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UNDERSTANDING THE PHYSIOLOGICAL BEHAVIOR OF INDUSTRIAL STRAINS THROUGH MOLECULAR FERMENTATION MAPS

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Microbial metabolism has been exploited for a millennia to produce useful compounds and is the core of human development in the past 50 years. Under the sequential argument “Increased output production→Lower production cost→Greater market penetration”, one of the main challenges for industrial microbiologists is the optimization of industrial strains. The tools used to address this can range from simplistic approaches, such as culture media conditions, to the design of sophisticated metabolic engineering strategies to redirect carbon to the pathway of interest. Without question, one of the main limitations of the optimization process is our lack of understanding of microbial physiology during industrial fermentation. In fact, it is still uncertain how the extensive knowledge of model microorganisms (*e.g.*, *E. coli* or *B. subtilis* under flask conditions) can be applied to an industrial fermentation. Currently, advances in sequencing technology have enabled us to study and analyze the full set of information encoded in the genome of industrial microorganisms. Access to this information is critical to determine their metabolic potential and even more important for the understanding of their physiological state throughout the fermentation. The core concept of systems biotechnology is relatively simple: the study and analysis of microorganisms at all molecular levels (gen -> protein -> metabolite) as the primary route to understand their physiological behaviour and develop strategies to improve their performance. Using systems biology we have developed detailed fermentation maps for two industrial strains and demonstrate how this tool can significant improve titers at industrial scale. I will present our work on the erythromycin producer actinomycete *Saccharopolyspora erythraea* and the production of the tetanus vaccine in *Clostridium tetani*.