Development agency: Process nº 2020/01529-9, Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP), Project CAPES-PRINT AUXPE 88881.310254/2018-01 and Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq).