



Deciphering the Pangenome of *Bacillus Sporothermodurans*, An Emerging Highly Heat Resistant Spore-Former

Rodney Owusu-Darko¹, Mushal Allam², Arshad Ismail², Carlos A. S. Ferreira³, Silvia Dias de Oliveira³, Elna Buys¹

¹University of Pretoria, Pretoria, South Africa. ²National Institute for Communicable Diseases, Johannesburg, South Africa. ³Pontifícia Universidade Católica do Rio Grande do Sul, Porto Alegre, Brazil

Abstract

Bacillus sporothermodurans is an emerging highly heat resistant endospore-forming bacterium that affects the quality of ultra-high temperature (UHT) milk products. *B. sporothermodurans* has been isolated in UHT processed milk products, evaporated milk, and other food products including soy, canned soups, and Indian curry. Diverse strains of *B. sporothermodurans* are known to have different heat resistance in UHT milk and other food products, with high heat resistance known to be clonal and because of mobile genetic elements. There is recent suggestion for the reclassification of this highly heat resistant spore former owing to its genetic variation. In this study, we have described for the first time the pangenome of *B. sporothermodurans*, with the inclusion of strains belonging to both the highly heat resistant spore (HRS) and non-HRS clones.

Whole genome sequencing was determined on the Illumina MiSeq platform, with subsequent genome and subsystem-based annotations undertaken by PGAP and RAST respectively. The core and accessory genomes were undertaken using Spine and AGEnt respectively.

The core genome covers 81.9% (69.9 – 92.2%) of the *B. sporothermodurans* pangenome, with the remaining 18% (7.8 – 30.1%) representing the accessory genome. Approximately 44% of the subsystem categories for the core genome was attributed to amino acid, carbohydrates and protein metabolism with 50% of the accessory genome accounting for DNA metabolism, membrane transport and mobile genetic elements. The core/pangenome ratio of 55% suggests that *B. sporothermodurans* has an open pangenome with sympatric characteristics. The presence of a complete prophage in strain B4102, which incidentally exhibited three times as much clustered regularly interspaced short palindromic repeats (CRISPRs) was identified.

The repertoire of subsystem categories and of genes in the core and accessory genomes show a pattern of MGE related systems, based predominantly in the accessory genome of *B. sporothermodurans* strains in the present study. The pangenome of *B. sporothermodurans* will assist in the deciphering of genes and their contribution to genetic variation and resultant phenotypic responses.

Biography: Rodney Owusu-Darko

Rodney Owusu-Darko is a Postdoctoral scientist at the Department of Consumer and Food Sciences at the University of Pretoria (UP) SA, under the supervision of Prof. Elna Buys (UP). Rodney received his B.Sc. (Hons) in Nutrition and Food Science from the University of Ghana, Legon and an M.Sc. in Food Biotechnology from the University of Strathclyde in Glasgow. His current research focuses on using Next-Generation Sequencing to identify to characterise microbes, of importance to the food industry. Rodney is especially interested in heat resistance and of the various mobile genetic elements that confer heat resistance to spore formers. His research also focuses on the thermal inactivation of these spore formers. Rodney's research hopes to shed light on the emergence of sub-specie heat resistance amongst spore-forming *Bacillus* species. Rodney is also very much interested in the application of Metagenomics as it applies to food safety, quality, and human health.