4 - 34 Progress of Ion Beam Breeding Research at IMP in 2016

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1. The mutation breeding of plants

In 2016, the mutation mechanism of various plant mutants including *Arabidopsis thaliana*, Geranium, *Tradescantia fluminensis*, *Taraxacum koksaghyz Rodin* and algae obtained by heavy ion beam mutation breeding techniques were investigated. The genome-wide profiling of an Arabidopsis mutant named *civar* (Carbon ion beams Induced Variegated) was revealed by using re-sequencing and the rough map-based cloning techniques. A phenotype screening of *Arabidopsis thaliana* irradiated by carbon ion beams based on high-throughput imaging technique combining the principal component analysis and scatter matrix clustering analysis was built and optimized which can screen the variation of plant mutant populations. The pigment components and quantities and expression profiles of key genes involved in anthocyanin biosynthesis of flower-color mutant of Geranium and leaf-color mutant of *Tradescantia fluminensis* were investigated. Mutation breeding of *Taraxacum koksaghyz Rodin* induced by carbon ion beam irradiations which is notable for its production of high quality rubber and inulin was started. In addition, the photosynthetic response of the mutants of *Scenedesmus quadricauda* with altered pigment features were analyzed.

2. The mutation breeding of microorganisms

The mutation breeding research of microbes including *Aspergillus niger*, *Saccharomyces cerevisiae*, and *Acidithiobacillus ferrooxidans* induced by heavy ion beam irradiations were investigated this year. Concerning *Aspergillus niger*, the cellulase production affected by aeration rate and the radioprotective effect of melanin from the spores were analyzed. In addition, the combination fermentation of *Aspergillus niger* mixed with *Trichoderma reesei* was carried out. Effects of carbon sources on the biomass accumulation of a high-yield strain of *Saccharomyces cerevisiae*, 100G-9, was studied.

3. Sweet sorghum industry chain of circular economy

Up to 2016, more than 1.12 million Chinese mu cultivation of sweet sorghum has been promoted in Gansu, Qinghai, Ningxia provinces and Xinjiang Uygur Autonomous Region in northwest of China. A perfect industrial chain of sweet sorghum which can produce various bio-products including yeast, ethanol, β-glucan, silage, *etc.*, was constructed. More important, the whole industry demonstration project of sweet sorghum benefits the development of local agriculture and pasturage aquaculture extremely.

4 - 35 Identification of Mutant Gene Induced by Carbon Ion Beams in *Arabidopsis* by Whole Genome Re-sequencing and Rough Map-based Cloning

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In recent years, heavy ion beams have been recognized as an effective and efficient physical mutagen due to their capacity to induce mutations with high frequency and broad spectrum. Nowadays, it is not so difficult to produce various mutants in plants. However, to mine the responsible mutated genes has been an important challenge. For mutation isolation, map-based cloning is one of the major traditional ways to isolate the mutant genes that control traits of interest in forward genetics studies. However, the process of map-based cloning is usually complicated and time-consuming. As the urgent demands of genome-wide studies, the High Throughput Sequencing (HTS) techniques have been rapidly developed and enabled rapid sequencing and mutation detection for genomic mutation identification, species evolution, genetic diseases, *etc.* But as everything has two sides, researchers do not know how to start when facing the huge data which produced by HTS. Since rough mapping is able to narrow down the screen ranges, while re-sequencing can reveal the genome-wide mutation profiling of carbon ion beams irradiation on *Arabidopsis*, association analysis of this two techniques will accelerate the identification of the mutant genes that are responsible for the phenotypes.

In the present study, an *Arabidopsis* mutant named *civar* (carbon ion beams Induced Variegated) displaying variegated stem, rosette and cauline leaves, sepals, and siliques, was induced by carbon ion beams accelerated by the Heavy Ion Research Facility in Lanzhou (HIRFL). Based on the IIlumina HiSeq2500 platform, whole genome re-sequencing of M_3 *civar* was performed in order to characterize mutations induced by heavy ion beams at DNA