into 5 generation fuel cell system based on structural and structural difference. I optionally named the biofuel cell with electron mediators prototype, that with electrochemical active bacterium 2nd generation, that with modified electrode with NR 3rd generation, that with catalytic active electrode 4th generation, and that using air as a catholyte instead of ion selective membrane and cathode, respectively. The electricity production was compared among 5 types biofuel cell and was confirmed to be 50-100% higher in 4th and 5th generation than in 1st to 3rd generation.

SL313

Universal Conservation of Factors Promoting Protein Synthesis

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A universally conserved step in gene expression is the initiation of protein synthesis at an AUG codon using a specific initiator tRNAMet. The delivery of the Met-tRNAMet to the ribosome is catalyzed in prokaryotes by the translation factor IF2, a single polypeptide of ~90 kDa, and in eukaryotes by the heterotrimeric factor eIF2. Therefore, it was surprising when a bacterial IF2 homolog was identified in both yeast and archaea. *S. cerevisiae* strains lacking the *FUN12* gene encoding the yeast IF2 homolog had a severe slow-growth phenotype, and polyribosome profiles revealed a translation initiation defect. This translation defect was also apparent in extracts prepared from the *fun12* deletion strains and could be rescued by adding back recombinant yeast IF2 protein. These results indicate that yeast IF2 is a general translation factor. We identified a human IF2 homolog and found that the human protein, as well as archaeal IF2, could functionally substitute for yeast IF2 both in vivo and in vitro. Thus, IF2 is a universally conserved translation initiation factor. Recent biochemical analyses revealed that the eukaryotic IF2 homolog, now known as eIF5B, is required for the ribosomal subunit joining step of translation initiation and possesses 60S ribosomal subunit-dependent GTP hydrolysis activity. In addition, using yeast two-hybrid, co-immunoprecipitation, and in vitro binding assays, as well as genetic analyses, we recently found that eIF1A (the eukaryotic homolog of the bacterial translation factor IF1) physically and functionally interacts with eIF5B. We propose that eIF1A and eIF5B locate in A site of ribosome and stabilize proper binding of the initiator Met-tRNAMet in the ribosomal P site. Thus the bacterial translation factors IF2 and IF1 are conserved in eukaryotes and functionally cooperate to promote protein synthesis. Our studies reveal both similarities and differences in the functions of the eukaryotic and prokaryotic IF2 proteins, and we believe they offer important insights into the development of antibiotics that target specifically bacterial or fungal IF2 proteins.

SL314

Production of Xylitol by Xylitol Dehydrogenase Defective Mutant of *Pichia stipitis*

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This study was carried out to develop

the xylitol dehydrogenase defective mutants (XDH) from *Pichia stipitis* CBs 5776 and investigate the characteristics of xylitol fermentation by a xylitol dehydrogenase defective mutant PXM-4 in an effort to determine the optimum conditions for the high yield production of xylitol from xylose. The XDH defective mutants were screened by a xylose assimilation test. Among about several hundreds mutant screened, the best mutant PXM-4 was selected. And also gluconic acid was selected as a appropriate co-substrate for the xylitol fermentation. Since gluconic acid neither blocked xylose transport nor repressed xylose reductase expression. An increase in gluconic acid concentration reduced the rates of xylitol production and cell growth by decreasing medium pH. The optimal concentration of gluconic acid for xylitol production was determined at 20 g/l with approximately 100% xylitol conversion yield. A fed-batch cell culture resulted in 42.4 g/l xylitol concentration with 97% yield based on xylose consumed.

SL315

Quantitative Immunoassay for Polychlorinated Biphenyl Compounds in Electrical Insulating Oils

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The development and performance of a competitive indirect immunoassay for the quantitative measurement of polychlorinated biphenyl compounds in insulating oils is presented. Reagent preparation and the assay characterisation, optimisation and validation steps are described. The dynamic range of the assay for Aroclors 1254 and 1260 in methanol was 50-800 μg/ml with 50% signal inhibition values of 217 and 212 μg/ml respectively. Impending legislation in the UK is likely to decree that oils containing >50 μg/ml PCB be considered contaminated. Assay sensitivity increased with the degree of PCB chlorination. The assay of structurally related compounds of environmental concern yielded cross-reactivity values of under 0.6%. The immunoassay proved reliable for the analysis of transformer oils containing >70 μg/ml PCB, but over-estimated PCB levels in oils containing <20 μg/ml of the analyte with the oils requiring pre-treatment using either solid-phase extraction techniques or washing with KOH-ethanol/sulphuric acid to remove matrix interferents. The analytical performance of the assay was compared against a commercially available semi-quantitative immunoassay kit for PCBs in soil and water.

SL316

A Molecular Biotechnology for Removal of Toxic Heavy Metals

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The thiosulfate reductase gene (*phsABC*) from *Salmonella typhimurium* was expressed in *Escherichia coli* in order to produce sulfide from inorganic thiosulfate and precipitate metals as metal sulfide complexes. A 5.1 kb DNA fragment containing the native *phsABC* and a 3.7 kb DNA fragment, excluding putative promoter and regulatory regions were inserted into expression vectors pTrc99A and pJB866, respectively. Upon