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Deep sequencing for identification of functional domains of plant viruses

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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. In the described study we used deep sequencing to characterize the evolution of BCTV populations during plant infection. Ion Torrent sequencing was used to characterize BCTV progeny isolated from upper non-inoculated leaves of plants infected with an infectious clone of BCTV. Our results show that Ion Torrent sequencing is sufficiently accurate for detecting SNPs in populations of progeny virus but that the platform is not useful for detecting indels in viral progeny due to the high error rate of the platform. As expected, we found that SNPs did not accumulate in known functional domains necessary for viral replication. Our results also reveal several additional 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 targetted in future studies examining viral replication.

Biography

Stephen F Hanson has completed his PhD in Plant Pathology from the University of Wisconsin at Madison in 1997 studying mechanisms of Geminivirus replication. Following Post-doctoral work in Molecular Virology and Viral Oncology he has held a Faculty Position in Molecular Plant Pathology at New Mexico State University. His current research includes molecular and biotechnology work on viruses, fungi, prokaryotes and nematodes affecting agricultural production.

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