

PSD2.02 In search of biomarkers for stress-induced robustness

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The microbial stability and safety of minimally processed foods is controlled by a deliberate combination of preservation hurdles. However, the hurdle preservation strategy is challenged by the ability of microorganisms to adapt to changing environments providing cellular robustness. Cellular biomarkers that are quantitatively correlated to stress-induced robustness will facilitate our ability to predict the impact of these adaptive traits, and therefore, will allow us to optimise minimal processing technologies. Here, we present a framework for identifying and selecting cellular biomarkers for bacterial robustness. To ascertain potential biomarkers, the genome-wide transcriptional expression profiles of cells that were exposed to various mild stressors were compared and revealed a remarkable confined overlap of transcriptional expression responses. This transcriptional signature of stress adaptation seemed to be stressor-independent and directed to potential biomarkers for stress adaptation. Subsequently, several candidate-biomarkers – including a transcriptional regulator (activating general stress responses), enzymes (removing reactive oxygen species), and chaperones (maintaining protein quality) – were selected and quantitatively measured in our model-organism *Bacillus cereus* on transcriptomic, proteomic and/or activity levels upon exposure to four mild adaptive stressors (heat, acid, salt and hydrogen peroxide) for various time intervals. Additionally, both unstressed and stress-adapted cells were exposed to lethal conditions (heat, acid and hydrogen peroxide) to determine their specific robustness. To evaluate if the selected candidate-biomarkers could predict the adapted cell status, the biomarker responses were quantitatively correlated to mild stress-induced robustness. Various short- and long-term biomarkers could be identified that were quantitatively correlated to thermal, acid or oxidative stress robustness, respectively, and are therefore potential predictive cellular indicators for stress-induced robustness. This study presents a framework for quantitatively deducing potential biomarkers for stress-induced robustness. Furthermore, it provides a mechanistic basis for adaptation-dependent behaviour and is thus a starting point towards mechanistic based-predictive modelling of bacterial robustness to optimise minimal processing strategies.