## Customer Success Story: Characterization of growth behavior and determination of optimal sampling points in different xylose-consuming strains using the CGQ

**Customer:** Prof. Dr. Lars M. Blank, RWTH Aachen University, Institute of Applied Microbiology (iAMB), Aachen, Germany)

**For more information:** Contact: lars.blank@rwth-aachen.de, +49 241 80-26600

**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. These different strains, which are able to consume xylose, were characterized in terms of growth and later synthesis of chemicals, especially 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 ensure the availability of a researcher when samples had to be taken, the optimal time to start the differently growing strains had to be planned. This required preliminary growth experiments, which were continuously monitored using a CGQ (aquila biolabs). The resulting growth curves showed the impact of the different xylose pathways and modifications. Further, they allowed a reliable planning of the following experiment with already fixed sampling times and thus minimized the effort considerably.

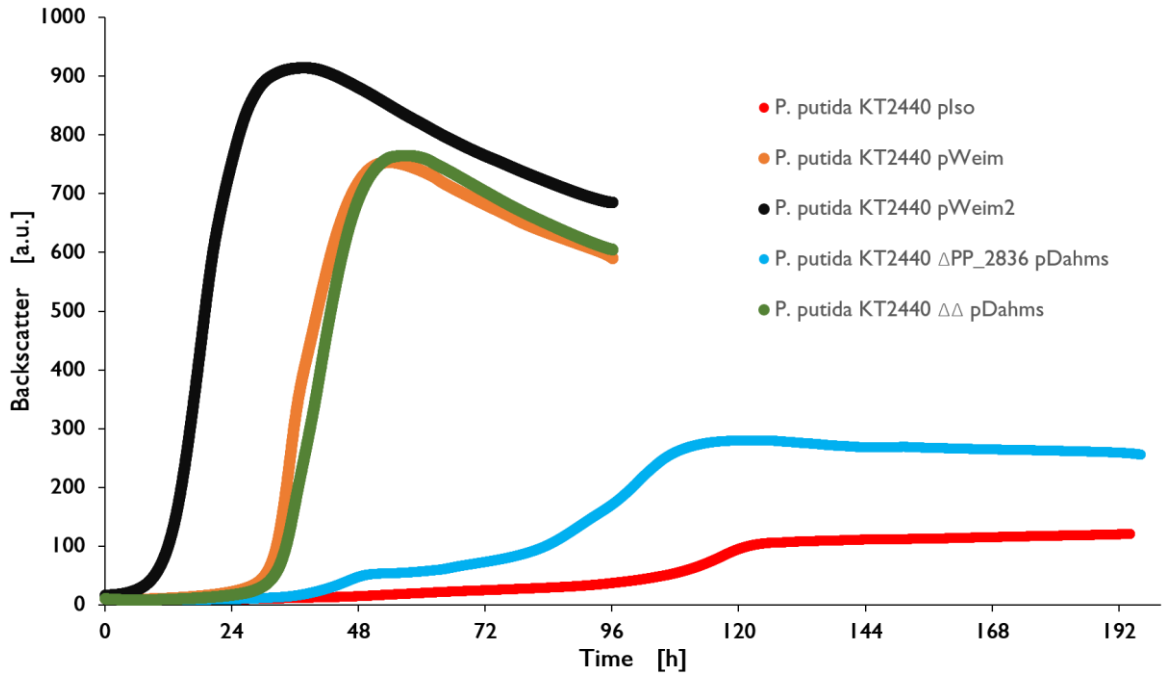


**Fig. 1** Growth curves of different genetically engineered *P. putida KT2440* strains. Backscatter values were measured by the aquila biolabs' *Cell Growth Quantifier* (CGQ). Displayed: mean from biological duplicates. Cultivation conditions: 30°C, 200 rpm, 50 mm shaking diameter, 500 mL shake flask, 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 on the wild-type strain was a great benefit for our research! Since we could not estimate the impact of different pathways and modifications on the organisms' growth, long cultivation times and 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 set up an efficient plan to start the experiments with already fixed sampling times to measure the substrate uptake of different strains. This planning minimized the effort considerably. 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