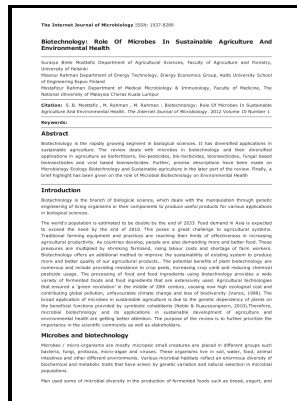


Diversity of genetic systems of industrial microorganisms

Kluwer - Exploration of genetic diversity of *Bacillus* spp. from industrial shrimp ponds in Vietnam by multi



Description: -

-Diversity of genetic systems of industrial microorganisms

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Antonie van Leeuwenhoek -- vol.64 (2)Diversity of genetic systems of industrial microorganisms

Notes: Special issue.

This edition was published in 1993



Filesize: 60.910 MB

Tags: #What #is #Agricultural #Biodiversity?

In

Anaerobic bacteria as producers of antibiotics.

Distribution and genetic diversity of functional microorganisms in different CANON reactors

Jornal of Antibiotics, 49, 349—354. The numbers above columns represent the passages of serial cultivation. Three colonies were used for base editing and the cells were mixed with an equal proportion before extraction of genomic DNAs, PCR amplification, and NGS.

Advances in Industrial Biotechnology Using CRISPR

Values and error bars reflect the mean \pm s.

Microbial diversity: the importance of exploration and conservation

No part of this content may be reproduced or transmitted in any form or by any means as per the standard guidelines of fair use. Moreover, for each locus, we found 11 to 19 alleles, which were counted on the basis of one-base difference. Serial cultivation and assay for xylose utilization Base-edited C.

Contributions of microorganisms to industrial biology

Thus, here comes the role of our tiny natural scavengers, in the form of microorganisms, which are widely distributed in nature for their treatment ability and maintain the ecological balance.

In

Increased phenylalanine production by growing and nongrowing *Escherichia coli* strain CWML2. After incubating at 37 °C for 1 h to remove RNA, DNA was further purified and concentrated into a 50-μL volume using Amicon Ultra 0.

Exploration of genetic diversity of *Bacillus* spp. from industrial shrimp ponds in Vietnam by multi

Cell pellet was then resuspended in 600 μL of Tris-EDTA 50 mM Tris pH 8. The tailored GGGGGGGG RBS was installed upstream of each target gene Supplementary Fig. Measures must be taken to estimate, record, and conserve microbial diversity, not only to sustain human health but also to enrich the human condition globally through wise use and conservation of genetic resources of the microbial world.

An anaerobic bacterium host system for heterologous expression of natural product biosynthetic gene clusters

Using BETTER, we highlight several samples of gene expression regulation for metabolic reprogramming. Selection and identification of non-pathogenic bacteria isolated from fermented pickles with antagonistic properties against two shrimp pathogens. Thus these fine organisms can be studied well and can be of varied use especially for the extracellular enzymes production as a byproduct.

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