

gustav / March 06, 2010 03:57PM

[\[International Cooperation\]\[Molecular Farming\] International Cooperation Project Aphid Genomic Analysis, in Which NTU Participated, Selected as Cover Story of 《PLoS Biology》](#)

[International Cooperation][Molecular Farming] International Cooperation Project Aphid Genomic Analysis, in Which NTU Participated, Selected as Cover Story of 《PLoS Biology》 ([Chinese Version](#))

NTU Newsletter (Issue 996) Associate Professor Chun-Che CHANG of Department & Graduate Institute of Entomology, College of Bioresources & Agriculture, NTU, participated in the aphid genomics project of the International aphid Genomics Consortium. The result of the international-cooperated project has recently been published in and selected as the cover story of the latest issue of PLoS Biology.

The aphid genome sequencing was conducted by the Human Genome Sequence Center of the Baylor College of Medicine, US. Scientists from over ten countries including the US, France, Japan etc., joined the project. Associate Professor Chun-Che CHANG was in charge of the team of reproductive genomics and responsible for the annotation of aphid's reproductive genes. Besides, CHANG and his team member Hsiao-ling LU (呂曉鈴) also participated in the analysis of aphid's developmental genes, which offered the important microbiological basis for studies of aphid's reproduction and early development. The aphid genomics project was a gigantic project; the results of the participated teams were separately and serially published in Insect Molecular Biology which were collected in a monograph. In the monograph, Associate Professor CHANG and his another team member Ting-yu HUANG (黃廷宇) presented an important article on the determination of the front-end of aphid embryos, exposing the possible new roles of "hunchback" gene in the specialization of the front-end of aphid embryos. Also, CHANG and the team members Hsiao-ling LU and Chi-wei LIN (林季瑋) participated in the genetic analysis project led by the National Institute of Basic Biology, Japan, too, and took the part of developmental genes analysis, which was also presented in the monograph. The results of the project were not only presented in the above-mentioned two journals but also reported in the major press media in UK, US, Japan, Spain, New Zealand etc.

The aphid genome sequencing is very helpful with understanding the special life history of the pest aphid. If the genome sequence of aphid is completed, we can utilize the functional genomics to further determine its alternation of generations, viral transmission, metabolic relation to the endosymbionts etc. Significantly, if the "switching sequence" about sexual and asexual generation is specified, ways to keep the aphids staying in the sexual generation for three to four months so that the total number of aphid can be effectively decreased, may be found.

Further Information:

[NTU Newsletter Issue 996](#) (Chinese)

Edited 3 time(s). Last edit at 03/06/2010 04:25PM by gustav.

---