S-72 Virus Evolution

21/08/18

Salon Darwin

Long-read sequencing reveals the full diversity and structure of host sequences integrated into AcMNPV baculovirus genomes during infection

LOISEAU V. [1], MOREAU Y. [2], LABROUSSE C. [3], HERNIOU E. [3], CORDAUX R. [4], GILBERT C. [1]
(1) Laboratoire Evolution, Génomes, Comportement, Écologie, Unité Mixte de Recherche 9191 Centre National de la Recherche Scientifique and Unité Mixte de Recherche 247 Institut de Recherche pour le Développement, Université Paris-Sud, 91198, Gif-sur-Yvette, F, Gif-Sur-Yvette FRANCE
(2) Cirad, UMR ASTRE Campus International de Baillarguet, 34398 Montpellier, France., Montpellier FRANCE
(3) Institut de Recherche sur la Biologie de l'Insecte, UMR 7261 CNRS-Université François Rabelais de Tours, Faculté des Sciences et Techniques, Avenue Monge-Parc Grandmont, 37200 Tours, France., Tours FRANCE
(4) Université de Poitiers, Laboratoire Ecologie et Biologie des Interactions, Equipe Ecologie Evolution Symbiose, 5 Rue Albert Turpain, TSA 51106, 86073, Poitiers Cedex 9, France., Poitiers FRANCE

AIMS:

Horizontal transfers (HTs) of genetic material is increasingly recognized as a major force shaping genomic evolution in some eukaryotes, but the mechanisms underlying these HTs are still unknown. It has been proposed that viruses could act as vectors of HT. Accordingly, we recently uncovered many host sequences, mostly transposable elements (TEs) integrated into AcMNPV baculovirus genomes using short read sequencing of AcMNPV particles extracted from the beet armyworm Spodoptera exigua. Here we further characterize the structure and full diversity of moth sequences carried by AcMNPV genomes using long-read sequencing. We detected no less than 68,375 host sequences integrated in AcMNPV genomes, among which are 30,196 transposable elements (TEs). We found all DNA TEs and LTR retrotransposons superfamilies previously identified using short read sequencing, as well as additional DNA TE and autonomous and non-autonomous non-LTR superfamilies. Expected target site duplication motifs could be identified for all these superfamilies, showing that bona fide transposition is the main mechanism underlying TE integration into viral genomes. Interestingly, the long read sequencing approach allowed us to show that a single viral genome may transport more than one host sequence. Our study of non-TE sequences is also revealing that host genes can jump into viral genomes during a single round of infection. Overall, our results suggest that about a quarter of AcMNPV genomes harbor at least one host sequence in AcMNPV populations, further supporting the role of viruses as vectors of HT between insects. We are currently characterizing in details the structure and genomic distribution of these insertions along the viral genome.