**APPLYING GENOME SCALE METABOLIC MODELS INTEGRATED WITH OMICS TECHNOLOGIES FOR IMPROVEMWENT OF COMMERCIAL CHO CELL CULTURE PROCESS**

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Although metabolic flux analysis has been established in microbial fermentation, their application in CHO cell culture is sparse. In general CHO cell culture process development is highly rely on empirical experience with limited cell and metabolite data without good mechanism understanding. The purpose of this research is to apply genome scale metabolic modeling for CHO cell culture process improvement. Recently we found that several medium components had significant impact on mAb production by BMSCHO1, a proprietary cell line (Fig. 1). Some of medium components at a low concentration, though within normal ranges for CHO cell culture, caused the BMSCHO1 crashed. Meanwhile some of the other medium components at a low concentration did not cause cell crash, but significantly decreased productivity. The preliminary genetic test results indicated no change in DNA copy number and southern blot integration profile under different medium conditions. Currently we are investigating both supernatant and cell pellets for metabolomics analysis using NMR and LCMS, and assessing epigenetic characteristics. In addition, transcriptomics data have been analyzed by RNA sequence and RT-PCR. Genome-scale modeling integrated with these OMICS datasets have been built and analyzed. In the presentation, we plan to share the investigation details of commercial cell-line and manufacturing process based on the application of genome scale modeling integrated with OMICS technology.

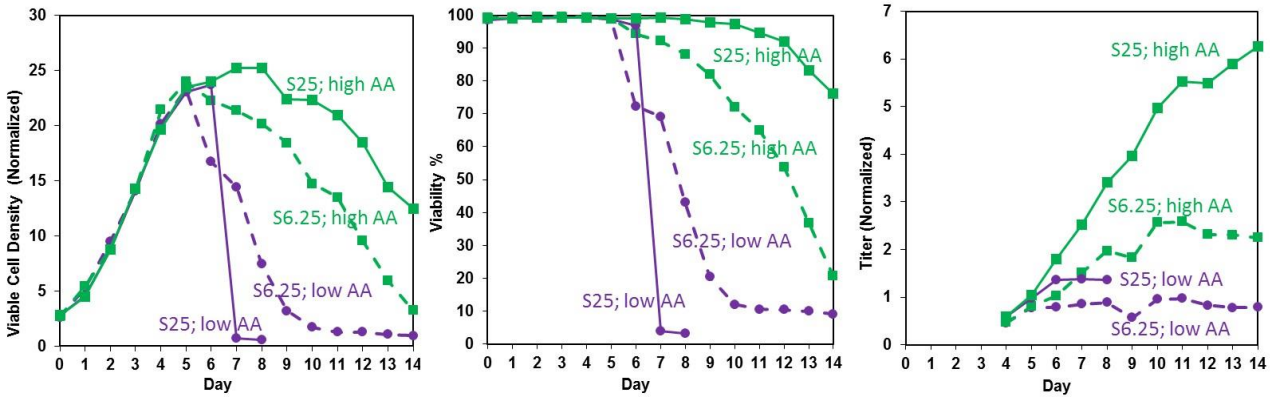


*Figure 1 – Impact of different medium component concentrations on BMSCHO1 cell growth, cell viability and titer using chemically defined media for fed batch production of a mAb*