



## Molecular Biotechnology in the development of cell-factories for the industrial production of bioethanol and recombinant proteins

## Lucília Domingues

IBB-Institute for Biotechnology and Bioengineering, Centre of Biological Engineering, Universidade do Minho, Campus de Gualtar, 4710-057 Braga, Portugal.

Currently, there is a global drive to promote white (industrial) biotechnology as a central technology to enable sustainable economic future of the modern industrialized societies. With the increasing shift towards a bio-based economy, there is rising demand for developing efficient cell factories that can produce fuels, chemicals, pharmaceuticals, materials, nutraceuticals, and even food ingredients. Strain improvement is a requisite for the efficient development of biotechnological processes. The genetic improvement of strains should be done as close as possible to the industrial conditions in which they will be applied in order to quarantee a good performance. An integrative approach for strain and process development should be followed. Moreover, the utilisation of renewable resources as substrates should be considered not only for the economic point of view but also for the positive impact on environment. Molecular biotechnology has been applied in this context for the improvement of microbial strains and processes. We have been using targeted metabolic engineering as a standard way of strain improvement followed by random metabolic engineering approaches[1] together with systems-level analysis of the metabolic characteristics of the mutant strains[2]. On the basis of the results of the analysis, further targeted metabolic engineering can be performed on random mutant strains for the improvement of their metabolic performance. Practical examples of the application of this approach will be given for bioethanol and recombinant proteins production.

## References

- [1] Guimarães PMR, François J, Parrou JL, Teixeira JA, Domingues L "Adaptive evolution of a lactose-consuming Saacharomyces cerevisiae recombinant", Appl. Environ. Microbiol. (2008) 74: 1748-1756.
- [2] Guimarães PMR, Le Berre V, Sokol S, François J, Teixeira Ja, Domingues L "Comparative transcriptome analysis between original and evolved recombinant lactose-consuming Saccharomyces cerevisiae strains. Biotechnol. J. (2008) 3: 1591-1597.