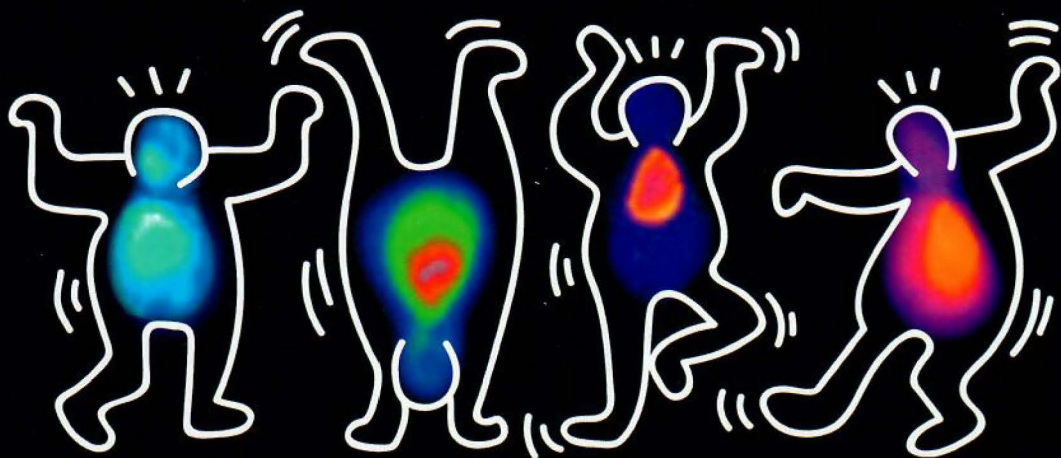


EMBO
Workshop



Experimental Approaches to Evolution and Ecology Using Yeast and Other Model Systems

17–20 October 2018 | EMBL Advanced Training Centre | Heidelberg | Germany

#EMBOevoeco



EMBL



42

New promoters for recombinant gene expression control in *Ashbya gossypii* identified through analysis of transcriptomic data

Tatiana Q. Aguiar, Lucília Domingues

Centre of Biological Engineering, University of Minho, Portugal

Presenter: Tatiana Q. Aguiar

The filamentous hemiascomycete commonly known as *Ashbya gossypii* has recently emerged as an interesting microbial factory [1-2]. Not only has it been safely and successfully used for more than two decades in the industrial production of riboflavin (vitamin B2), as it combines several attributes that makes it an attractive host to produce other added-value bio-products in addition to riboflavin [1-3]. The availability of its genome sequence and of molecular tools to manipulate it [1] have allowed the development of metabolic engineering approaches that have significantly increased its production titres [1-2]. However, the design of novel and more complex metabolic engineering approaches is hampered by the limited range of well-characterized promoters available for the recombinant expression of genes in *A. gossypii* [1,3]. Well-defined modular gene expression regulation elements are crucial tools in metabolic engineering, as the optimal balance in the expression of the individual genes forming the biosynthetic pathway of a target compound is essential to achieve maximal yields. Considering that endogenous promoters provide the main regulatory elements for gene expression control, in this work we analysed the transcriptomic data available for *A. gossypii* under different conditions to identify endogenous uni- and/or bidirectional promoters that drive high to moderate constitutive/semi-constitutive gene expression. Selected promoters were then used to drive the expression of a recombinant gene encoding a model protein [3]. Using this strategy, the bidirectional promoter AgCCW12/HOG1p was already characterized and found to drive relatively strong expression through the CCW12 side and moderate expression through the HOG1 side. The characterization of other selected promoters is under way.

References:

- [1] Aguiar et al., *Biotechnol Adv* 2015; 33:1774-1786.
- [2] Aguiar et al., *Bioengineered* 2017; 8:309-315.
- [3] Magalhães et al., *Biotechnol Prog* 2014; 30:261-8.