ABSTRACT

We performed improvement of the system function and maintenance task for the link and expand information registration system services in The National Agricultural Biotechnology information Center.

I. Introduction

The English-language neologism omics informally refers to a field of study in biology ending in -omics, such as genomics, proteomics or metabolomics. The related suffix -ome is used to address the objects of study of such fields, such as the genome, proteome or metabolome respectively. Omics aims at the collective characterization and quantification of pools of biological molecules that translate into the structure, function, and dynamics of an organism or organisms.

Functional genomics aims at identifying the functions of as many genes as possible of a given organism. It combines different -omics techniques such as transcriptomics and proteomics with saturated mutant collections.[1]

II. Related research

Over the last decades, technological advances in genome sequencing, namely development of Next Generation Sequencing technology, improvements in genomics technology and the endless availability of online-based resources, have allowed the construction of omics system from related genome projects. Also, the costs of genome sequencing dropped rapidly, production of genome data began in earnest. In order to use these data, researcher needed a integrated database with standardized[2].

In this study, we constructed integrated information system for omics data that can be stored for each species and objects. The platform was developed using MYSQL and JAVA language. The large amount of data, such as next-generation genome sequencing(NGS) and transcripts(transcriptome), obtained from result of current National Agricultural Genome Program researches carried out. The integrated and standardized omics data was gathered according to the standardized format established information system. Also, we performed improvement of the system function and maintenance task for the link and expand information registration system services in The National Agricultural Biotechnology information Center.

References

[2] Reinhardt IA, Baltrus DA, Nishimura MT, Jeck WR, Jones CD, Dangl JL. De novo assembly using low-coverage short read sequence data from the rice