Customer Success Story: Characterization of growth behaviors and determination of optimal sampling points in differently modified microbial strains using the CGQ

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Background: Preliminary tests for (accepted) manuscript: **"Comparison of Three Xylose Pathways in *Pseudomonas putida KT2440* for the Synthesis of Valuable Products"**
Pseudomonas putida KT2440 is a well-established chassis in industrial biotechnology. To increase the substrate spectrum, we implemented three alternative xylose utilization pathways, namely the Isomerase, Weimberg, and Dahms pathways. Before and after adaptive laboratory evolution, these strains were characterized in terms of growth and synthesis of mono-rhamnolipids and pyocyanin.
The strain characterization required information about their growth which is determined by measuring the biomass, as well as substrate uptake rate, measured by HPLC. To determine the optimal sampling times to measure the substrate uptake and characterize the growth behavior, growth experiments were continuously monitored using a CGQ (aquila biolabs). The resulting growth curves were used to only samples at important time points, but also proved the impact of the modifications on growth rates and formation of biomass.

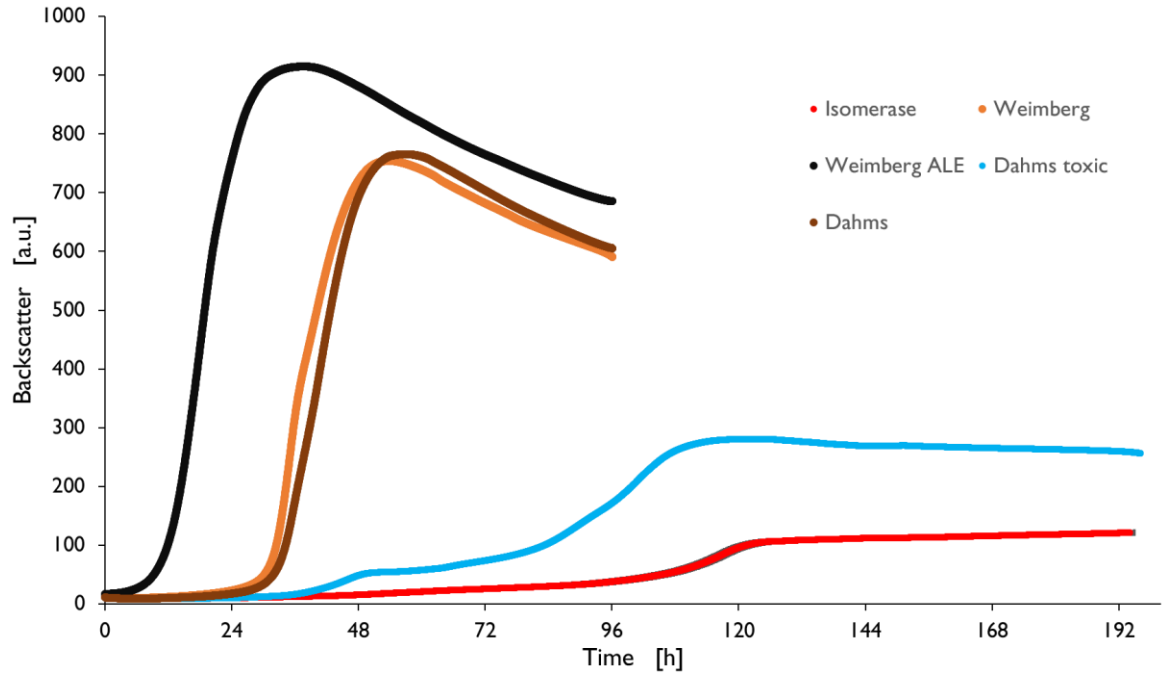

Fig. 1 Growth curves of differently genetically engineered *P. putida KT2440* strains. Backscatter values were measured by the aquila biolabs' *Cell Growth Quantifier* (CGQ). Displayed: mean from biological duplicates. Cultivation conditions: 30°C, 200 rpm, 50 mm shaking diameter, 500 mL shake flask, 50 mL filling volume. Medium: M9 + xylose.

Our opinion about the CGQ:

"The possibility to observe the growth of several organisms at once and compare the impact of genetic modifications with the wild type strain was a great benefit for our research! Since we could not estimate the impact of a modification on the organisms' growth, long cultivation times and a high sampling numbers would have been required. The automated system CGQ provided accurate growth curves with a very dense sampling interval and gave us the opportunity to identify differences in the growth behaviors. Using these data, we were able to determine the optimal sampling time to measure the substrate uptake from different modifications. The CGQ made this very easy and had a big impact in understanding the organisms and, eventually, the finalization of the publication."

Prof. Dr. Lars M. Blank