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INVESTIGATING ENRICHMENT OF LIGNITE SOLUBILIZING-BACTERIA SPECIES THROUGH ILLUMINA HIGH THROUGHPUT SEQUENCING TECHNOLOGY

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Coal is a traditional fuel that has evolved from ancient plants in the underground for thousands of years. The degree of coal mineralization determines the quality of coal. Low-quality coal seams, such as lignite and leonardite, have a low development value. Kazakhstan has very rich reserves of low-rank coal resources, lignite, as a low-calorie coal with the lowest degree of coalification, has strong chemical reactivity and is easily weathered in the air and difficult to store and transport. As a fuel for power plants, lignite is a low-value fuel with a low return. Therefore, the development of energy-saving and environmental protection applications and new products for lignite can not only greatly increase the benefit of lignite, but also protect the environment. The research on the bioconversion and bioutilization of low-rank coal has opened up a new path to achieve benign and sustainable development of green energy.

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.

Illumina Hiseq high-throughput sequencing technique was used to investigate the bacteria species community with lignite solubilizing activities. No less than 91074 valid reads and 417 operational taxonomic unites (OTUs) were obtained from enrichment method for the cultivation of bacteria communities respectively. *Firmicutes* (95.38%), *Proteobacteria* (0.92%), *Actinobacteria* (2.65%) and *Cyanobacteria* (1.05%) were the supreme phyla in the samples. *Bacilli* (94.04%) was dominant population among lignite solubilizing-bacteria. The sequencing covers a larger amount of data and detects the low-abundance lignite species that cannot be found by traditional pure culture and non-culture techniques. The foundation for enriching the microbial theory of microbial transformation, as well as the research and application of genetically engineered bacteria as the biofactories of biohumic substances for further studies was developed. *Bacillus* sp. may be useful in the coal-bed for *in situ* bioutilization of low-rank coal in order to improve the content of humified organic compounds in soil.

Scientific advisor: prof., Zhubanova A.A.

EVALUATION OF GRAIN PROTEIN CONTENT IN SPRING WHEAT MUTANT LINES

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Wheat is a main crop with global importance for food safety and is one of the major cereal source of nutrients for both human and animal. Mutagenesis is a powerful tool for generation of genetic variability and therefore crop improvement. Over the past 80 years this technique has been applied for development of new mutant varieties of seeds. According to the FAO/IAEA Mutant Variety Database in 2014 there were more than 3000 mutant plant varieties of 214 plant species all round the world. Grain protein content (GPC) is a major property to estimate the quality of nutrition and quality of final utilization of wheat.

In addition, in a large number of practical studies, it is found that the protein content of wheat varieties has a direct relationship with the nitrogen element. So it is very key to develop more higher N-use efficiency, which include N-intake, and N-remobilization of the breeding wheat genotypes. Whether the nitrogen element component can effectively transfer from the vegetative organs to the panicle is the key to affect the protein content of wheat. The content of wheat protein is quite sensitive to environmental changes from heading to maturity, which is also the main factor leading to large protein differences in wheat varieties.

Genetically stable mutant spring wheat lines (M_7 generation) generated from Almaken standard (parent seed) given two doses of radiation (100 and 200 Gy) from a ⁶⁰Co source at the Kazakh Nuclear Centre. 30

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