Compact and optimized metabolic pathway design in yeasts

Implementing natural and synthetic pathways into microorganisms provides new opportunities for the production of valuable chemicals. We developed a strategy to smartly design and quickly implement such pathways in yeasts

BACKGROUND

An emerging challenge nowadays is not to produce single proteins only, but multiple ones in sufficient amounts and with balanced activities along the pathway to avoid the accumulation of side products or intermediates. Commonly, multi-gene expression is based on co-expression constructs harboring the pathway genes under the separate control of the (same) promoter and terminator. This usually works sufficiently well for proof-of-concept studies. However, the transformation rates of microbial cells generally decrease with the increasing size of the expression construct, while on the other hand technological difficulties and the costs for labor and materials increase. More importantly, the repeated use of homologous sequences can result in recombination events, and thus in genetic instability.

TECHNOLOGY

We exploit self-processing 2A sequences for polycistronic pathway expression, i.e. the production of multiple proteins from one single transcript. This approach allows the design of compact expression constructs which facilitates not only their construction, but all further molecular biologic steps. Thus, multi-gene pathways can be generated in 2-3 days instead of several days or weeks. In addition, the resulting production strains are genetically stable as the repetitive use of long homologous sequences is avoided. Finetuning of pathway expression can be modulated by the order of the genes within the polycistron.

BENEFITS

- Compact pathway design
- Fast and simple pathway assembly
- Generation of stable production strains
- Possibility for pathway fine tuning

AVAILABLE FOR

- License Agreement
- Joint Research Project
- Contract Research

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DEVELOPMENT STATUS

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