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| **refs itemname** | Journal Article |
| **Bibliography** | Olmedo-Velarde, A.; Loristo, J.; Kong, A.; Waisen, P.; Wang, Koon-Hui; Hu, j.; Melzer, M. (2022) Examination of the virome of taro plants affected by a lethal disease, the alomae-bobone virus complex, in Papua New Guinea, In: Viruses, Vol.14 (7), 1-12, URL: https://doi.org/10.3390/v14071410 |
| **Associated conference** |  |
| **Abstract / Content summary** | Alomae-bobone virus complex (ABVC) is a lethal but still understudied disease that is limited to the Solomon Islands and Papua New Guinea. The only virus clearly associated to ABVC is Colocasia bobone disease-associated virus (CBDaV). Taro (Colocasia esculenta) plants with and
without symptoms of ABVC disease were sampled from two locations in Papua New Guinea and examined for viruses using high-throughput sequencing (HTS). Similar to previous reports, isolates of CBDaV were present only in symptomatic plants, further supporting its role in the disease. The only other viruses consistently present in symptomatic plants were badnaviruses: taro bacilliform virus (TaBV) and/or taro bacilliform CH virus (TaBCHV). If ABVC requires co-infection by multiple viruses, CBDaV and badnavirus infection appears to be the most likely combination. The complete genomes of two isolates of CBDaV and TaBCHV, and single isolates of TaBV and dasheen mosaic virus, were obtained in this study, furthering our knowledge of the genetic diversity of these relatively understudied taro viruses. HTS data also provided evidence for an agent similar to umbra-like viruses that we are tentatively designating it as Colocasia umbra-like virus (CULV).
Keywords: Colocasia esculenta; alomae-bobone virus complex; cytorhabdovirus; badnavirus
Note: Special Issue Next-Generation Sequencing in Plant Virology |
| **identifier** |  |
| **Library Locations** |  |
| **files** |  |
| **External web link** | https://doi.org/10.3390/v14071410 |
| **File info** | 2.73 MB, PDF |