

GENETIC SIMILARITY PROFILE OF CRONOBACTER SPP. ISOLATES FROM A WHEY CONCENTRATION AND DRYING INDUSTRY

Cleiton Margatto Aloisio¹, Rafaela de Melo Tavares², Caio Fialho de Freitas², Amanda Rosário Alvim Santos², Layza Mylena Pardinho Dias¹, Luis Augusto Nero², Luciano dos Santos Bersot¹

¹. Universidade Federal do Paraná, Setor Palotina, Palotina/Paraná, Brasil

². Universidade Federal de Viçosa, Viçosa/Minas Gerais, Brasil

Cronobacter spp. are pathogenic microorganisms capable of surviving adverse environmental conditions. They have already been isolated from several food categories, including seasonings, fruits, vegetables, cereals, instant soups, and mainly dry mixes. Currently in Brazil, *Cronobacter* spp. is used as a mandatory requirement only in infant formulas. Whey powder and its derivatives have been used in several products as an ingredient to promote dairy flavor, and applied in fillings, cake mixes, ice creams, sports nutrition, infant formulas, and formulas for immunosuppressed patients. Knowing that whey in its different protein concentrations is used as the main ingredient in several ready-to-eat products, *Cronobacter* spp. can be considered a microorganism of great relevance for monitoring in the production chain. As the natural environment of *Cronobacter* spp. is not known, its omnipresence in different environments makes it difficult to control this pathogen in food production areas. Therefore, understanding the subtyping of this microorganism becomes necessary for the epidemiological understanding of the occurrence of strains of *Cronobacter* spp. throughout food production processes. The objective of this study was to identify the degree of clonal diversity of *Cronobacter* spp. isolated from a whey concentration and drying industry from December 2022 to October 2023. The 40 isolates obtained during the study were subjected to pulsed-field gel electrophoresis (PFGE) as described by PulseNet (Centers for Disease Control and Prevention, Atlanta, GA, USA) for species of *Cronobacter* spp. Electrophoresis was conducted following CHEF-DR III conditions. The dendrogram was created using the unweighted pair group method with arithmetic mean (UPGMA) with Dice coefficient and analyzed using BioNumerics software version 6.6, (Applied Maths, Sint-Martens-Latem, Belgium). The 40 isolates of *Cronobacter* spp. subjected to PFGE analysis were characterized into 13 groups with a similarity level of 94.5%. Despite the high genetic diversity observed among the isolates, it was possible to identify isolates with highly similar restriction profiles during the sampling period: isolates 8, 17 and 28 - sampled in the months of Dec./2022, Jan. and Feb/2023 respectively (CIP water samples and equipment surfaces); isolate 11 - sampled in Dec/2022 (CIP water sample), 12 and 13 - Jan/2023 (product samples), 27 (equipment surface sample) and 32 (CIP water) - Feb/2023 and 36 - Oct./2023 (product sample); isolates 9 and 10 - sampled in Dec./2022 (CIP water samples), 16 and 19 (equipment surface samples), 21 and 22 (CIP water samples) - Jan./2023, 24 and 25 (samples of product) and 26 (equipment surface sample) - Feb/2023, 38 and 40 (product samples) - Oct/2023. The similarity between the isolates obtained from different stages of the process and in different months indicates potential reintroduction of these subtypes or temporary persistence in different areas of the whey concentration and drying factory. Failures in the hygiene process of equipment and processing environments, as well as failures in the hygiene procedures of food handlers can contribute to cross-



contamination and the development of *Cronobacter* spp. biofilms, justifying the results obtained. Future stages of this study, such as the identification of the species of the isolates, will allow us to understand the pathogenicity of these microorganisms.

Agradecimentos: CAPES (Coordenação de Aperfeiçoamento de Pessoal de Nível Superior), CNPq (Conselho Nacional de Desenvolvimento Científico e Tecnológico).

