Novogene Company: Product of Identification of virus siRNA

Xiao Dong*
Novogene Bioinformatics Technology Co., Ltd., Beijing, P.R. China, 100083

Introduction
Novogene Bioinformatics Technology Co., Ltd was founded in March, 2011, in Beijing Life Science Park. Exclusively focusing on genome research and bioinformatics development, Novogene aims to distinguish it as one of the world’s leading genomic solution providers.

Recently, more and more results show that high throughput small RNA sequencing has used to identify unknown virus and viroid in host. As Virus small RNA molecular overlaps from each other, contigs can be assembled to genome sequence. High throughput small RNA sequencing has been a rapid virus identification method, which not involves isolated culture and enrichment of virus and greatly cut down the period. The technology has widely applied to the pathogen monitoring with insect-borne infectious disease and authentication, test or the whole genome sequencing of animals and plant virus, etc.

Technological advantage

✓ Convenient sample collection: no isolated culture, extract total RNA of virus infection tissue directly.
✓ No reference sequence: identification virus without host reference sequence.
✓ Accurate and reliable: Experimental verification rate has reach more than 80%.

Analysis of the content
Firstly: siRNA splice and assembly
Secondly: Map and annotate to virus database, select candidate virus
Thirdly: Assessment of candidate virus database

*: Xiao Dong: Master, Major in Molecular Biology
Tel: 86-010-82837567  Fax: 86-010-82837567
E-mail: support@novogene.cn
Program process

The test of the sample, advance payment in place → Small RNA library building in 3 days → HiSeq 2500 sequencing in 15 days → Information analysis in 27 days → Result (45 days)

Information analysis process

Raw data → Quality control → Length selection → PFOR analysis (identify virus not depend to sequence similarity) → Map to reference sequence → Assembly by velvet (a assembly method basic to De Bruijn graph) → Length distribution of the mapping sRNA → Distribution to chromosome of sRNA → Contig classification and annotation → PFOR unclassification contigs → Unredundancy virus nucleotide sequence in NCBI → Host genome → virus RefSeq database of GenBank → Candidate virus bank summerization and assessment

Details see Website: http://www.novogene.cn/en/