Società Italiana di Virologia

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A Joint Meeting with the SPANISH SOCIETY FOR VIROLOGY (SEV)

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PROGRAMME and ABSTRACT BOOK

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SIV – Italian Society for Virology
Dept. SPVSA, Istituto Superiore di Sanità,
Viale Regina Elena, 199
00161 Roma
www.siv-virologia.it

MZ CONGRESSI SRL
Via C. Farini, 81 - 20159 Milano
Tel. 02/66802323 Fax 02/6686699
www.mzcongressi.com

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General Information

OFFICIAL LANGUAGE
The official language of the Congress is ENGLISH.

CERTIFICATE OF ATTENDANCE
The certificate of attendance will be issued for the number of days a registrants has actually attended the congress.

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GRAPEVINE PINOT GRIS VIRUS: IS PATHOGENICITY RELATED TO GENETIC DIVERSITY?

M. Morelli3, A. Giampetruzzi3, P. Bianchedi2, P. Saldarelli3, V. Gualandri2, G. Martelli1

1Dipartimento di Scienze del Suolo, della Pianta e degli Alimenti, Università degli Studi Aldo Moro, Bari
2FEM-IASMA, Centre for Technology Transfer, San Michele all'Adige (TN)
3Istituto per la Protezione Sostenibile delle Piante del C.N.R. UOS Bari

Grapevine Pinot gris virus (GPGV) is a recently characterized member of the genus Trichovirus, putatively associated to a new grapevine disease whose symptomatology consists of chlorotic mottling, stunting and deformation of the leaves. Firstly identified through high-throughput sequencing of a cv Pinot Gris accession in the Trento's area (northern Italy), GPGV was later frequently detected in vineyards of northern and southern Italy, Slovenia, South Korea, Czech Republic and Slovak Republic.
Despite the high occurrence and the fast rate of natural spreading, GPGV role in the induction of mentioned aetiology is under study. With these premises, the present study aimed at further characterizing GPGV pathogenicity, starting from NGS analysis of two Pinot gris accessions, one showing symptoms of leaf mottling, the other asymptomatic. Virome profile analysis consistently duplicated what already described, unravelling the presence of GPGV together with Grapevine rupestris stem pitting virus (GRSPaV), Grapevine Rupestris vein feathering virus (GRVFV) and the two viroids Hop stunt viroid (HSVd) and Grapevine yellow speckle viroid 1 (GYSVd-1), without relevant differences between the two vines. Derived consensus sequences were therefore submitted to whole genome pairwise and phylogenetic comparison, additionally including GPGV isolates originating from Italian and Czech-Slovak vineyards. Phylogenetic reconstruction strongly clustered strains associated to symptom expression, clearly distinguished from those characterized by latent behaviour. On that account we extended the analysis to a sample population comprising grapevine accessions known to be free from viruses associated to leafroll, infectious degenerations or rugose-wood diseases and found a 84% of association of GPGV with symptoms. Maximum likelihood and Bayesian analyses were focused on two GPGV genomic regions, i.e. the RNA polymerase RNA dependent domain of the replicase gene, and a segment comprised between the movement protein and the coat protein genes. We ascertained that the lineage grouping symptomatic vines is distinct from those of symptomless plants, thus hypothesizing that an evolutionary dynamic, independent from the vine genotype, could have selected for virulent or latent GPGV strains.

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IDENTIFICATION OF RNA AND DNA VIRUSES IN PIG FECES BY NGS

G. Vaccari1, I. Di Bartolo1, G. Angeloni1, G. Zaccaria1, F.M. Ruggeri1

1Dept. of Veterinary Public Health & Food Safety, Istituto Superiore di Sanità, Rome, Italy

Pigs represent one of the most important sources of food worldwide. Nevertheless, swine frequently acts as reservoir for zoonotic viruses or other viruses that cause a range of diseases or sub-clinical infections, determining a risk for consumers and affecting pig health. The present study aimed to investigate RNA/DNA viruses in a fecal sample from a pig affected with diarrhea by Next Generation Sequencing.
Methods: feces of a 30 days old pig affected by diarrhea were made a 10% suspension, and used to extract RNA by QiampViral RNA MIDI kit (Qiagen). Sample was prepared by SISPA-method. Purified random amplified (100–1000 bp) samples were sequenced on Ion Torrent (Lifetechnologies).
Results: by NGS 1.2 mega reads with an average sequence length of 195 were obtained. A de novo assembly was carried out, resulting in a total of 8623 contigs, of which 3311 showed with a coverage ranging from 10 to 11264 X. Contigs were checked for sequence identities with viral genomes available in the NCBI GenBank including the calculation of tBLASTYx E scores. Only sequences with a score E≤10-5 were included. By this 339 contigs obtained corresponded to known viral genomes. Overall, a total of 16 different viruses with sequence identity with mammalian viruses were identified. This included: astrovirus (most representative 157 contigs), enterovirus, sapelovirus, hepatitis E, kobuvirus, torovirus, the closely related parechovirus and pasivirus, PEC, picobirnavirus, posavirus. Moreover, DNA viruses were also detected: teschovirus, torovirus, circovirus, bocavirus and the novel stool associated circular ssDNA Virus (SCV). Bocavirus, astrovirus, PEC were associated to diarrhea in pigs either alone or in mixed infections.
Conclusion: the novel technology of NGS is of great utility in studying viral community in feces and detecting viruses with little o no sequence information, without molecular detection methods, including zoonotic pathogens such as the HEV detected in the study.