454/Roche GS FLX. The reads were subjected to pre-processing, with filtering according to quality criteria using PrinSeq. Single-nucleotide polymorphisms (SNPs) analysis was done using Geneious 9.1.2 software with the following parameters: minimum coverage of 100, frequency of 0.001 and a quality value of 30. We obtained 13 WSMV whole-genome sequencing resulting in average coding depth between 404 and 1654 reads per base across the coding region. This deep coverage creates a high-resolution view of resulting in the distribution and frequency of mutations within viral population. We obtained low SNPs frequency in 10 of the 13 viral populations. We found different number of SNPs according to the sequences of the protein. However, three isolates of WSMV from wheat were distinguished by their high SNPs frequency and distribution throughout all of the coding sequencing. Comparison of the SNPs patterns between the different host (Wheat, triticale, *Avena fatua* and *Digitaria sanguinalis*) not presented difference as it was reported for other virus. The knowledge of the spectrum of spontaneous mutations of WSMV is important given that small changes have implications in the pathogenicity, epidemiology and viral resistance-breaking.

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Palavras-chaves: SNPs, whole-genome sequencing , intra-host genetic diversity , pyrosequencing, wheat

Exploring virus diversity in grapevines

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Resumo

The knowledge about diversity and ecology of viruses has increased in recent years. Consequently, this increase has shown that viruses set up several relationships with other organism beyond of parasitism. The study of viral diversity has been expanded in last years, special due to improvements in sequencing technology. In this work we analyzed viral diversity in an RNA-Seq data from grapevine plants from several different places. Twelve grapevines samples were collected from experimental filed in Brazil. The dsRNA total was extract and cDNA library and sequenced using Illumina Hiseq 2000 platform. The reads obtained was analyze for FastQC, and Trimmomatic was use for clear and trimming. Trinity was use for *de novo* assemble. The identities of contigs from *de novo* assemble was analyze through NCBI Blastn against the RefSeq and EMBI databases. We found representatives of families *Tymoviridae, Betaflexiviridae, Peribunyaviridae, Phycodnaviridae, Siphoviridae, Baculoviridae, Podoviridae, Myoviridae, Phycodnaviridae, Siphoviridae, Reoviridae, Phasmaviridae, Tospoviridae, Iridoviridae, Peribunyaviridae, Closteroviridae, Luteoviridae, Caulimoviridae, Chysoviridae, Partitiviridae* and *Totiviridae*. The families *Tymoviridae, Betaflexiviridae, Podoviridae, Myoviridae* and *Partitiviridae* shows more prevalence than the other families. Interestingly we also found some Nucleocytoplasmic large DNA viruses and viroids classified as *Pospiviroidae*. We identified 25 species of mycoviruses from which 12 species were *Chysoviridae*, followed by eight species of *Partitiviridae* and three species of *Totiviridae*. In addition, we identified three species of unclassified