МИИСТЕРСТВО ОБРАЗОВАНИЯ И НАУКИ РЕСПУБЛИКИ КАЗАХСТАН
КОМИТЕТ НАУКИ

НАЦИОНАЛЬНЫЙ ЦЕНТР БИОТЕХНОЛОГИИ

АСТАНА БИОТЕХ 2018
МЕЖДУНАРОДНЫЙ СИМПОЗИУМ

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АСТАНА БИОТЕХ 2018

МАТЕРИАЛЫ
Астана, 12-13 июня 2018 г.

PROCEEDINGS
OF THE INTERNATIONAL SYMPOSIUM
Astana Biotech 2018

УДК 60 (063)
ББК 30.16
А 89

А 89 АСТАНА БИОТЕХ 2018: Материалы Международного Симпозиума «Астана Биотех 2018» - Астана: НЦБ, 2018 – 194 с.

ISBN 978-601-7343-37-8

Материалы Международного Симпозиума «Астана Биотех 2018», приуроченного к 20-летию г. Астана, освещают достижения ученых и специалистов в области биотехнологии здравоохранения, сельского хозяйства и охраны окружающей среды.

УДК 60 (063)
ББК 30.16

ISBN 978-601-7343-37-8

UDC 577.212.3

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SCREENING OF LIGNITE DEPOLYMERIZING BACTERIAL SPECIES THROUGH ILLUMINA MISEQ HIGH-THROUGHPUT SEQUENCING TECHNOLOGY

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16S rRNA is located on the small subunit of the ribosome of prokaryotic cells, including 10 conserved regions and 9 hypervariable regions. The conserved regions are not very different among bacteria, and the hypervariable regions are genus or species. Thus, 16S rDNA can be used as a characteristic nucleic acid sequence to reveal biological species, and is considered to be the most suitable indicator for bacterial phylogenetic development and classification. 16S rDNA Amplicon Sequencing usually select one or several variation regions use the conserved region design universal primer for PCR amplification, and then the high-change region for sequencing analysis and identification of bacteria, 16S rDNA sequencing technology has become an important means to study the microbial community structure in environmental samples.

With the continuous development of the high-throughput sequencing platform, the upgraded HiSeq sequencing platform achieves the PE250 strategy of double-ended sequencing to achieve the same read length as the MiSeq platform and has a large amount of throughput and sequencing quality compared to MiSeq Enhance, become more suitable for 16S amplicon sequencing of the new platform. HiSeq PE250 has high sequencing depth and is more favorable for the identification of low-rich community species and improves the integrity of microbial community research. It will be the first choice to study the diversity of microbial community.

Through the use of Reads splicing filters, Operational Taxonomic Units (OTUs) clustering, and species annotation and abundance analysis, the sample species composition can be revealed; further alpha diversity analysis, beta diversity can be dig the differences between the samples.

For screening of lignite depolymerizing dominant species, Illumina Miseq high-throughput sequencing technique was used to measure the sequence of 16S rDNA-V4 variable region of bacteria diversity in coal-contaminated soil in Karaganda city (Kazakhstan) and enrichment method for the cultivation of bacteria communities that has lignite as a sole carbon source. No less than 72840 valid reads and 1416 OTU were obtained from two samples, with each samples in three replications. *Proteobacteria, Verrucomicrobia, Bacteroidetes, Acidobacteria, Actinobacteria* and *Firmicutes* were the dominant phyla among two samples. It provide an exact and relevant information for the screening of lignite depolymerizing bacteria as the biofactories of biohumic substances for further studies.