Session: Ecology

Heidy M.W. den Besten[1,3], Roy Moezelaar[2,3], Marcel H. Zwietering[1], and Tjakko Abee[1,3*] (*presenting author)
[1] Wageningen University and Research Centre, Laboratory of Food Microbiology, Wageningen, The Netherlands
[2] Wageningen University and Research Centre, Food and Biobased Research, Wageningen, The Netherlands
[3] Top Institute Food and Nutrition (TIFN), Wageningen, The Netherlands

Title: Prediction of stress induced robustness using molecular biomarkers

Microorganisms are constantly facing changing environmental conditions and have evolved sophisticated stress adaptation mechanisms to be prepared for challenges even before they arise. Prediction of mild stress induced enhanced robustness will allow to control and/or exploit these stress adaptive traits.

We designed a framework for identifying molecular biomarkers for mild stress induced microbial robustness towards lethal stresses. Candidate-biomarkers were selected by comparing the genome-wide transcriptome profiles of our model organism *Bacillus cereus* upon exposure to four mild stress conditions (mild heat, acid, salt and oxidative stress). These candidate-biomarkers – the transcriptional regulator σ^B (activating general stress responses), catalases (removing reactive oxygen species), and chaperones and proteases (maintaining protein quality) – were quantitatively measured at transcript, protein and/or activity level upon exposure to mild heat, acid, salt and oxidative stress treatment for various time intervals. Exposure of unstressed and mildly stressed cells to subsequent lethal stress conditions (severe heat, acid and oxidative stress) allowed for quantification of the robustness advantage provided by mild stress pretreatment. The induction levels of the candidate-biomarkers σ^B protein, catalase activity and proteases transcripts upon mild stress treatment were significantly correlated to mild stress induced enhanced robustness towards lethal heat stress, lethal oxidative stress, and lethal acid stress, respectively, and were therefore suitable to predict these adaptive traits.

The identified molecular biomarkers are widely conserved in microorganisms and have indispensable roles in stress responses. Therefore, they might also serve as biomarkers for stress adaptive behaviour in other microorganisms than *B. cereus.* Our study provides a systematic, quantitative approach to search for these biomarkers for stress induced robustness and to statistically evaluate their predictive potential in order to select biomarkers with high predictive quality that can serve to early detect and predict adaptive traits.

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