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Journal of Molecular Catalysis B: Enzymatic 28 (2004) 137

JOURNAL OF MOLECULAR CATALYSIS B: ENZYMATIC

www.elsevier.com/locate/molcatb

Editorial

Combinatorial bioengineering—Development of molecular evolution

As genome research on many species including humans has rapidly progressed, the diversity of gene pools, including DNA resources obtained from difficult-to-culture organisms, available for use in various types of research has increased. New sciences and industrial techniques using DNA information as resources are growing out of conventional industries that consumes fossil fuel. Surface display techniques with the potential to convert known DNA information into bioactive proteins and to generate novel proteins using random DNA information are expected to be useful as molecular tools to convert DNA information into novel bioactive molecules. These tools have yielded scientific breakthroughs that enable design or discovery of tailor-made bioactive polymers and cells as directed by researchers. Researchers can select a new, simple, rapid and optimal combination of methods to convert an information molecule into a bioactive molecule from a molecular library in high-throughput and systematic fashion, using molecular tools such as phages, bacteria, yeasts, ribosomes and PCR, which have advantages over the tools used in combinatorial chemistry since they can make use of the productive capacities of live cells and enzymes. We have termed these techniques making use of the above-mentioned molecular tools 'combinatorial bioengineering', and the Combinatorial Bioengineering Study Group (http://www.prmvr.otsu.shiga.jp/ACB/), a study group to create novel bioactive molecules and cells using molecular information libraries with the key word 3-D (diversity, display and directed selection) rather than discover substances from natural resources has been established in Japan. In 2002, the session of combinatorial bioengineering has been taken place in the international conference SCI2002 in Florida. From 2004 to 2006, the International Conference of Combinatorial Bioengineering will be taken place in Osaka, Japan, every year. Furthermore, we have a big session of combinatorial bioengineering in PACIFICHEM 2005 (http://www.pacifichem.org/) in Hawaii.

Live cells have evolved over several billion years since the beginning of life into high specialized units secreting bioactive molecules coded by DNA chains that have been selected during evolution while exposed to environments with limited resources. Conventional bioactive molecules available for bioengineering research have been limited to substances included in the dendrogram of live cells, but with the new tools of combinatorial bioengineering we can break through limits of evolution and attain an entirely new level of biotechnological research. We hope that the research in this issue will illuminate ways to new directions in science and prove useful to scientists in the future.

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doi:10.1016/j.molcatb.2004.03.001