Comparative genome sequences analysis of Bacillus sonorensis 112 isolated from a primary starter used for production of Sudanese traditional bread, Gergoush, and B. licheniformis DSM13T

Adimpong, David Bichala; Sørensen, Kim I.; Nielsen, Dennis Sandris; Rasmussen, Thomas B.; Thorsen, Line; Derkx, Patrick M.F.; Jespersen, Lene

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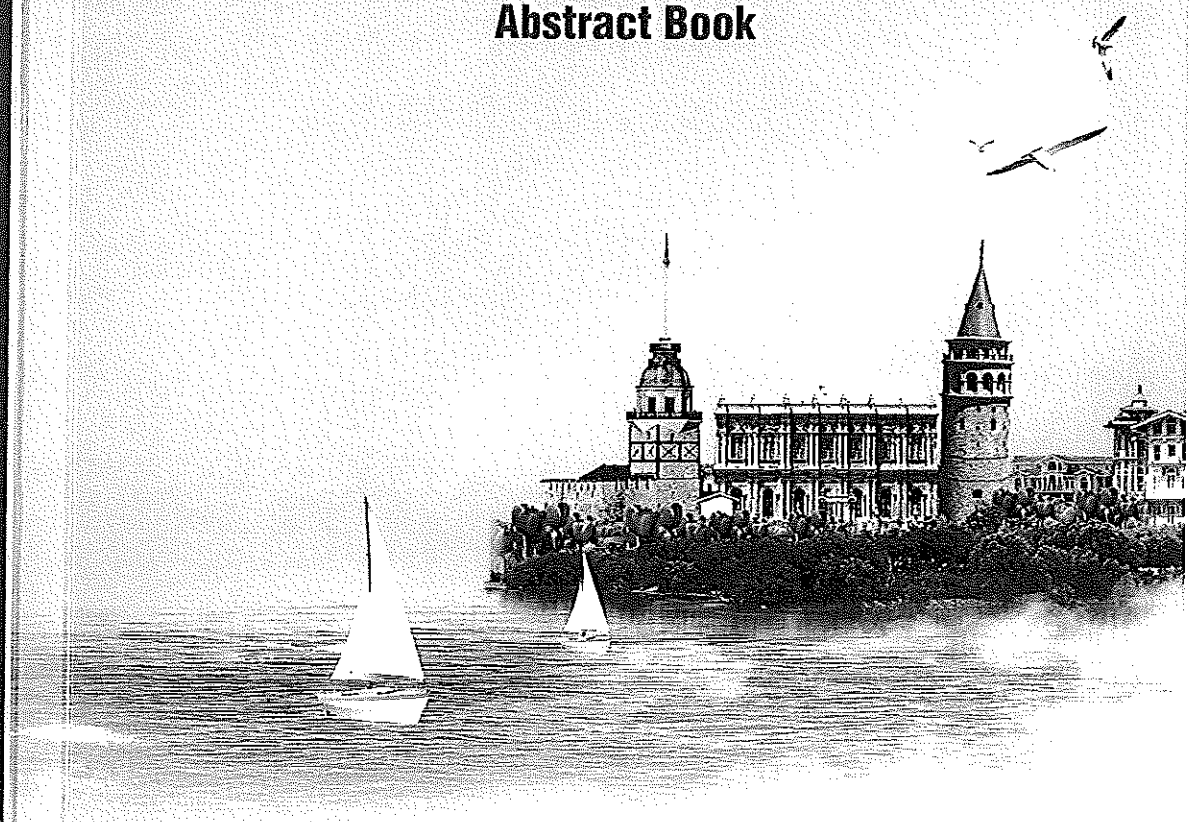

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P-392

Comparative genome sequences analysis of *Bacillus sonorensis* l12 isolated from a primary starter used for production of Sudanese traditional bread, Gergoush, and *B. licheniformis* DSM13T

David B. ADIMPONG[1], Kim I. SØRENSEN[2], Dennis S. NIELSEN[1], Thomas B. RASMUSSEN[2], Line THORSEN[1], Patrick M.F. DERKX[2]
LENE JESPERSEN (SE POSTER FOR PROOF)
1: University of Copenhagen, Food Science, Frederiksberg C, DENMARK
2: Chr-Hansen, Discovery, Hørsholm, DENMARK
Corresponding author: dadimpong@life.ku.dk

Bacillus sonorensis was first isolated from the Sonoran Desert soil. Taxonomic studies have indicated is closely related to *B. licheniformis*. The two species can be phenotypically distinguished based on colonies pigmentation, but in general little is known about the genomic, evolutionary and phylogenetic status of *B. sonorensis* species. The closely related species *B. licheniformis* is exploited industrially for large-scale production of many enzymes such as proteases, amylases and lipopeptide surfactants. These enzymes are used; to produce detergents, for liquefaction of starch, for oil recovery and in the paper and textile industries. *B. sonorensis*, *B. licheniformis* and *B. subtilis* species strains were isolated in high numbers from a primary starter used for the production of African traditional bread; Gergoush in Sudan. An earlier study on the antimicrobial susceptibility profiles of these species strains to frequently used antibiotics indicated that *B. sonorensis* and *B. subtilis* species were susceptible to clindamycin whereas *B. licheniformis* species strains were intrinsically resistant. To further enhance our limited knowledge and to explore the technological relevance of *B. sonorensis* species, strain L12 from our previous study was completely genome sequenced using the Illumina Hiseq platform. The sequences were assembled into contigs using CLC genomic workbench (CLC Aarhus, Denmark) which was also used to determine the nucleotides sequences statistics. Transfer RNA genes and rRNA operons were predicted using rRNAscan-SE and RNAmmer programs respectively. Open reading frames (ORFs) were predicted using IOGMA® software version 3.8 (Genostar Bioinformatics Software & Services©). Auto-annotation of the predicted ORFs was based on BLASTP analysis against GenBank database. Evolutionary dynamics of strain L12 and *B. licheniformis* DSM13T were further observed using the Mauve software for Multiple Genome Alignment. The latest data on the complete genome sequence of *B. sonorensis* strain L12 and comparative analysis with *B. licheniformis* DSM13T will therefore be presented. To our knowledge, this is the first genome sequence of a *B. sonorensis* strain. The information obtained from the genome of this species will provide valuable insight for both evolutionary and phylogenetic aspects of these two closely related species.

P-393

The effect of hea genetically modified

Ozge OZGEN ARUN, K

1: Istanbul University, Veterina TURKEY
Corresponding author: oarun

Genetically modified organisms of food safety area. Although tl since they were first commercia rapidly. Because of this strong r on labelling of GMOs and GM(enforce the labelling of food developing reliable methods for food science area since early 20 which is based on detection of r novel DNA are used for this pu conditions ELISA methods are n methods are proved to be the mo because of the degradation effec yield, there are limits of PCR m well. The aim of the present stu detection of GM soya in cookies. of GM soya were prepared and ba heat on DNA quality of these s sequence which is a novel sequenc present in both GM and non GM s GMO screening PCR is signific presence of practically low levels c