

Academy of Agricultural Sciences: Garlic Genome Was Sequenced

Recently, the Southern Protein Feed Plant Resource Development and Utilization Team of the Bast Research Institute of the Chinese Academy of Agricultural Sciences joined relevant universities and enterprises to complete the sequencing and assembly of the garlic genome in 4 years. Related research results were published online in "Molecular Plants".

According to research team members, garlic is one of the important vegetable crops. The annual sown area of garlic in my country has reached more than 10 million mu. Garlic has an enlarged bulb and is rich in allicin. It can not only be used as vegetables and seasoning food, but also widely used in the pharmaceutical industry. But cultivar garlic is generally sterile, which seriously hinders garlic biology research and garlic breeding.

As a unique compound in allium crops, this study established the allicin biosynthesis pathway through genome expansion and contraction analysis, combined with transcriptome data.

It is reported that the species sequenced this time is early purple garlic, also known as Sichuan garlic. Mr. Liu explained that the reason why the early purple garlic was selected as the first sequenced variety is because of its wide applicability and the widest cultivation area in my country.

Mr. Liu said that as the first genome sequenced in an Allium species, the completion of the sequencing and assembly work of the garlic genome is of great significance to the study of species evolution. The research was funded by the National Key Research and Development Program, the Science and Technology Innovation Project of the Chinese Academy of Agricultural Sciences and the National Natural Science Foundation of China.

[China garlic suppliers](#) provide consumers around the world with reasonable [China Garlic Price](#) and high quality garlic and garlic products.