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Use of deep sequencing for analysis of virus replication

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Viruses are pathogens that replicate much more rapidly than their hosts and often utilize error prone genome replication mechanisms which function to produce large populations of diverse progeny. This replication strategy has been proposed as a mechanism that enables rapid evolution and adaptation of viruses. Recent advances in deep sequencing methodologies have enabled the observation of viral populations as they replication during infection of individual hosts. Beet Curly top virus (BCTV) is a typical geminivirus that causes substantial disease on a wide variety of crops which has previously been shown to have error prone replication. Here we describe the use of Ion Torrent sequencing to characterize BCTV progeny isolated from upper non-inoculated leaves of plants infected with an infectious clone of BCTV. The analysis pipeline included steps for sequence error correction, alignment construction and quality checking, SNP detection and confidence sorting. Our results show that this methodology sufficiently accurate for detecting SNPs in populations of progeny virus but that the platform is not useful for detecting indels in viral progeny. As expected, we found that SNPs did not accumulate in known functional domains necessary for viral replication. Our results also reveal several protected areas of the genome that likely represent novel and previously undescribed functional domains. Thus, deep sequencing is proving to be a versatile tool not only for estimating viral mutation rates but also for identifying functionally important regions of the genome that could be targeted in future studies examining viral replication.

Biography

Hua Zhong has completed his M.S. at the age of 23 from Department of Computer Science in New Mexico State University. Now he is a Ph.D student of Department of Computer Science in New Mexico State University

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