



## Domestication Of Pantoea Sp. Through Genome-Scale Metabolic Modelling And A Genetic Toolbox

van der Heijden, Lies; van der Maas, Lucas Nicolaas Ludovic; Gorter de Vries, Philip Johannes; Özdemir, Emre; Ingemann Jensen, Sheila

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## POSTER PRESENTATIONS

### [58] DOMESTICATION OF PANTOEA SP. THROUGH GENOME-SCALE METABOLIC MODELLING AND A GENETIC TOOLBOX

Lies van der Heijden\*,<sup>1</sup>, Lucas van der Maas,<sup>1</sup>, Philip de Vries,<sup>1</sup>, Emre Özdemir,<sup>2</sup>, Sheila I. Jensen,<sup>3</sup>

<sup>1</sup> Technical University of Denmark, Dtu Biosustain, Kgs. Lyngby, Denmark, <sup>2</sup> Technical University of Denmark, Denmark, <sup>3</sup> Technical University of Denmark, Novo Nordisk Foundation Center for B, Kgs. Lyngby, Denmark

The genus *Pantoea* comprises a versatile group of Gram-negative bacteria belonging to the family of *Erwiniaceae*. The species in this genus have been isolated from several environments, such as water, soil, plants and animals. The ubiquity and versatility of *Pantoea* isolates make it an ideal genus for exploring niche-specific adaptation and opportunism, as well as for developing commercially relevant therapeutic, agricultural and environmental products.

Our fundamental understanding of *Pantoea*, however, remains limited due to the absence of a standardized genetic toolbox for this genus. Additionally, only approximately 30 genome-sequenced strains are available to date and no genome-scale metabolic model is available.

In this study, a *Pantoea* strain was isolated from soil samples and characterized as a newly discovered strain; *Pantoea* sp.. To further develop *Pantoea* strains into fully optimized microbial chassis, an in-depth, systems-level understanding of metabolism is required, for which genome-scale metabolic models are essential. We have developed a draft genome-scale metabolic model using CarveMe (Machado et al., 2018). The model is curated using additional data derived from wet-lab experiments.

Additionally, Synthetic biology and metabolic engineering require the ability to alter the genome of the strain in question. Limited research has been conducted in strain engineering tools specific for *Pantoea* strains. Preliminary experimental results are promising for the application of Lambda-Red recombineering, which is an easy and efficient method for generating genetic modifications.

In conclusion, this study aims to provide a base-level understanding of *Pantoea* as a genus and pave the way for its application in various fields.