

NABIC의 새로운 농업 바이오 정보 시스템 소개

Introduction to agricultural bio-information new resources in NABIC

김도완, 이동준, 오재현
국립농업과학원 농업생명자원부

Do-Wan Kim, Dong-Jun Lee*, Jae-Hyeon Oh
National Institute of Agricultural Science

ABSTRACT

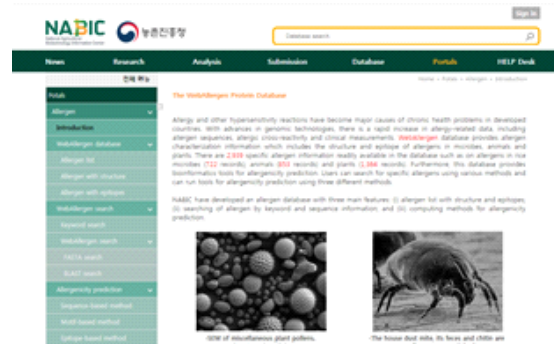
NABIC(National Agricultural Biotechnology Information Center) established integrated management system of agricultural omics information to achieve and analyze a agricultural bio-information resources in Korea.

I. Introduction

The amount of bio-information is enormously increasing due to emergence of NGS(Next Generation Sequencing) technology. We are building, maintaining and providing agricultural bio-information databases and information services. Various data type for submission is available such as genome, proteome, transcriptome, metabolome, molecular marker, etc. We issue the submission confirmation which is available for research achievement. Currently, the amount of data submitted on our system is 30Tb. We are also providing various analysis pipelines such as NGS analysis(denovo, rna-seq, reference assembly), Gene annotation, GWAS, marker analysis for breeding, Microbial community analysis and differential expression profiling analysis using submitted data through web[1]. We have a plan to provide bioinformatics education portal in this year.



▶▶ Fig.1. NABIC Home



▶▶ Fig.2. NABIC Portal

II. NABIC

In this study, we constructed integrated information system for omics data that can be stored for each species and objects.

본 성과물은(논문, 산업재산권, 품종보호권 등)은 **농촌진흥청 포스트게놈다부처유전체연구사업 (PJ013693022018)의 지원에 의해 이루어진 것임**

■ References ■

- [1] Reinhardt JA, Baltrus DA, Nishimura MT, Jeck WR, Jones CD, Dangl JL. De novo assembly using low-coverage short read sequence data from the rice pathogen *Pseudomonas syringae* pv. *oryzae*. *Genome Research*. 2009;19(2):294-305.