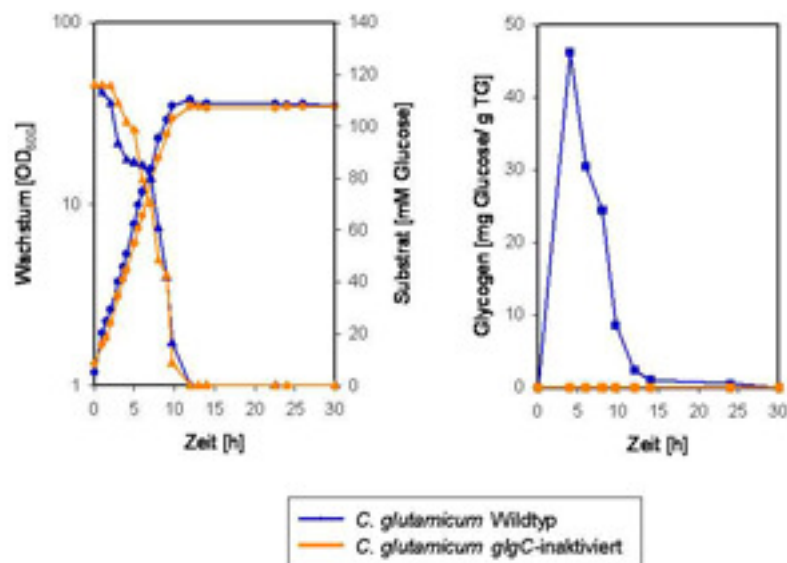


Analyzing the Role of Glycogen in Amino Acid Production

The **Institute of Microbiology and Biotechnology at the University of Ulm** has gained new knowledge about the role of Glycogen formation and degradation in *Corynebacterium glutamicum* and its impact on industrial scale amino acid production.

Professor Bernhard Eikmanns and his group first investigated the role of the *glgC* (ADP-Glucosepyrophosphorylase) gene, encoding the key enzyme in glycogen synthesis. They compared results of the *glgC* inactivated mutant with the wildtype using the DASGIP Parallel Bioreactor System. DASGIP system allowed tight control of the determined parameters and the direct comparison of the performances between the wildtype and the mutant in four parallel-operated 250 mL units. "Due to the parallel technology and the outstanding precision of the DASGIP we could rely on reproducible and comparable results. This reduced the time for our competitive experiments by 50 % compared to earlier experiments", says Eikmanns.



His group found a relatively low effect of glycogen formation on growth and vitality of *C. glutamicum* as well as on its amino acid production. On the other hand, the key enzyme's activity was observed to have notable impact on fast adaptation to hyperosmotic stress. This could be of great interest for large scale production, as great amounts of added glucose raise the ionic strength of media used in industrial processes. Results of glycogen formation indicate that the *glgC* gene prevents the *C. glutamicum* from being negatively affected by hyperosmotic stress.

Further studies focused on the role of glycogen degradation: While glycogen degradation in the well studied *E. coli* was known as been accomplished by the interplay of four enzymes, none of them had been identified in *C. glutamicum*.

Growing *E. coli* and *C. glutamicum* in the DASGIP system, Eikmanns again was able to precisely control external variables such as pH, agitation speed and oxygen supply in order to compare performance between the conventional organisms and the rather unknown in frame of glycogen degradation.

The *glgX* gene product was shown to encode a functional glycogen debranching enzyme. The early increase of glycogen in the *glgX*-inactivated mutant was even found as an indicator for parallel synthesis and degradation of glycogen in *C. glutamicum*.

Eikmanns team also investigated the impact of the glycogen debranching enzyme on growth after a shift to hyperosmotic conditions. They found that maltodextrins, derived from degradation of intracellular glycogen, positively affect the performance of *C. glutamicum* in industrial production. This is due to the fact that the formation of trehalose from maltodextrin provides the organism with a mechanism of fast adaptation to hyperosmotic conditions without the uptake of carbohydrates.

Eikmanns concluded: "Results showed clearly that the role of glycogen degradation is even more important than glycogen formation when it comes to industrial production. As *Corynebacterium glutamicum* is not only the number one working horse for amino acids but also of interest as model organism for the group of mycolic acid-containing actinomycetes, studies may be of value for drug development, too".

References:

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2. Seibold G.M. & Eikmanns B.J. (2007) The *glgX* gene product of *Corynebacterium glutamicum* is required for glycogen degradation and for fast adaptation to hyperosmotic stress. *Microbiology* 153:2212-2220