

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

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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.

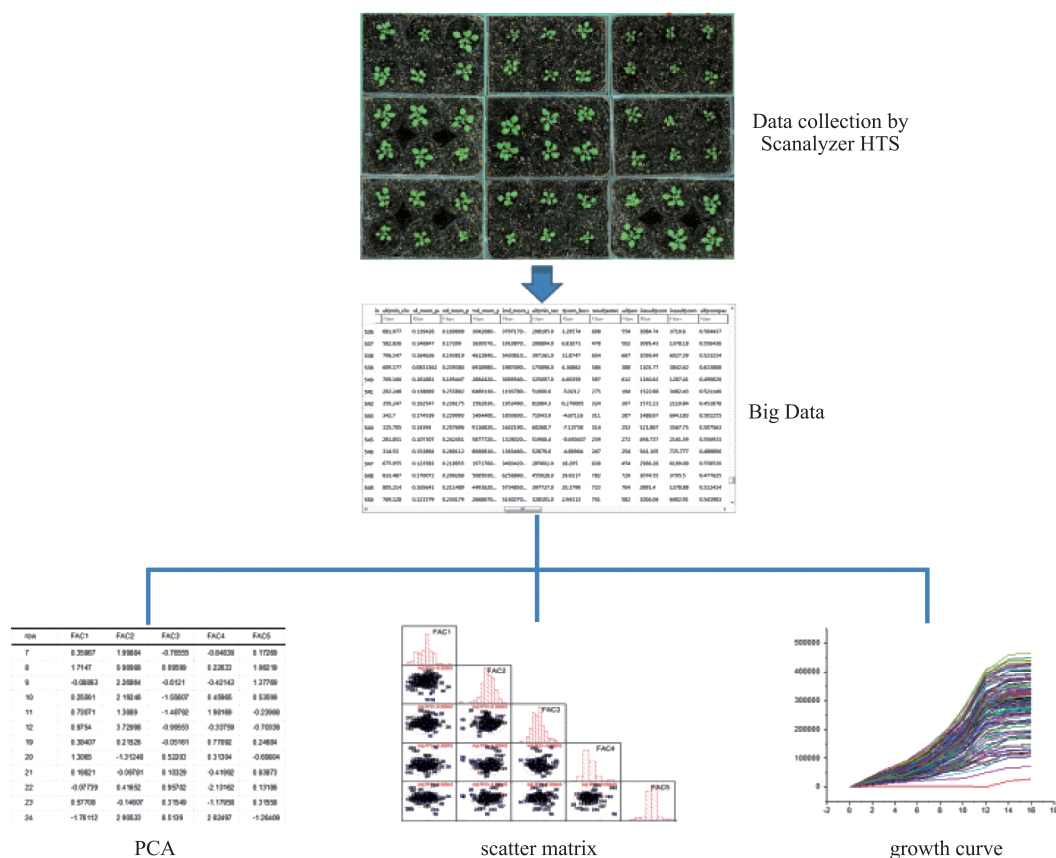


Fig. 1 The analysis route of mutant screening system with large data processing.