



First report of barley virus G infecting corn in Greece

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In June 2019, corn plants exhibiting leaf mosaic, interveinal yellowing and yellow streak were observed in a field trial in Thermi, Greece. To identify possible agent(s), total RNAs of five individual plants were extracted (Norgen Biotek Corporation, Canada) and subjected to high-throughput sequencing separately on an Illumina NextSeq500 (SeqMatic, Fremont CA) in USA. The *de novo* contigs were assembled with SPAdes and subjected to a local BLASTn similarity search using an up-to-date nr/nt database. In addition to sugarcane mosaic virus identified in all samples, barley virus G (BVG, a tentative member of *Solemoviridae*, genus *Polerovirus*) was identified in one of them. This sample had a total of 23,825,417 reads (after QC 23,825,378), while the number of reads mapped to BVG was 133,521. The four BVG *de novo* contigs were assembled into a 5,530 nt long scaffold (MW657364), covering almost the complete genome (with only the first 90 nt missing), which was ~98% identical to BVG isolates Gimje and Uiseong (KT962089.1, LC259081.1, respectively). To confirm BVG infection, a primer pair was designed based on the contig sequence. Primers BVG3646up(5'-AACACTTCAGGAGGATCTGGA-3') and BVG4247down(5'-AACTCGGAATTCTTCGTGA-3'), amplifying a 602 nt coat protein/movement protein/P5 segment, were used in a one-step RT-PCR on a new RNA extract obtained from the infected plant in Greece. Sanger sequencing (MT672307) confirmed BVG infection, as the nucleotide identity between the amplicon and the *de novo* contig was 100%. The virus was not detected by RT-PCR in any of the other four corn plants tested. BVG was

initially reported in barley in Gimje, South Korea in 2016 (Zhao et al. 2016). Outside Korea, BVG was also identified in other hosts in few countries, including corn in Kenya (Wamaitha et al. 2018). This is, to our knowledge, the first report of BVG in corn in Greece, thus further expanding the geographic distribution of the virus.

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Declarations

Conflict of interest The authors have no conflicts of interest to declare that are relevant to the content of this article.

References

- Wamaitha MJ, Nigam D, Maina S, Stomeo F, Wangai A, Njuguna JN, Holton TA, Wanjala BW, Wamalwa M, Lucas T, Djikeng A, Garcia-Ruiz H (2018) Metagenomic analysis of viruses associated with maize lethal necrosis in Kenya. *Virology* 15:90. <https://doi.org/10.1186/s12985-018-0999-2>
- Zhao F, Lim S, Yoo RH, Igori D, Kim SM, Kwak DY, Kim SL, Lee BC, Moon JS (2016) The complete genomic sequence of a tentative new polerovirus identified in barley in South Korea. *Arch Virol* 161:2047–2050. <https://doi.org/10.1007/s00705-016-2881-0>

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