

Plant Genomics Group, BioGreen 21 Program, RDA (Ramada Plaza Jeju, November 2–3, 2005)

과제 일련번호: 17

## Structural and Functional Genomics of Viruses Infecting Major Crops in Korea

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When faced with a new disease of probable viral etiology, practically the first goal to obtain the beginning of an understanding is to diagnose, identify, and obtain some nucleotide sequence information of the virus(es), if possible. That information usually reveals what the virus is most closely related to and immediately suggests solid hypotheses for a multitude of biological parameters including vectors, host range, stability, mutability, variation, and the success prospects for various means of control. This approach is often not successful because our database of viral genome sequences does not contain the complete information for all recognized plant viruses in Korea. To obtain viruses or virus-infected tissues from the major crops in Korea and conduct the complete nucleotide sequencing of the genomes of all recognized viruses, we'll screen major crops including rice, soybean, pepper, potato, sweet potato, cucumber, etc. for virus infection, obtain virus-infected tissues and sequence whole genome of each virus isolates. Currently, we have obtained more than 100 different virus-infected samples that have been assigned to virus genera including potyviruses, cucumoviruses, tobamoviruses, potexviruses, alfamoviruses, and several unclassified groups based upon results from virion observation, host ranges, ELISA, and RT-PCR. A large majority of these viruses remaining to be sequenced. The complete genome data as well as virus stocks will be deposited into National Gene Bank and Korean Agricultural Culture Collection (RDA). These virus stocks and genome data will be efficiently applicable to manipulation (maintenance and distribution of viruses), to development of reliable diagnosis and control practices for virus disease, and to develop a mechanistic model of replication and the evolution of viruses in Korea.

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† 주관과제명 (과제책임자): 우리나라 주요작물 바이러스의 구조 및 기능유전체 연구 (김국형)

‡ 총연구기간 (년차): 2005년 - 2007년 (1년차)