especially early genes *CHS*, *CHI* showed the significantly down-regulated transcriptional level and the expression of late gene *ANS* almost be suppressed. The down-regulated or inhibited transcription of these key genes blocked the biosynthesis of anthocyanin, and that was the crucial reason for the deficiency of anthocyanin which lead to the depigmentation of mutant.

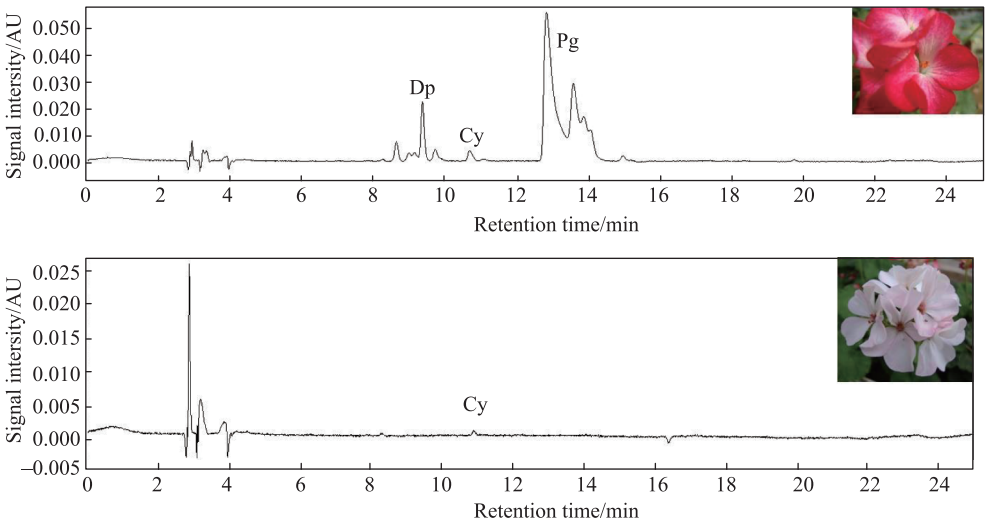

Fig. 2 Comparison the compositions and contents of pigments in flowers of wild type and mutant of geranium. Dp: Delphinidin; Cy: Cyanidin; Pg: Pelargonidin.

These results above provided part of the explanation of the mechanism of coloration change in mutant and established the research foundation for the follow-up design and color improving in geranium. At the same time, we can deduce that heavy ion beam irradiation may be utilized as a mutagen for flower color improvement and may be proposed as an effective approach for mutation breeding of ornamental plants.

4 - 43 Effect of Aeration Rate on the Cellulase Production of *Aspergillus niger* and Mixed Fermentation with *Trichoderma reesei*

Dong Miaoyin, Wang Shuyang, Li Qiaoqiao, Chen Jihong and Li Wenjian

In recent years, growing attention has been devoted to maximize the yield for the cellulase production in a bioreactor depending on the specific process. However, there are many factors that affected the fermentation performance and cellulase production, such as aeration rate, agitation speed, pH value, temperature[1]. The aeration rate is a key factor for mycelia growth and enzyme production, due to aeration rate conditions influence mass transfer by affecting the bubble size, air hold up and turbulance within the vessel as well as biomass production[2], and provides air flow, oxygen transfer, and removal of generated carbon dioxide under submerged fermentation. Therefore, aeration rate optimization plays a crucial role in cellulase production.

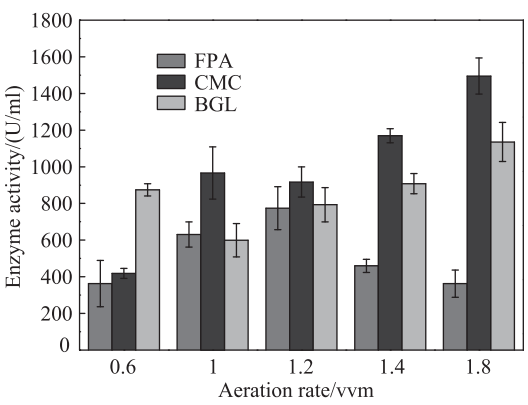

Fig. 1 The effect of aeration rate on the cellulase production.

The aim of this study is to evaluate how aeration rate affect cellulase production of *Aspergillus niger* and mixed fermentation with *Trichoderma reesei*. The fermentation was carried out in a 10 L stirred tank bioreactor, and filter paper assay (FPA), endoglucanase (EG) and β-glucosidase (BGL) activities was analyzed.

Fig. 1 showed that the filter paper assay (FPA) activity increased with increasing aeration rate and reached the maximum enzyme activities (773.85 U/ml) at 1.2 vvm, and then decreased with the increasing of aeration rate. While endoglucanase (CMC) activities correlated positively with increasing aeration rate. The highest endoglucanase (CMC) and β-glucosidase (BGL) activities were obtained at aeration rate (1.8 vvm) after 48 h fermentation, reached 1 495.2 U/ml and 1 135.43 U/ml,

respectively. The results suggested that the aeration rate had significant impact on the cellulase production of *Aspergillus niger* and mixed fermentation with *Trichoderma reesei.*

References

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[2] Mostafa Seifan, Ali Khajeh Samani, Aydin Berenjian, Appl Microbiol Biotechnol, 101(2017)3131.

4 - 44 Phenotype Screening of *Arabidopsis thaliana* Irradiated by Carbon Ion Beams Based on High-throughput Imaging Technique

Mu Jinhu, Chen Yuze, Du Yan, Yu Lixia, Yang Jiangyan, Luo Shanwei, Feng Hui, Cui Tao, Chen Xia, Li Wenjian and Zhou Libin

In recent years, with the development of robotics, sensors and kinds of imaging apparatuses, researchers have developed varieties of automation, high precision and throughput phenotype analysis platforms by ceaselessly hard working and exploring[1,2]. Although these platforms have improved the development of phenomics to some degree, there are still some problems in need of resolution. For example, researchers have not yet carried out an effective evaluation of the relationship between plant phenotype and genotype. Certainly, it is the key to solve these problems that how to analyze thoroughly and availably the "big data" obtained from the "high throughput" of the phenotypic analysis platform[3]. Based on these issues, we attempted to analyze the huge amounts of data produced by Scanalyzer HTS, and summed up a set of research methods to analyze phenomics data.

An analysis route of phenomics with large data processing and a useful mutant screening system was established (Fig. 1). An effective mutant screening system was built eventually through integrating the mutant information. It is necessary to reduce the dimension of big proteomics data obtained by Scanalyzer HTS and compress the data amount at first. Then based on logistic function of plant growth curve, a synthetic method of principal component analysis (PCA) and scatter matrix clustering analysis were optimized which can screen the variation of plant populations.

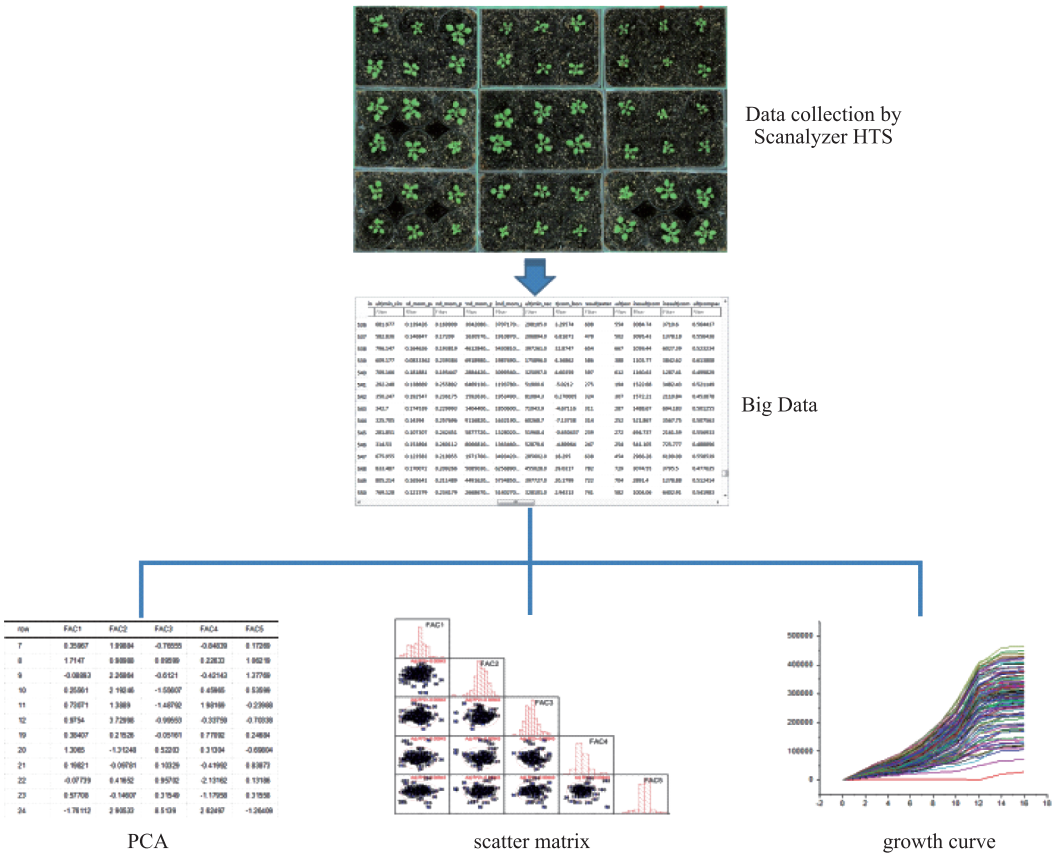

Fig. 1 The analysis route of mutant screening system with large data processing.